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em\_sy:\* em\_un:\* em\_vi:\*

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em\_pl:\* em\_ro:\* em\_sts:\* gb\_vil:\*
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db\_sy:\*

gb\_htg6:\* gb\_htg7:\* gb\_htg8:\*

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October 26, 2001, 15:20:44; Search time 3927.32 Seconds (without alignments) 5616.301 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|        | Description           |        | AX021809 Sequence    | AF295325 Synthetic | A19452 phytase cDN | Il3430 Sequence 33 | 133881 Sequence 19 | AX000634 Sequence | U59804 Aspergillus | Z16414 A.niger phy |
|--------|-----------------------|--------|----------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
|        | ID                    |        | AAUZ18U9<br>AF295325 | A19452             | 113430             | 132881             | AXOUGESA           | SELLEGEOA         | ANDHVAC            |                    |
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|        | Length                | 3071   | 1350                 | 1404               | 1404               | 1404               | 1571               | 1812              | 2000               |                    |
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|        | Score                 | 1342.8 | 790.8                | 622.2              | 622.2              | 622.2              | 619.6              | 619.6             | 618.2              |                    |
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| 9 618.2 43.4 2363 9 AR018076<br>10 618.2 43.4 2363 9 AR051916<br>11 618.2 43.4 2379 9 AR051934<br>12 618.2 43.4 2379 13 ASNPHYTAS<br>13 618.2 43.4 6756 9 A19451<br>14 618.2 43.4 6756 9 A19451<br>15 618.2 43.4 6756 9 A19451<br>16 599.6 42.0 1518 13 AF018813<br>16 599.6 42.0 1518 12 AB022700<br>18 597.6 41.9 1559 14 AY013315<br>19 595.8 41.8 1553 12 AB042805<br>20 580.4 40.7 1931 9 AX000630<br>21 580.4 40.7 1931 9 AX000632<br>22 553.4 37.4 1567 9 AX00636<br>23 549 38.5 1845 9 AX00636<br>24 549 38.5 1845 9 AX00636<br>25 533.4 37.4 1567 9 AX00636<br>27 533.4 37.4 1567 9 AX00636<br>28 533.4 37.4 1770 14 ATU60412 | 533.4 37.4 2327<br>512 35.9 11922<br>510 35.8 11684<br>412.4 28.9 4898<br>35.6 25.0 2200<br>292.6 25.0 853<br>265.2 18.6 3995<br>265.2 18.6 3995<br>265.2 18.6 3995<br>265.2 18.6 3995<br>265.2 4.9 7 806<br>64.8 4.5 1107<br>64.8 4.5 1604<br>64 4.5 1904<br>64 4.5 3913   | T. 1  809  XX021809  XX021 | Ouery Match Best Local Similarity 96.4%; Pred. No. 0; Back Local Similarity 96.4%; Pred. No. 0; Matches 1374; Conservative 0; Mismatches 52; Indels 0; Gratches 1 tatatgaattcatgggggttcgtcgtgtcgtgctactgfccattgccacttgttcggttcca Qy |

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Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy of Agricultural Sciences, Guangzhou, Guangdong 510640, China (bases 1 to 1350)
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STEADDLIPPEGEOLVUSGIKEYPTDSKGKKYSALIEEIONATTPFDKYAFLKYYN

SIGADDLIPPEGEOLVUSGIKEYORYESLCFRNIVDPFIRSSGSSRYLASGKKFIEGFO

STEKKRPRAGPGOSSEKIDVUISESSSNNTLDPGTCTVFEDSELADTVEARFIEGFO

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YLOSLKKYYGHGAGNPLGPTGVYGYANELJARLTHSPVHDDTSSNHTLDSSPATFPLN

STLYADFSHDMGIISTLFALGLYNGTKPLSTTVENITQTOGFSSSMATVPPASRIYVE

MMQCQABGOEPLVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFRIXVE
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cttcttggactgttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctg 1260
                                                                                      1261 aaaaggaaccattggttagagttttggttaacgacagagttgttccattgcacggttgtg 1320
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Synthetic sequence of phytase gene for expression in Pichia
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55.58; 74.78;

Best Local Similarity 74.7 Matches 993; Conservative

Query Match

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DGFSSAWIVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGCPVDALGRCTRDSFV

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artificial sequence.
1 (Assa 1 to 1404)
van Gorcom, R.F.M., van Hartingsveldt, W., van Paridon, P.A.,
venstra, A.E., Lulten, R.G.M. and Selten, G.C.M.
Cloning and expression of microbial phytase
Patent: EP 0420358-A 41 03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1404;
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/db_xref="taxon:32630"
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|---|--------|--|--|------|--------|--------|----------|--|------------------------------|---------|--------|--|--------|---|-------------------------|------------------------------------|--------|---|---------|--|---|-----------|---------|---|---------|-----|---|-----------|-----------|--|---|---|
| Qy       1212 gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca       1271         Db       1201 GTTCCGTTTCCTTCCCGTTTCTACATCATCATCATCATCATCATCATCATCATCATC |        |  | Db 1321 TTGGGGACATGTACCCGGGATAGCTTTGTGAGGGTTTGAGCTTTGCTAGATCTGGGGGT 1380 | 1414 |        |        | RESULT 4 | 113430 1404 bp DNA Sequence 33 from nation; in carrier | N 113430<br>113430 CT:010771 | Unknown | NISM   | REFERENCE 1 (bases 1 to 1404) AUTHORS Van Corror P. F. |        | JOURNAL Patent: US 434615510H OI PHYTASE from aspergillus FEATURES LOCATION/OIL 1995, | Source 1. John Manifels | BASE COUNT 293 a 436 C 344 g 331 t |        | Query Match 43.6%; Score 622.2; DB 10; Length 1404; Best Local Similarity 65.2%; Drod No. 15.2%; Local Similarity 65.2%; Drod No. 15.2%; Length 1404; | Matches | 12 atgggcgtgttćgtcgtgctactgtccattgccaccttgttcggttccacatccggtac | 1 ATGGGGGTCÍCTGCTGTTCTTCCTTTGTATCTCTGTCTGGAGTCACC |           |         | 132 tteccagaaatttetcacttgtgggtcaatactetccattettetttggetgacgaa | 121     | 192 | DD 181 FCGGTCATCTCCCCTGAGGTGCCGGATGCAGATCACTTTCGCTCAGTTCTCC 240 |           | 241       | VY 312 gotaticaaaagaacgetactgeitteaagggtaagtacgeitteitgaagacitacaac 371<br>  1   1   1   1   1   1   1   1   1 | Db 361 TACAGCTTGGGTGCAGATGACTCGCTTCGGAGAACAGAGCTAGTGTGT 431 |   |

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1 ATCAAGTICTACCAGCGGTACGAATCGCTCACAAGGAACATCGTTCCATTCATCCGATCC 480
               2 aagtiggoigacccaggigciaacccacaccaagciictccagiiattaacgiiatii 611
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Van Ooijen, A.J.J., Rietveld, K., Hoekema, A., Pen, J., Sijmons, P.C. and Verwoerd, T.C.
Expression of phytase in plants
Patent: US 5593963-A 19 14-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672 tctgaattgggtgacgacgttgaagctaacttcactgctgttttcgctccacctattaga 731
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Pred. No. 1.5e-154;
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                                                                                                               Location/Qualifiers
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           Unknown.
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                                                                 AUTHORS
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/translation="WYTLTFILSAAYLLSGRVSAAPSSAGSKSCDTVDLGYQCSPATS
//translation="WYTLTFILSAAYLLSGRVSAAPSSAGSKSCDTVDLGYQCSPATS
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SQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASOL
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                                                                                                                841 Trengreaceretreaceargaegaargaarcaacracgaeracacereceagreerraaaa 900
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Van, L.A. and Wyss.M.
Modified phytass.M.
Patent: EP 0897010-A 5 17-FEB-1999;
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join(43. .89,147. .1497)
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SPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHT
STNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLXNGTFPLSRTSVEGAKELDG
YSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLNDFVKG
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Bukaryota, Fungi, Ascomycota, Pezizomycotina; Eurotiomycetes; Eurotiales; Fungi, Ascomycota, Mitosporic Trichocomaceae; Aspergillus. I doses i to 1800.

Pasamontes, L., Haiker, M., Wyss, M., Tessier, M. and van Loon, A.P. Gene cloning, purification, and characterization of a heat-stable phytase from the fungus Aspergillus fumigatus

Appl., Environ. Microbiol. 63 (5), 1696-1700 (1997)
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SQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLWDMCSFDTVARTSDASQL
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Submitted (02-JUN-1996) Luis Pasamontes, VFCB, F.Hoffmann-La Roche
AG., Basel 4070, Switzerland
                                            1106 ggittictatiticiticgcittigggittigtacaacggiactaagccattgictactactic 1165
                                                                                                                                 1166 tgttgaatctattgaagaaactgacggttacgctgcttcttggactgttccattcgctgc 1225
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/db_xref="taxon:5085"
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join(<284. 330,388. 51738)
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/Ec_number"3,1,3,8"
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/db_xref="G1:2108354"
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STNSTLYSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSFTSVESAKELDG
YSASWVVPFGARAYFETMQCKSEKEFLVRALINDRVVPLHGCDVDKLGRCKLNDFVKG
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Submitted (05-OCT-1992) van Hartingsveldt W., TNO Medical Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. 1 (bases 1 to 2000)
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                                                                                                       ggtttctattttcttcgcttttgggtttgtacaacggtactaagccattgtctactacttc 1165
1046 cccagctactttcccattgaacgctactttgtacgctgacttctctccacgacaacatt 1105
                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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/db_xref="taxon:5061"
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/translation="MORNALISA" (**ATANGSCOTVDGGYQCFSET SHIMOGYAPPESLANESVISPEVPLATILISGYPSGLAVPASRNQSSCOTVDGGYQCFSET QONATFEGGYPFESLANESVISPEVPAGCRVTFAQVLSHRGARFTDSKGKKYSALIEET QONATFEGGKYAFLKTYNSTGADDITPFGEGELNNSGIKFYQRYESLIFNIVPFIRS EDSELADTVEANFTATFVPSTRADFAGPGGSFKTIDVTFSTRSSSSRNTLDPGTCTVPF KLSPFCDLFTHDEWINYDYLQSIRKYYGHGAGNPLGPTQGYGYTNIDDGSFDTISTSTYDT DGTSSNHTLDSSPATFPLNSTLYABGGNAGCGTALFTRADFAGNATTATFVPSTRANGSTRATIONFSPHINGSTRANGSFDTISTSTYDT DGFSSAWNTVPFASSTRANGSTRANGSFDTISTSTYDT DGFSSAWNTVPFASSTRANGSTRANGSFDTISTSTYDT CONTROL OF ATANGSTRANGSFORMATTATFVBNTTQT CONTROL OF ATANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRANGSTRA
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Pred. No. 1.8e-153;
0; Mismatches 483; Indels 0;
                                              /db_xref="SWISS-PROT:P34752"
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/protein_id="CAA78904.1"
/db_xref="GI:2393"
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Nevalainen, H.K.M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K., Torkkell, T.K., Cantrell, M., Piddington, C.S., Rambosek, J.A., Turunen, M.K. and Fagerstrom, R.B.
Production of phytate degrading enzymes in trichoderma Patent: US 5780292-A 7 14-UUL-1998;
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Nevalainen, H.K. M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K., Torkkell, T.K., Carlell, M., Piddington, C.S., Rambosek, J.A., Turunen, M.K., Fagerstrom, R.B. and Houston, C.S. Nucleic acid molecules encoding phytase and pH2.5 acid phosphatase Patent: US 5830733-A 7 03-NOV-1998;
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                                                                                                                                  384 gotgacgacttgactccattcggtgaacaacaaatggttaactctggtattaagttctac 443
                                                                                                                                                                                                                                                                                                                                                     1118 TCATCCAACAACACTCTCGACCAGGCACCTGCACTGTCTTTGAAGACAGGGAATTGGCC 1177
                                                                                                           818 AACGTGACCACCTTTGATGGAAAATATGCCTTCCTGAAGACATACAACTACAGCTTGGGT 877
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Tobaces 1 to 2379)
Nevalainen, H.K.M., Paloheimo, M.T., Fagerstrom, R.B.,
Miettinen-Oinonen, A.S.K., Turunen, M.K., Rambosek, J.A.,
Piddington, C.S., Houston, C.S. and Cantrell, M.A.
Recombinant cells that express phytate degrading enzymes in desired
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                       1778 TIGGITAATGATCGCGTTGTCCCGCTGCATGGGTGTCCAATTGATGCTTTGGGGAGATGT 1837
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                                                                                                                                                                                                                                                                                                                                       Patent: US 5834286-A 1 10-NOV-1998;
                                                                                                                                                            ARU53934 2379 bp DNA
Sequence 1 from patent US 5834286.
AR053934
                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
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Matches 908; Conservative
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1224 gctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaaccattggttagagtt 1283
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1014 CGCGTGATCGCCTCCGGCGAGAAATTCATTGAGGGCTTCCAGAGCACCAAGCTGAAGGAT 1073
                                                                                                                                               744 gctcacttgccaggtgttaacttgactgacgaagacgttgttaacttgatggacatgtgt 803
                                                             624 ggttacaacaacactttggaccacggtttgtgtactgctttcgaagaatctgaattgggt 683
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RESULT 12
ASNPHYTAS ASNPHYTAS 2379 bp DNA PLN 23-MAR-1994
LOCUS
DEFINITION ASPECTALLUS niger var awamori phytase gene, complete cds.
DEFINITION L02421
L02421
L02421
L02421
L02421
L02421
REYWORDS
PHYTASE.
SOURCE
ASPECTALIUS niger (strain ALK0243, sub_species awamori) DNA.
SOURCE
ASPECTALIUS niger
ORGANISM
ASPECTALIUS niger
BUKATYOTA; Fungi; Ascomycota; Pezizomycotina: Eurotiomycetes;
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KLSPPCDLFTHDEWIHYDYLOSLKKYYGHGAGNPLGPTOGYGYANELIARLTHSPVHD
DTSSHHTLDSNPATPPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTYVENITOT
DGFSSAWTVPFASRLYVENMOCQAEQEPLVRVLVNDRYVPLHGCPIDALGRCTRDSFV
                                                                                                                                                                                                                                                                                                                                                                                                         /function="conversion of phytate to inositol and inorganic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDGGYQCFSET
SHLWQQYAPPFSLAMESAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEI
QONVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYORYESLTRNIIPFIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSSRVIASGEKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDSELADTVEANFTATFAPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDT
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                   1 (Sites)
Piddington, C.S., Houston, C.S., Paloheimo, M., Cantrell, M.,
Piddington, C.S., Houston, A., Nevalainen, H. and Rambosek, J.
The cloning and sequencing of the genes encoding phytase (phy) and phy 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
                                                                                                                                                              Carter,J.R., Franden,M.A., Aebersold,R.H. and McHenry,C.S.
Molecular cloning, sequencing and overexpression of the gene
encoding the psi subunit of E. coli DNA polymerase III holoenzyme
Unpublished (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 ccagacgitccaaagggttgtagagitactitcgitcaagitttgictagacacggtgct 263
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Pred. No. 1.8e-153;
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                                                                                                                                                                                                                                                              /organism="Aspergillus niger"
/db_xref="taxon:5061"
                                                                                                                                                                                                                                                                                                                                 /evidence=experimental
join(420. .463,566. .1925)
/EC_number="3.1.3.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="phytase"
/protein_id="AAA16898.1"
/db_xref="GI:166519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=experimental
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735 c
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954 CAGGGATACGAATCGCTCACAAGGAACATCATTCCGTTCATCCGATCCTCTGGCTCCAGC 1013
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834 AACGTGACCACCTTTGATGGAAAATATGCCTTCCTGAAGACATACAACTACAGCTTGGGT 893
                                                                                444 agaagatacaaggctttggctagaaagattgttccattcgttagagcttctggttctgac 503
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Eukaryotta: Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. I to 2665)

Mullaney, E.J., Gibson, D.M and Ullah, A.H.
Positive identication of a lambda gtll clone containing a region of fungal phytase gene by immunoprobe and sequence verification Appl. Microbiol. Biotechnol. 35, 611-614 (1991)
                                         ASPERGILLUS niger myo-inistol hexaphosphate phosphohydrolyase gene,
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SCSRVIAZGAGKKEIGEPGSTKLKDPFGGELVNISGIKEYORYEELTEI
SCSRVIAZGAGKKEIGEPGSTKLKDPFAQPGGSSPKIDVVISEASSSNNTLDPGTTYPFIRS
EDSELADIVEANFTAFVPSIRQALENDLSGYTUDTEVILADMGSFDTISTSTVDT
KLSPFCDLFTHDEMINYDXLOSLKKYYGHGAGNPLCPTGGYZTVDT
DGFSSPANTLDSSPATFPLNSTLYADFSHDNGIISILEALGENDRGSPDTISTSPYDD
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DGFSSAMWTUPFASRLYVEMQCQAEQEPLVRVLVNDRVVPLHGCPVDALGRCTYBSFV
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SHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEI
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/product="myo-inositol hexaphosphate phosphohydrolyase"
808 c 574 g 650 t
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Mullaney,E.J.
Sequence of the Aspergillus niger (ficuum) phytase gene
Unpublished (1992)
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43.4%; Score 618.2; DB 13; Length 2665;
al Similarity 65.3%; Pred. No. 1.8e-153;
908; Conservative 0; Mismatches 483: Indels 0.
                                                                                                                                                            myo-inositol hexaphosphate phosphohydrolyase; phytase.
Aspergillus niger (library: EMBL 3; NRRL 3135) DNA.
Aspergillus niger
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0; Mismatches 483; Indels
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<683. 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Aspergillus niger"
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/note="phytase gene"
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1937 ACCGTGGAGAATATCACCCAGACAGATGGATTCTCGTCTGGTTGGACGGTTCCGTTTGCT 1996
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1037 CGGTATCCGACCGACTCCAAGGGCAAGAATACTCCGCTCTCATTGAGGAGATCCAGGAG 1096
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                                                         2117 ACCCGGGATAGCTTTGTAGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCGGAG 2176
2057 ITGGTTAATGATCGCGTTGTCCCGCTGCATGGGTGTCCGGTTGATGCTTTGGGGAGATGT 2116
                                     10-JUN-1994
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phytase gene locus of plasmids pAF 2-3, pAF 2-6, pAF 2-7.
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65.3%; Pred. No. 1.9e-153;
tive 0; Mismatches 483;
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Wan Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.A., Venstra,A.E., Luiten,R.G.M. and Selten,G.C.M. Cloning and expression of phytase from aspergillus Patent: US 5436156-A 31 25-JUL-1995; 43.4%; Score 618.2; DB 10; Length 6756; 65.3%; Pred. No. 1.9e-153; tive 0; Mismatches 483; Indels 0; PAT /organism="unknown" 1714 c 1712 g 1715 t 113429 6756 bp DNA Sequence 31 from patent US 5436156. Location/Qualifiers I13429.1 GI:910770 al Similarity 65.3 908; Conservative .6756 1404 tgtttcgctta 1414 1704 rGTTTTGCTTA 1714 Unclassified. 1615 a Unknown. Unknown I13429 13429 Query Match DEFINITION source ORGANISM RESULT 15 BASE COUNT TITLE JOURNAL ACCESSION Matches REFERENCE AUTHORS KEYWORDS FEATURES VERSION I13429 ORIGIN Q g δ g òγ Db ŏ à. δ q δă g qq ò qq δ g δy

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Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634 Tel: 864 655 5737 Fax: 864 656 4293

High quality sequence stop: 408. Location/Qualifiers Seq primer: GGAAACAGCTATGACCATG Class: BAC ends Email: rdean@clemson.edu

source

FEATURES

Contact: Dean RA Clemson University Genomics Institute

Unpublished (1998)

JOURNAL

COMMENT

| Description   | 7.25  |  |
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| Result<br>No. |   |  |

AQ324539 802 bp DNA GSS 08-JAN-1999 mgxb0019c01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic 1 (bases 1 to 802) Tu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome Eukaryota: Fung: Ascomycota: Pezizomycotina: Sordariomycetes; Sordariomycetes incertae sedis: Magnaporthaceae; Magnaporthe. clone mgxb0019C01r, DNA sequence. AQ324539.1 GI:4116391 Magnaporthe grisea. Magnaporthe grisea DEFINITION AQ324539/c ORGANISM ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE SOURCE

Anote—"Vector: pBACWICH; Site\_1: HindIII; Site\_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library kb was constructed. This library represents size of 130 kbm was constructed. 5, than 25% genome coverage. High density colony filters are available upon request." 1 others 995 tcactctccagttcaagaccacacttctactaaccacactttggactctaacccagctac 1054 1055 tttcccattgaacgctactttgtacgctgacttctctcacgacaacactatggtttctat 1114 755 aggigitaacitgactgacgaagacgitgitaacitgaiggacaigigicalicgacac 814 614 AGGGTGAAACCTCACGGCCAAGCAAGCGGTGCAGATCATGAGCTTCTGCCGGTTTGAGAC 555 1115 tttcttcgctttgggtttgtacaacggtactaagccaitgtctactacttctgttgaatc 1174 1175 ta-----ttgaagaaactgacggttacgctgcttcttggactgttccattcgctgctag 1228 875 cgaatggattcaatacgactacttgcaatctttgggtaagtactacggttacggtgctgg 934 10.6%; Score 151; DB 227; Length 802; 55.2%; Pred. No. 5.7e-33; Live 0; Mismatches 266; Indels 12; Gaps 815 igitigetagaactictgacgctactcaattgictccattctgigactigitcactcacga 874 554 CGTGGCAGATCCNCAAGCCAC-----CCTGTCGCAGTTCTGCACGCTGTTTACGCAACG 501 380 CCAAAAAGCCGTTGAAGACCACACAAAATACCAACTGACGCTCGACACGCACCCATCGAC 321 320 GTTCCCACTAGACAAAAAGCTGTACGCCGACTTTAGCCATGATAACGATATGCTGGGCAT 261 260 craceccececressarraraacsccaceseccecearressressaaaassassas 201 200 AAGGAGCGCGCAGGAGCTCAGCGGGTTCTCGTCCAGCTGGGCGGTACCGTTCGCAGCGG 141 /clone="mgxb0019C01r"
/clone\_lib="CUGI Rice Blast BAC Library"
/tissue\_type="Protoplasts"
/lab\_host="E. coli DH108" 1. .802 /organism="Magnaporthe grisea" /strain="70-15" /db\_xref="taxon:148305" Best Local Similarity 55.29 Matches 342; Conservative 166 Query Match BASE COUNT ORIGIN óγ qq δλ Q δ g δ q δ g δ g

g ŏ

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130
                                                                                                                                                                                                                                                                     AQ255459 837 bp DNA GSS 23-OCT-1998 mgxb0014M15r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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248 a 154 c 188 g 243 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                          1289 taacgacagagttgttccattgcacggttgtggtgttgacaagttgggtagatgtaagag 1348
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Sordarlomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
  81
                                                                  140 GATGTTTGTTGAAAAATGACTTGCGCAGGGCAGAACGAGGAGCTTGTGAGAATCCTGGT
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
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56.2%; Pred. No. 2.9e-23;
Live 0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="CUGI Rice Blast BAC Library"
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/lab_host="E. coli DH10B"
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/strain="70-15"
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High quality sequence stop: 277.
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                                                                                                                                  1349 agacgacttcgttgaaggtt 1368
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/clone_lib="Metarhizium anisopliae ARSEF 2575"
/note="Vector: Unizap; Metarhizium anisopliae was grown on insect cuticle for 24 hours. A cDNA library was constructed in the unidirectional Lambda Vector, Unizap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (Massa 1 to 581)
Screen, S. B., Mathur, P. and St. Leger, R.J.
EST analysis of the insect pathogenic fungus Metarhizium anisopliae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AJ274007 581 bp mRNA EST 29-DEC-1999
AJ274007 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae
CDNA clone Ma#1628, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                        .048 cagctactttcccattgaacgctactttgtacgctgacttctctcacgacaacactatgg 1107
                                                                                                                                                                                                                                                                                 988 gattgactcactctccagttcaagaccacacttctactaaccacactttggactctaacc 1047
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                                                                                                                                                                                                                                                                                                                                  380 GATTAACCCGAAGCCCAGTCCAAGATCAAACCATGTCCAATACGACATTGACATGAACC 439
                                                                                                                                                                                                                                320 GAAACGGTAATCCTTTGGGCCCCAACTATGGGCGTGGGATGGGTAAACGAACTTATTGCAC 379
868 ctcacgacgaatggattcaatacgactacttgcaatctttgggtaagtactacggttacg 927
                                                                                                                               260 CGGAAGCAGATTGGGTAAAATATGGTTACTTGTCCAGCGTGCAAAAATGGTACAGATACG 319
                                                                                                                                                                                University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.0%; Score 113.8; DB 104; Length 581; 58.5%; Pred. No. 3.8e-22;
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/strain="ARSEF 2575"
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/clone="Ma#1628"
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Metarhizium anisopliae
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7

DP OY OY OY

275 ttcttctaagtctaagaagtactctgctttgattgaagctattcaaaagaacgctactgc 334

249 GTATGCACCATTTTTGGTTGCACCGTCAGCACCATCGGATTATGATTCCTCTGCTACCTT 308

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AQ163004 753 bp DNA GSS 09-SEP-1998 mgxb0021D19r_CUGI_Rice Blast BAC_Library_Magnaporthe_grisea_genomic
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M. Wing,R.A. and bean,R.A.
                                         340 GACTATGGGAAGGGCTTCGAGTTTCTCAAAGATTACAAGTATACTCTAGGTTCTGACGAC 399
333 gctttcaagggtaagtacgctttcttgaagacttacaactacactttgggtgctgacgac 392
                                                                                      393 tigaciccaticggigaacaacaaatggitaaciciggiatiaagiictacagaagatac 452
                                                                                                             453 aaggettiggetagaaa---gatigitecatiegitagagettetggiteigaeagagit 509
                                                                                                                                                                                                                   460 cagaagiraccgaggarrccarccarccrrrgrrcaagccrcgggcrcrgaaggagrc 519
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Tel: 864 656 5737
Fax: 864 656 4293
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Clone="mgxb0021019r"
/clone_lib="cug1 Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                               510 attgcttctgctgaaaagttcattgaaggtttccaatctgctaag 554
                                                                                                                                                                                                                                                                                                         520 GICAIGICAGCGCAAGAITITIGIICAIGGCIICIACAAAGCCAAG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Magnaporthe grisea"/strain="70-15"
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Clemson University Genomics Institute
Clemson University
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Location/Qualifiers
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Magnaporthe grisea
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AQ162040 699 bp DNA GSS 09-SEP-1998
mgxb0010F06r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
369 cgcicaaaccggcggaaaiicicgaacacgaiicaccgaciccaaaccicacgiacg 428
                                                                         395 gactecattoggtgaacaacaaatggttaactetggtattaagttetacagaagatacaa 454
                                           335 tttcaagggtaagtacgctttcttgaagacttacaactacactttgggtgctgacgactt 394
                                                                                                                                                                       489 GAATGATTTGGGCCGTCGGCAAACAGAGAACTCCGGGTATTNATTTTACCAAAGATACCA 548
                                                                                                                                                                                                                     455 ggctttggctagaaagattgttccattcgttagagcttctggttctgacagagttattgc 514
                                                                                                                                                                                                                                                             549 AAATCTGGCCAGAAGGAACGAACCATTTATTCGCTATGATGACAAANAACGCGTGTTTGA 608
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette.R., Gavle a Frinch.
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100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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/clone_lib="CuGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
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Clemson University Genomics Institute
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Class: BAC ends
High quality sequence stop: 285.
Location/Qualifiers
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6; Gaps

6.2%; Score 88.6; DB 225; Length 753; 51.3%; Pred. No. 9.4e-15; ative 0; Mismatches 212; Indels 6;

Best Local Similarity 51.3 Matches 230; Conservative

Query Match

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Query Match
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/lab.host="E. coll DH10B"
/note="Vector: pBACWICH: Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ361474 769 bp DNA GSS 03-FEB-1999 mgxb00004112f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
a haploid genome (n-7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request. "
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A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1309 igcacggitgiggigttgacaagttgggtagatgtaagagagacgacttcgttgaaggtt 1368
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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/clone="mgxb0004112f"
/clone_lib="CUGI Rice Blast BAC Library"
                                                                                                                                                                                                                                                                                         92; Indels
                                                                                                                                                                                                                                                  Score 81.8; DB 22:
Pred. No. 8.8e-13;
0; Mismatches 92.
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High quality sequence stop: 416.
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Fax: 864 656 4293
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                                 of files would when the state of approximately 40 Mbp. Rice a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying blast is an important model fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters har available upon request.

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A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
It is a filamentous ascomycete with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 ATTGAATGATTTGGGCCGTCCGCAACAGAGAAC-CTCGGGTATATTTTACCAAAGATA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 caaggotttggotagaaagattgttccattcgttagagcttctggttctgacagagttat 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            632 CCAAAATCTGGCCAGAAGGAACGAACCATTTATTCGCTATGATGACAAAAAACGCGTGTT 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 ----agggttgtagagttactttcgttcaagttttgtctagacacggtgctagataccc 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 CTTGCCAGGGTGTAGGATTACGTTTGCCCAAGTCCTTCAGAGGCACGGGGCTCGATACCC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 aacttottotaagtotaagaagtactotgotttgattgaagotattcaaaagaacgotac 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 AACGGCTCAAACCGGGGGGAAATTCTCGAACACGATTCACCGACTCCAAACCTCACGTAC 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 CTGTTTTGATGCGCCAGCCGGGTTTTCAATTTAAAGCAGCAATCACTCATAATTGGGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 5.6%; Score 79.4; DB 227; Length 769; 51.7%; Pred. No. 4.6e-12;
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Tel: 864 656 5737
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Anotes "Vector: Data With Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1190 cggttacgctgcttcttggactgttccattcgctgctagagcttacgttgaaatgatgca 1249
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Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 655 5737
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/clone=lib="CuGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76; DB 225;
Pred. No. 4.6e-11;
                                                                                                                                                                  /organism="Magnaporthe grisea"
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Clemson University Genomics Institute
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/db_xref="taxon:148305"
                                           Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 321.
                                                                                                                    Location/Qualifiers
                         Email: rdean@clemson.edu
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Fax: 864 656 4293
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order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater area available upon request. " 1 others
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tive 0; Mismatches 321; Indels 14; Gaps
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/clone_lib="CUGI Rice Blast BAC Library"
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                                            Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 465.
Location/Qualifiers
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                         Email: rdean@clemson.edu
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Fax: 864 656 4293
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthonopha; Acanthopterygii; Percomorpha; Tetraodontidae; Tetraodon.

1 (bases 1 to 1016)

1 (bases 1 to 1016)

Bouneau, L., Billault, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="G"
/note="Genoscope sequence ID : C0BG105AH08LP1-end : T7"
/note="Genoscope sequence ID : C0BG105AH08LP1-end : T7"
                                                                                                                                                                      Tetraodon nigroviridis genome survey sequence T7 end of clone
105015 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 cttctccagttattaacgttattattccagaaggtgctggttacaacaacactttggacc 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             782 CIGCIGITGITACIGCIGITGITACIGCIGITGITACIGAIGITACIGCIGITGITA 841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tetracdon nigroviridis"
/db_xref="taxon:99883"
/clone="105015"
                                                                                                                                                         GSS
                                                                                                                                                                                                                                                                              GSS, genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                         DNA
    1044 aacccagctactttcccattgaa 1066
                        27 AATCCGAAAACGTTTCCGTTGGA 5
                                                                                                                                                                                                                                                              AL287459.1 GI:8025953
                                                                                                                                                                                                                                                                                                                                Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 a
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KEYWORDS
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1 (bases 1 to 545)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                       AQ140737 545 bp DNA GSS 24-SEP-1998 HS_3124_A2_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=20 Row=G, DNA sequence. AQ140737
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 taagtotaagaagtaototgotttgattgaagotattoaaaagaacgotaotgotttoaa 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 ATGTAACAGCTCAGTACAAGGTTAAGTAAACCATTATTTTCTATCTGTGAAACAAG--AA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 115; Indels
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/clone="Plate=3124 Col=20 Row=G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 545.
Location/Qualifiers
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                                                                                                                                                                                                                                                    AQ140737.1 GI:3531390
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Fax: (206) 616-3887
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06
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962 CIGCIGITGITACT 975
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Class: BAC e
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ORGANISM
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JOURNAL
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                                                                                                                                                       REFERENCE
AUTHORS
        ACCESSION
                                                 KEYWORDS
SOURCE
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                               VERSION
                                                                                                                                                                                    Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 468)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores-Jeres,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula leaf library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                              NF049F02LF1F1016 Developing leaf Medicago truncatula cDNA clone
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AV054552 Mus musculus pancreas C57BL/6J adult Mus musculus CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 AGAATGTTTTGAGTGTATTGTTTGACATTTTTGTTACATCTAGTGTACTGTCAGACTTTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               571 ctaacccacaccaagcttctccagttattaacgttattattccagaaggtgctggttaca 630
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                                                 19-DEC-2000
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/note="Vector: Lambda Zap; Contains a mixture of young, developing, mature and senescing leaves."
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7391
Fmail: gdmay@noble.org
Insert Length: 468 Std Error: 0.00
Plate: 049 row: F column: 02
Seq primer: TCACACAGGAAACAGCTAATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
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/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3880"
/clone="NF049F02LF"
                                                                                    NF049F02LF 5', mRNA sequence.
                                              mRNA
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                                                                                                                          BF637070.1 GI:11901228
                                            468 bp
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ORGANISM
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                                                              DEFINITION
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                                                                                                        ACCESSION
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RESULT 1
BF637070
                                                                                                                               VERSION
KEYWORDS
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Email: genome_resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                           Carninol, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kaikuchi, N., Kojima, Y., Matsuyama, T., Nitteuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Mutanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 341)
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PCII-48J14.TK RPCI-11 Homo sapiens genomic clone RPCI-11-48J14,
DNA sequence.
AQ202816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreas C57BL/6J adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pancreas"
clone 1810031C08, mRNA sequence.
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/clone="1810031C08"
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60 c 101 g
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                        AV054552
AV054552.1 GI:5154299
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN Mouse ESTs
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.6#
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
                                                                                                                                  Mus musculus
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KEYWORDS
SOURCE
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ORGANISM

REFERENCE AUTHORS

TITLE

COMMENT

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trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                       (bases 1 to 231)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara,
A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigemcto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N.,
Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV064132 Mus musculus small intestine C57BL/6J adult Mus musculus cDNA clone 2010009L02, mRNA sequence.
                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1165 ctgttgaatctattgaagaaactgacggttacgctgcttcttggactgttccattcgctg 1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 CCGCCGCCCCAGCTGAGGAGAAGAAGTGGAGGCAAAGAAGAAGTAGTCCCGAGGAGTCTG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1285 tggttaacgacagagttgttccattgcacggttgtggtgttgacaagttgggta 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mus musculus C57BL/6J 11-day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 AAGAIGACATGGGCTTCGGTCTTTTGACTAAACTGCTTTTGTTAAGTTGGCTA 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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51 c 66 g 55 t
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/clone="2700068B02"
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AV129427.1 GI:5315662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Conservative
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                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
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                                                                                                1 (bases 1 to 481)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu): Clones may be purchased from
ABCPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from
Attp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
1 99 c 81 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1097 caacactatggtttctattttcttcgctttgggtttgtacaacggtactaagccattgtc 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   977 attgattgctagattgactcactctccagttcaagaccacacttctactaaccacacttt 1036
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AV129427
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45.5%; Pred. No. 0.38;
tive 0; Mismatches 177; Indels 0;
                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GDB:7518277"
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Other_GSSs: RPCI11-48J14.TJ
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                                                                                                                                                                                                                                                                                                 Contact: Mark Adams
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Fax: 301 838 0208
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Scarinci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahibata, S., Akiyama, T., Fukuda, S., Fukuda, S., Fukuda, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Cawai, J., Shigemoto, Y., Suzuki, H., Oda, H., Owa, C., Y., Suzuki, H., Suzuki, H., Yamamura, T., Yokota, T., Tominaga, N., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Tominaga, N., RIKEN Mouse, ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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2.9%; Score 41.2; DB 109; Length 234;
Best Local Similarity 52.3%; Pred. No. 0.44;
Matches 91; Conservative 0; Mismatches 83; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="small intestine"
/dev_stage="adult"
45 c 72 q 62 t
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/organism="Mus musculus"
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 protein search, using sw model OM protein

Run on:

October 26, 2001, 13:24:54; Search time 48.78 Seconds (without alignments) 729.264 Million cell updates/sec

1 MGVFVVLLSIATLFGSTSGT.......DFVEGLSFARSGGNWEECFA 467 Perfect score: Scoring table: Sequence:

US-09-488-265-26

BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | )<br>E  | -phytase (EC | ouytase (EC | cid phosphatas | cid phosphatas                             | cid phosphatas | phosphatas | onata | >~     | acid phosphatase ( |        |        | acid phosphatase ( | ebress  |        |       | u      |        | יי     | netical pr | acid phospharase ( |        | pitospita Lase | nypounetical prote | brootbots of contract | Allocation prote | glucose-I-phosphat | aldehyde dehydroge |
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| SUMMARIES | . QI          | TNORRO                                  | .TN0656 | TN0482       | יכ          | 553476         | 34 8 9 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | DARYCC         | 552495     | 2001. | JC4285 | COSUNI             | A05306 | 514110 | 330000             | TEO 260 | AB6103 | 00000 | 113116 | A33395 | 716883 | S14742     | S06167             | JH0152 | F21241         | A36715             | F16455                | TV0087           | 385636             | 144987             |
|           | DB            | :<br>:                                  | ,       |              | -           | 10             |  |                |            |       |        |                    |        |        |                    |         |        |       | ۷ ۸    |        |        |            |                    |        |                |                    |                       |                  |                    |                    |
|           | Length        | 467                                     | 467     | 441          | 467         | 467            | 467  | 467            | 468        | 479   | 468    | 479                | 453    | 463    | 463                | 465     | 468    | 7.50  | 449    | 423    | 380    | 421        | 423                | 381    | . 354          | 602                | 730                   | 413              | 413                | 496                |
| æ         | Query         |   |         | N            | 9           |                | 16.2                                       |                | 5          |       | 4      | 4                  |        |        |                    |         |        |       |        |        |        | 4.8        | 4.6                | 4.4    | 4.4            | 4.4                | 4.3                   | 4.2              | 4.2                | 4.2                |
|           | Score         | 1866                                    |         | 1801         | 403         | 399            | 399  | 394            | 370        | 350.5 | 350    | 346.5              | 326    | 301    | 301                | 156     | 154.5  | _     | 130    | 122.5  | 119    | 117.5      | 112.5              | 108.5  | 108            | 107.5              | 90                    | 04               | 104.5              | 03                 |
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| S61067<br>T16346   | \$64682<br>T20556  | E69144                                   | JH0610<br>T37690   | S77346             | G36793             | C75105             | S54770             | T27570             | T46726              | A71444                | 574407             | KSPSCY            |
| 7                  | 01 00              | ο,                                       | <b>→</b> ~         | 7                  | 7                  | 7                  | 7                  | 7                  | ~                   | 7                     | ~                  | 1                 |
| 693                | 438                | 642                                      | 386<br>844         | 630                | 1350               | 374                | 537                | 721                | 888                 | 1433                  | 433                | 609               |
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| 1 0 |
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3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
N.Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C;Species: Aspergillus awamori
C;Date: 14-0ul-1994 #sequence\_revision 19-oct-1995 #text\_change 11-Jun-1999
C;Accession: JNO889
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A. Gene 133, 55-62, 1993
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-op

A; Accession: JN0889

A; Molecule type: DNA
A; Residues: 1-467 <PIDA
A; Cross-references: 68:102421; NID:9166518; PIDN:AAA16898.1; PID:9166519
A; Bayerimental source: strain ALK0243
A; Note: part of the sequence, including the amino end of the mature protein, was conf C; Genetics:
A; Gene: phyA
A; Introns: 15,2
C; Genetics: A; Gene: phyA
A; Introns: 15,2
C; Superfamily: yeast acid phosphatase
C; Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F; 1-19,7 Domain: signal sequence #status experimental AMAT>
F; 20-467/Product: 3-phytase A #status experimental AMAT>
F; 20-467/Product: 3-phytase A #status experimental AMAT>
F; 20-467/Product: 3-phytase A #status predicted
F; 82/Active site: His (phosphohistidine intermediate) #status predicted

0; Gaps Length 467; Indels 75.5%; Score 1866; DB 1; 74.5%; Pred. No. 8.3e-142; tive 44; Mismatches 75; Local Similarity 74.5 ies 348; Conservative Query Match Best Local S Matches

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1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60 qq

61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIOKNATAFKGKYAFLKTYN 120 δλ

g

121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180 Ωÿ

q

181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240 δ

241 ARLEAHLPGVNLTDEDVVNLAMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300 òγ

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Query Match
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A. Note: parts of the sequence, including the amino end of the mature protein, were conficionment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and ind conficion of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A forms: phyA had a form of the phosphatase construction of the phosphopistic phosphopistic phosphopists; 15/2 cyporfamily: yeast acid phosphatase cysuperfamily: yeast acid phosphatase cysuperfamily: yeast acid phosphoprotein; phosphopistic extracellular protein; glycoprotein; phosphopis: stracellular protein; glycoprotein; phosphores: stracellular protein; glycoprotein; phosphores: stracellular protein; phosphores: stracellular protein; phosphores: stracellular protein; phosphores: carbohydrate (Asn) (covalent) #staf: $1,351,501,051,120,207,230,339,352,376,388,fallofing site: carbohydrate (Asn) (covalent) #staf: $1,351,Active site: Arg, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger NAlternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein C; Species: Aspergillus niger C; Species: Name 1994 #sequence_revision 19-oct-1995 #text_change 11-Jun-1999 (C; Accession: JN0656; S28456 R; Van Hartingsveldt, W.; Van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVISPEVPAGCRVTFAQVLSRHGARYPIDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120
                                                                                                                   361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                                                                                 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300
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                                                                                                                                                                                                                                                                                                                                                                           LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                     75.4%; Score 1862; DB 1; 74.5%; Pred. No. 1.7e-141; Live 44; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348; Conservative
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A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Residues: 48-70 <UL2>
C;Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phyt
C;Superfamily: yeast acid phosphatase
C;Reywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
C;Reywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
C;Reywords: extracellular protein; glycoprotein; phosphohistidine site: arbohydrate (Asn) (covalent) #sta
F;S8,338/Active site: Arg, His #status preddicted
F;S9/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 192, 747-753, 1993
A;Title: Aspergillus ficuum phytase. Complete primary structure elucidation.by chemic
A;Reference number: JN0482; MUID:93249451
A;Accession: JN0482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-441 <ULL>
A; Note: authors state that the 9 Asn followed by Thr or Ser after an intervening resi
R; Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 178, 45-53, 1991
A; Title: Cyclohexanedione modification of arginine at the active site of Aspergillus
A; Reference number: PN0023; MUID:91298982
                                                                                                                                                                                                                                                                                                                                                                         3-phytase (EC 3.1.3.8) A - Aspergillus ficuum N.Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein C.Species: Aspergillus ficuum C.Species: Aspergillus ficuum C.Species: 30-Sep-1993 #sequence_revision 19-oct-1995 #text_change 07-May-1999 C.Accession: JN0482, PN0023 R.Ullah, A.H.J.: Dischinger Jr., H.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 DIISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
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361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                       27 NSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF
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                                                                                                                                                                             421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.9%; Score 1801; DB 1;
76.0%; Pred. No. 1.3e-136;
Live 42; Mismatches 63;
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                                                                                                       A;Cross-references: EMBL:235962; NID:9536364; PIDN:CAA85046.1; PID:9536365; GSPDB:GN0000
R;Arima, K.; Oshima, T.; Kubota, I.; Nakamura, N.; Mizunaga, T.; Toh-e, A.
Nucleic Acids Res. 11, 1657-1672, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-35, Y', 37-129, 'G', 131-293, 'O', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467 <AF
A; Cross-references: EMBL: V01320; NID: 94158; PIDN: CAA24630.1; PID: 94159
A; Accession: A38793
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A. Molecule type: DNA
A. Residues: 1-30, T', 32-51, S', 53-75 < MEY>
A. Residues: 1-30, T', 32-51, S', 53-75 < MEY>
A. Cross-references: EMBL:M24178 NID:9172156; PIDN:AAA34868.1; PID:9172157
B. Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G
Mol. Cell. Biol. 6, 1855-1865, 1986
A. Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within A. Reference number: A93074; MUID:87064474
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Mol. Cell. Biol. 6, 2298-2304, 1986
A, Title: A DNA fragment containing the upstream activator sequence determines nucleosome
A, Reference number: A25367; MUID:87064526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55598.1; PID:g476051
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: 845927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of A;Reference number: A00777; MUID:83168913
A;Accession: A00777
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A;Residues: 18-26, X',28 <AR12>
R:Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinnen, A.
EMBO J. 1, 675-680, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S48255; MUID: 95208357
A; Accession: S48260
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A;Residues: 1-2,'Y',4-43,'T',45-51 <BER>
424 DSFVRGLSFARSGGDWAE 441
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A; Residues: 1-467 <MAN>
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A; Residues: 1-44 <TAI>
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C; Superfamily: yeast acid phosphatase
C; Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydr
E;1-1/7Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase, repressible #status experimental <MAT>
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (co
                                                                                                                               can enter the secretory pathway without its N-ter
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R;Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; submitted to the EMBL Data Library, February 1994
A;Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 DDDDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVPKGCRVTFVQVLSRHGARYPTSŠKSKKYSALIEAIQKNATAFKGKYAFLK-TYNYTLG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAEKFIEGFQSAKLADPGANPHQASPVINVII-----PEGAGYNNTLDHGLCTAFEESEL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 TAQYFIDG-----LGDQ------FNITLQTVSEAESAGANTLSACNSCPAW-DYDA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCD 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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R;Silve, S.; Monod, M.; Hinnen, A.; Haguenauer-Tsapis, Mol. Cell. Biol. 7, 3306-3314, 1987
Astritle: The yeast acid phosphatase can enter the secretaries in water the secretary and phosphatase can enter the
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A;Cross-references: SGD:S0000297; MIPS:YBR093c
                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-51,'S',53-60 <SIL>
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:M17306
                                                                                                                                                                                                                                             A; Accession: A27774
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A; Reference number: S46671
                                                 A; Molecule type: DNA
A; Residues: 1-467 <MAC>
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A/Gene: SGD:PH011
A/Gene: SGD:S0000094; MIPS:YAR071w
A/Map position: 1R
C;Superfamily: yeast acid phosphatase
C;Superfamily: yeast acid phospholatildine; phosphoprotein; phosphoric monoester hydrola
E;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase #status predicted <MAT>
F;74/Active site: ANG #status predicted <MAT>
F;74/Active site: His (phosphohistidine intermediate) #status predicted
F;97,162,192,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                   R;Chen, J.Y.; Gong, Y.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A;Title: The primary structure of acid phosphatase gene PHO11 in S. cerevisiae and compa
A;Reference number: JC1018
                                                                                                    A;Cross-references: EMBL:L28920; NID:91616966; PIDN:AAC09508.1; PID:9456155; MIPS:YAR071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 NPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSNRCHDTAQYFIDG-----LGDK- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANPHQASPVINVII----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNTMVSIFFALGLYNGTKPLSTISVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 ARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLK-----TYNYTL-----GADDL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 ERYPTVSKAKSIMTTWYKLSNYTGOFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIDILNYLITIGIIDDKNNLTAEHVPFMENT--FHRSWYVPQGARVYTEKFQC--SNDTY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 PLGKLSDIDKIGTQTEIFPPL---GGSGPYYSFPGDYGISRDLPESCEMKQVQMVGRHG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 PRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 -----FNISLQTISEAESAGANTLSAHHSCPAWDD-DVNDDILKKYDTKYLSGIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 TPF-GEQQMVNSGIKFYRRYKALARKIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 RINKENKGLNLTSSDANTFFAWCAYEINAR----GYSDICNIFTKDELVRFSYGQDLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 YYQTGPGYDVVRSVGANLFNASVKLLKESEVQDQ------KVWLSFTH
                                                                                                                                                                                                                                                                              A;Residues: 1-16,'L',18-149,'H',151-353,'Q',355-422,'G',424-467 <CHE>A;Note: this paper is in Chinese, with an English abstract C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.2%; Score 399; DB 2; Length 467; 26.1%; Pred. No. 3.8e-24; Live 63; Mismatches 203; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 VRVLVNDRVVPLHGCGVDKLGRCKRDDF-----VEGLSFAR 457
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A; Description: The sequence of S. cerevisiae cosmid 9177.
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                                                   A; Molecule type: DNA
A; Residues: 1-467 <BUS>
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                              A; Accession: S53476
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A.C.ossine to the EMBL: U00029; NID: 9551322; PIDN: AAB69729.1; PID: 9458917; MIPS: YHR2 R.X. L. submitted to the EMBL: Data Library, January 1995
A.R.C.ossion: S59658
A.A.C.ossion: S59658
A.A.C.oss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (Saccharomyces cerevisi N.Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR092c C; Species: Saccharomyces cerevisiae C; Species: Saccharomyces cerevisiae (C; Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999 C; Accession: S48259; S45960; S05794; A25241; S44674 #text_change 05-Nov-1999 P; Wannhaupt, G; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 10, 1363-1381, 1994 # 370 kb. region on the right arm of yeast chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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A;Residues: 1-467 < AMAN>
A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 TPF-GEQQMVNSGIKFYRRYKALARKIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNIMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPL 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 PRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PLGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDLPESCEMKQVQMVGRHG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 ANPHQASPVINVII----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK
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A; Accession: S48259
A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.2%; Score 399; DB 2; Length 46
26.1%; Pred. No. 3.8e-24;
Live 63; Mismatches 203; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 ARYPISSKSKKYSALIEAIQKNATAFKGKYAFLK-----TYNYTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 VRYVINDAVVPIETCSTGPGFSCEINDFYGYAEKRVAGTDFLK 436
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A.Map position: 8R
C.Superfamily: yeast acid phosphatase
C.Keywords: phosphoric monoester hydrolase
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Best Local Similarity 26.18
Matches 121; Conservative
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RESULT
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A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994 submitted to the Processions, G:; Schwarzlose, C.; Vetter, I.

A; Reference number: S45927
A; Reference number: S45927
A; Molecule type: DNA
A; Residues: 1-467 - CFE2>
A; CFC5S-references: EMBL: Z35961; NID: 9536362; PIDN: CAA85045.1; PID: 9536363; GSPDB: GN000C
A; Molecule type: DNA
A; Residues: 1-2771-7739, 1984
A; Reference number: S05794; MUID: 85037940
A; Reference number: S05794; MUID: 85037940
A; Reference number: S05794; MUID: 94148; PIDN: CAA25557.1; PID: 9758281
A; Molecule type: DNA
A; Residues: 1-218, MRT, 222-467 < RAJI>
A; Molecule type: DNA
A; Residues: 1-218, MRT, 218, 
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A;Gene: SGD:PH03; MIPS:YBR092c
A;Gross-references: SGD:S0000296; MIPS:YBR092c
A;Map position: 2R
C;Superfamily: yeast acid phosphatase
C;Superfamily: yeast acid phosphatase
C;Reywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
F;1-17,Domain: signal sequence #status predicted <SIC>
F;18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;337/Active site: His #status predicted
F;337/Active site: His #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 FKGKYAFLK-TYNYTLGADD------LT-PF-GEQQMVNSGIKFYRRYKALAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 FNGSLSFLNDDYEFFIRDDDDLEMETTFANSDNVLNPYTGEMDAKRHAREFLAQYGYMFE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 KIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 HG-LCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 ETQD------LKVWLSFTHDTDILNYLTTAGIIDDKNNLTAEXVPFMG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 ETDGYAASWIVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF- 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 394; DB 1; Length 467; 27.0%; Pred. No. 9.7e-24; Live 62; Mismatches 191; Indels (
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A;Residues: 1-44 <TAI>
C;Genetics:
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A;Residues: 1-468 - CURR>
A;Cross-references: EMBL:274072; NID:91430996; PIDN:CAA98583.1; PID:91430997; MIPS:YD
A;Experimental source: strain $288C
                                                                                                                                                          R;Andre, B.; Vissers, S.; Urrestarazu, L. submitted to the EMBL Data Library, February 1995
A;Description: The sequence of a 42 kb segment located on the left arm of chromosome A;Reference number: $52492
A;Accession: $52495
acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D2815
C;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C;Accession: $52495; $67556
                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-468 <AND>
A;Cross-references: EMBL:248432; NID:g683669; PIDN:CAA88335.1; PID:g683673
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N:Alternate names: pH 2.5-optimum acid phosphatase
C;Species: Aspergillus ficuum
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 FKGKYAFLKT-YNYTL------GADDLTPF-GEQQMVNSGIKFYRRYKALAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 YEGSLSFLNNGYEFFIPDESLLEMETTLONSIDVLNPYTGEMNAKRHAREFLAKYGKLME 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Mismatches 174; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 KIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 NCINFPIFIINSKRIYDTAQYFAEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- DDVEANFTAVFAPPIRARLEAHLPGVNLT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 ----TLSENSSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLENISDRLNDENKGLNLS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 DEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDXLQSLGKYYGYGAGNPLGP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AQGVGFVN---ELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMYSIFF 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 RKDAAALFSWCAFEL----NAKGYSNICDIFSAAELIHYSYETDLTSFYQNGPGYKLIK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 SIGANLFNATVKLIRQSAH--------LDQKVWLSFTHDTDILNYLT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 ALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRV 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 TAGLIDDIRNLTINHVPFRDHS--YHRSWYIPQGARVYIEKFQC--SNDSYVRYVVNDAV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%; Score 370; DB 2; Length 468; 25.1%; Pred. No. 8.2e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 VPIESCSSGPGFSCEEGTFYEYAKDRLRGVSF-----YEDC 439
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental Source: Strain S208C
R; Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
A; Reference number: S67535
A; Accession: S67556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 4L
C; Superfamily: yeast acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 HGLCTAFEESELG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gene 163, 19-26, 1995
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                                                                                                             DNA
                                                                                                             A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                   A; Gene: phol
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                                                                                                                                                                                                                C; Genetics:
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F;81,337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;introns 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosp
F;1-19/Domain: signal sequence #status predicted <SIG>
C; Accession: JN0715; PN0594; PN0460
R; Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
Biochem. Biophys. Res. Commun. 195, 53-57, 1993
A; Title: Identification and cloning of a second phytase gene (phyB) from Aspergillus nig A; Reference number: JN0715; MUID:93371452
                                                                                                                                                                                                                                                      A;Molecule type: protein.
A;Residues: 20-101;133-146;376-399 <EH2>
R;Ullah, A.H.J.; Dischinger Jr., H.C.
Blochem. Blophys. Res. Commun. 192, 754-759, 1993
A;Title: Identification of active-site residues in Aspergillus ficuum extracellular pH A;Reference number: PN0460; MUID:93249452
A;Accession: PN0460
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein.
A;Residues: 65-66,68-93 <ULL>
C;Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho C;Species: Pichia pastoris
C;Date: 14.Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY--NGTKP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 FEESELG------DDVEANFTAVFAPPIR---ARLEAHLPGVNLTDEDVVNLMD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 MASFELNAR----PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 LSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 L-----DRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDKGTYVRLVLNEAVLPFNDC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 EYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 SESEVMGADSLIPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KEAGP-----LFFNLAHDTNITPILAALGVLIPNEDLP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKY-SALIEAIQKNAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GEQOMVNSGIKFYRRYKAL--ARKIVPF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 VRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----FGYNYSTNAALNII 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.2%, Score 350.5; DB 1
27.9%, Pred. No. 3.1e-20;
ative 53; Mismatches 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: JC4285
R; Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                        A;Cross-references: GB:L20567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-479 < EHR>
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                                                                                                                                                                                                                                                   A; Accession: PN0594
                                                                                                                                                     A; Accession: JN0715
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Matches 117;
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R; piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A. Gene 133, 55-62, 1993
A; Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-op A; Reference number: JN0889; MUID:94040796
A; Accession: JN089
A; Molecule type: DNA
A; Residues: 1-479 <PID>
                                                                                                                                                                                                                                                                                                                                                                              Ciscoperfamily: yeast acid phosphatase
Ciscoperfamily: yeast acid phosphatase
Ciscoperds: glycoprotein; phospholistidine; phosphoprotein; phosphoric monoester hydr
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-468/product: acid phosphatase #status predicted <MAT>
F:84/Active site: His (phospholistidine intermediate) #status predicted
F:163,196,256,321,360,453/Hinding site: carbohydrate (Asn) (covalent) #status predict
F:345/Active site: His #status predicted
A;Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterizati A;Reference number: JC4285; MUID:96001238
A;Accession: JC4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 GYAASWIYVPFAARAYVEMMQC--EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 SFKSTEIVPMGARLLIBRLLCTVEGEEKYYVRTILNDAVFPLSDCSSGPGFSCPLNDYVS 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIE-AIQKNATAFKGKYAFLKTY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 SEI-----ESCTIDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVEVPTGPLSFFQDY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 DYFVSDAAWYEQETTKGFYSGLNTAFDFGTTLRERYDHLINTSEEGKKL--SVWAGSQER 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VYDTAKYFAQGFMKSNYTD------MVEVVALEEEKSQGLNSLTARISCPNYNSHI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 FEESELGDDV---EANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 YKDGDFPNDIAEREAD------RLNTLSPGFNITADDIPTIALYCGFELNVRGE- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 ATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 HISTNHTLDSNPATEPLNATLYADFSHDNTMVSIFFALGLYNGTK-PLSTTSVESIEETD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VLLSIATL---FGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPF--FSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 IILALATLQSVFAVELQHVLGVNDRPYPQRT-DDQYNILRHLGGL-GPYIGYNGWGIAAE 67
                                                                                                                                                                    A;Residues: 1-468 <PAY>
A;Cross-references: GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 VIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPE---GAGYNNTLDHGLCT----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 NYTLG----ADDLTPFGEQQMVNSGIKF----YRRYKAL-----ARKIVPFVRASGSDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.2%; Score 350; DB 2; Length 468; 25.4%; Pred. No. 3.3e-20; Live 79; Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
C;Species: Aspergillus awamori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 25.4%
Matches 125; Conservative
                                                                                                                                                                                                                                                            A; Experimental source: GS115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 RLEALNEDSDFAE 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 GLSFARSGGNWEE 464
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C;Superfamily: yeast acid phosphatase
C;Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;68/Active site: Arg #status predicted
F;69/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 25.49
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SPBC428.03c
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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A;Cross-references: GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482
A;Experimental source: strain ALK0243
C;Comment: The highly similar enzyme from A. ficuum has been shown to have 3-phytase (EC Genetics:
C;Genetics: A;Gene: aph
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protain; glycoprotein; phosphohistidine; phosphoprotein; phosp F;119/pomain: signal sequence #status predicted <ANT>
F;10-479/product: 3-phytase #status predicted <ANT>
F;81.337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid phosphatase (EC 3.1.3.2), precursor [similarity] - fission yeast (Schizosaccharomyce C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: A25326; T50405 T50405 R;Elliott, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J. B:Elliott, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J. A;Title: Isolation and characterization of the structural gene for secreted acid phospha A;Reference number: A25326; MUID:86140050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: EMBL:AL137099; PIDN:CAB68657.1; GSPDB:GN00067; SPDB:SPBP4G3.02
A:Experimental source: strain 972h(-); clone pl p4G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKY-SALIEAIQKNAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 GPYSERVSY----GIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINTT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 EYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AFKGKYAFLKTYNYTL-----GADDLT-PF-CEQQMVNSGIKFYRKYKAL--ARKIVPF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 VRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 FEESELG------DDVEANFTAVFAPPIR---ARLEAHLPGVNLTDEDVVNLMD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FGYNYSTNAALNII 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 SESEVMGADSLIPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 MASFELNAR-----PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY--NGTRP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 LSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 L----DRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AGSLFFNFAHDTNITPILAALGVLIPNEDLP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-453 <ELL>
A; Residues: 1-453 <ELL>
A; Cross-references: GB:M11857; NID:g173422; PIDN:AAA35321.1; PID:g173423
R; Rieger. M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A; Reference number: 225068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%; Score 346.5; DB 1; Length A Similarity 27.4%; Pred. No. 6.5e-20; L5; Conservative 54; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 F-SSGYGRVIETARKFGEGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 SLTLLNQGPKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: pho1; SPDB:SPBP4G3.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-453 <RIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 2
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Cispecies: Schlzosaccharomyces pombe
Cispecies: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1999
Ryang, J.; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990
A; Title: The structural gene coding for thiamin-repressible acid phosphatase in Schiz A; Reference number: S14119; MUID:91064763
A; Reference number: S14119; MUID:91064763
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-463 < YAN>
A; Cross-references: GB:X56939; NID:95006; PIDN:CAA40258.1; PID:g5007
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
A; Reference number: Z21931
A; Accession: T40455
A; Reference number: Z21931
A; Accession: T40455
A; Residues: 1-463 < LYN>
A; Residues: BMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03C
C; Genetics: Strain 972h-; cosmid c428
                                                                                             ..
8
                                                                                                                                                                                                                                                                                                                                                                   82 DAVGIANFQORLLINGSVPIDYSVSGNPLSFVPTWTPVIEAANADALSSSGRVELFDMGRQ 141
                                                                                                                                                                                                                                                                                                        --NATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                             143 FYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 FYERYHELFNASTYNIYTAAQQRVVDSALWYGYGMF-----GEDVHNFTNYILVSENA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 TAGSNSLSSYNACPASDADDFTTPALEAWRNYYMPPIRQRLNPYFSNYNLTNDDILNLYG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLS 382
                                                                                             48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 LANSL--RSVENNTQ------QVFFAFTHDANIIPVETALGFFTDNTPEN 351
                                                                                                                                                35 DGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKK 94
                                                                                                                                                                                                                  27 DGKFDFKEHLISRSPYHKPYF----YGPSIDFPTTCKIKQVHTLORHGSRNPTGGNAAF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 ITSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 PLPTSYQVHSHSMKASEFVFFAGNLITELFQCEDSKY-YVRHLVNEEVFPLSDCG 405
13.2%; Score 326; DB 1; Length 453; 24.8%; Pred. No. 2.6e-18; Live 63; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 2
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphoric monoester hydrolase
                                                                              Conservative
                                                                                                                                                                                                                                                                                                    95 YSALIEAIQK-----
                                       Best Local Similarity
Matches 103; Conserv
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14;

Gaps

58;

Length 463;

12.2%; Score 301; DB 2; Length 463 25.4%; Pred. No. 2.7e-16; Live 66; Mismatches 185; Indels

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Search completed: October 26, 2001, 15:10:27 Job time: 6333 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thiamin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T39929
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
submitted to the EMBL Data Library, May 1998
A;Reference number: 221857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 ACPVFKDNNFHKNATDAAHAVWRNIFIEPIVNRLAKYFDSSYKLTINDVRSLFYICEYEI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 VARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 IEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRRYKALARKIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 YDINTAEQERVVESAKWFTYGLFGDKMYE-----KTNFILISEGKAAGANSLSMYN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 LCTAFEESEL ---- GDDVEANFTAVFAPPIRARLEAHL - PGVNLTDEDVVNLMDMCPFDT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 NGSIPVNFSYPENPLCFIKQWTPVIDAENADQLSSRGRLELEDLGRQLYQRYYKLFDSYV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEG--AGYNNTLDHG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 388
                                                                                                   101 --AIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRRYKALARKIV 155
                                                                                                                                  98 NGSIPVNFSYPENPLYFVKHWTPVIKAENADQLSSSGRIELFDLGRQVFERYYELFDTDV 157
                                                                                                                                                                                                   156 PFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPE--GAGYNNTLDHG 213
                                                                                                                                                                                                                                                  158 YDINTAAQERVVDSAEWFSYGM----FGDDMQNKTNF----IVLPEDDSAGANSLAMYY 208
                                                                                                                                                                                                                                                                                                    214 LCTAFEESELGDD-VEANFTA---VFAPPIRARLEAHL-PGVNLTDEDVVNLMDMCPFDT 268
                                                                                                                                                                                                                                                                                                                                                209 SCPUYEDNNIDENTTEAAHTSWRNVFLKPIANRLNKYFDSGYNLTVSDVRSLYYICVYEI 268
                                                                                                                                                                                                                                                                                                                                                                                                  269 VARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAOGVGFVNELIARLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                       269 ALRDN-----SDFCSLFIPSEFLNFEYDSDLDYAXWGGPASEWASTLGGAYVNNLANNL- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 YSPFFSLADESALSPDVPKGCRVTFVQVLSRHGARYPTS--SKSKKYSA-----L 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 HEPYFDGLDSA-----FPETCEIQQVHLLQRHGSRNPTGDVTATDVYSSQYLNNFQEKLL 97
51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSS-----KSKKYSALIE---- 100
                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 NIFTYSLKTSSFVPFAGNLITELFLC-SDNKYYVRHLVNOQVYPLTDCGYGPSG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 IEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.2%; Score 301; DB 2; Length 463; 24.3%; Pred. No. 2.7e-16; tive 71; Mismatches 198; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T39929
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _
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C;Superfamily: yeast acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-463 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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histidine acid phosphatase (EC 3.1.3.-) - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) : C.Species: Arabidopsis thaliana (mouse-ear cress) : C.Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 C.Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 C.Accession: Je0369; A.H.J. Blochem. Biophys. Res. Commun. 251, 252-255, 1998 A.Title: Identification of a histidine acid phosphatase (phyA)-like gene in Arabidops A.Accession: Je0369; MuID:99009256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 AQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFA-L 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 NVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDED 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 --VISENRASDIKLRFFECC-----ONY-----KSYRKAKEPAVDKLKEP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 VVNLMDMC---PFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 VLNKITASVAKRYDLKFTKQDISSLWFLCKQVALLEW-----TDDLEVFLLKGYGNSLNY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 KMGVPLLEDVL----HSMEEAIKAREEKLP--PGSYE-KARL--RFAHAETIVPPFSCLL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 GLYNGTKPLSTTSVESIE------ETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 GLF-----LDGSEFEKIQKEKPLELPPQPPKTRDFRGSTMAPFGGNNILVLYSCPAESSP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 MESLAGREKELVRDAEARKLPSDKIPGWLGQWK--SPWEGKVKGGELIRQGEDELYQLGI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 KEYRRYKALARK----IVPFVRASGSDRVIASAEKFIEGFQSAK-LADPGANPHQASPVI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RVRERFFPSLFEEDYHPDVYTIRATQIPRASASAVAFGMGLFSEKGNLGPGRNRAFA---- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 YSAL---IEAIQKNATAFK------GKYAFLKTYNYTLGADDLTPFGEQQMVNSGI 141
                                                                                                                                                                                                              368 NIYIYSQKISSFVPFAGNLITELFFC-SDSKYYVRHLVNQQVYPLIDGGYGPSGTSDGLC 426
269 AIKDH-----SDFCSIFTPSEFLNFEYDSDLDQAYGGGPVSEWASTLGGAYINNLADSL- 322
                                                              329 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 388
                                                                                                                323 -----RNVTNPDFDRK------VFLAFTHDSNIIPVEAALGFFPDITPQNPLPTDK 367
                                                                                                                                                                               389 IEETDGYAASWIVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGR----C 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 DGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 DGGFDVRHHLSTV-TRYSTSKDVTQNLIEGSNVPSECTPIHLNLVARHGTRSPTKKRLRE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.3%; Score 156; DB 2; Length 465; 22.2%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 KYFVQVLHNEHPIAVPGC--DGKDFCPLEDF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 -- LVRVLVNDRVVPLHGCGVDKLGRCKRDDF 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Superfamily: yeast acid phosphatase C, Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                       427 ELQAYLNSPIRANSTSN 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.3%
Best Local Similarity 22.2%
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                               445 KRDDFVEGLSFARSGGN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-465 <MUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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OM protein - protein search, using sw model

Run on:

October 26, 2001, 15:10:34; search time 29.88 Seconds (without alignments) 535.385 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-488-265-26 2470 1 MGVFVVLLSIATLFGSTSGT......DFVEGLSFARSGGNWEECFA 467

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

|           | , to 500         | The section of the se | ın         | Sper       |             | Saccharon  |            |            |            |              |            | P52291 pichia past |            | P52289 kluyveromyc |            |            |            |          |            | P11117 homo sapien | rattı    | erwinia    | escherio  |            |            | schiz           |            | υ          | P52986 synechocyst |            |            |            |            | 75 baciline f | 5438 homo sapie |   |
|-----------|------------------|--|------------|------------|-------------|------------|------------|------------|------------|--------------|------------|--------------------|------------|--------------------|------------|------------|------------|----------|------------|--------------------|----------|------------|-----------|------------|------------|-----------------|------------|------------|--------------------|------------|------------|------------|------------|---------------|-----------------|---|
| SUMMARIES | II               | -  | PHYA_ASPAW | PHYA_ASPNG | PHYB_EMENI  | PPA5_YEAST | PPAB_YEAST | PPAC_YEAST | PPA3_YEAST | PPAD_YEAST   | PHYB_ASPNG | - 1                | PHYB_ASPAW | PPA5_KLULA         | PPA1_SCHPO | PPA2_SCHPO | PPAX_CAEEL | PPAL_RAT | PPAL_MOUSE | PPAL_HUMAN         | PPAP_RAT | PEHX_ERWCH | AGP_ECOLI | LYS4_YEAST | PPAP_HUMAN | YDZ5_SCHPO      | VG72_HSVI1 | NICA_CAEEL | DHOM_SYNY3         | COPA_PSESM | TRG1_ECOLI | TYCB_BACBR | PPAY_CAEEL | ATPX BACFI    | MRP3_HUMAN      |   |
|           | Length DB        | •  | 29         |            |             |            |            |            |            |              |            |                    |            |                    |            |            |            |          |            | 423 1              |          |            |           |            |            |                 |            |            |                    |            |            |            |            |               |                 | • |
| оNР       | Query<br>Match L |  | ٠<br>ر     | 'n.        | ω.          | ė.         | ė.         | 16.2       | ė          | 'n.          | ⊸.         | ÷.                 | •          | m .                | ÷.         | · ·        |            |          |            | 4.6                | 4.4      | 4.4        | 4.2       | 4.1        | 4.0        | 4.0             | თ.<br>თ.   | ω (<br>0 ( | υ.<br>0.0          | י<br>טי    | æ.         | 3.8        | 3.8        | 3.8           | 3.8             |   |
|           | Score            | 1 0  | 1866       | 1862       | 1813.5      | 403        | 399        | 399        | 394        | 370          | 352.5      | 3,00               | 340.0      | 340.5              | 326        | 301        | 134        | 122.5    | 117.5      | 112.5              | 108.5    | 107.5      | 104.5     | 100.5      | 80 0       | χ) (ζ<br>(Σ) (ζ | 76         | ט<br>סו    |                    | 0.0<br>0.0 | 55         | 92         | 94         | 94            | 94              |   |
|           | Result<br>No.    |  | <b>⊣</b> ( | 7 (        | <b>-</b> 0. | 4          | i, us      | ا ع        |            | <b>x</b> 0 ( | D (        | 2 -                | 1 .        | 77                 | 13         | # F        | 15         | 97       | 17         | <b>20</b> 0        | 61.0     | 20         | 21        | 7.7        | 570        | 7 C             | 520        | 970        | 7 0                | 0 0        | 67         | 30         | 31         | 32            | 33              |   |

| Off908 aguifox ago | D24007 min minus: | Ologo Para mascala | poogs nomo sapien | F098/O CTOSTIGIUM | F23984 Infections | 009451 caenorhabdi | P32473 saccharomyc | 03/002 ctaching | ODDE SCAPING TOCOC | COZEUS TENCODOSTOC | P38132 saccharomyc |           | P30672 murine cyto |  |
|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|-----------------|--------------------|--------------------|--------------------|-----------|--------------------|--|
| ARS1 AOUAE         | TRG1 MOUSE        | DTNT HITMAN        | THOID SOLD        | MAY TENTE         | V F 4 0 T T T V T | PPAW_CAEEL         | ODPB_YEAST         | GSA STAAH       | BCAL LEITLA        | מחחקק העסקה        | CC47_YEAST         | AGP_PRORE | DNBI_MCMVS         |  |
| 396                | 646 1             | 1 2485             | 526 1             | 1 1 2             | 2                 | 413 1              | 366 1              | 428 1           | 626 1              | 1                  | 845 I              | 417 1     | 191 1              |  |
|                    |                   | •                  | 3.7               |                   |                   |                    |                    |                 |                    |                    |                    |           | _                  |  |
| 93.5               | 93.5              | 93.5               | 91.5              | 7                 |                   | 7                  | 06                 | 90              | 90                 |                    | 0 4<br>0 1         | 68        | 68                 |  |
| 34                 | 35                | 36                 | 37                | 33                |                   | υ.<br>υ.           | 40                 | 41              | 42                 |                    | 7.                 | 44        | 45                 |  |

# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 QRLENDLSGYTLTDTEVTYLMDMCSFDTISTSTYDTKLSPFCDLFTHDEWIHYDYLQSLK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=93252284; PubMed=8387447; MEDILINE=93252284; PubMed=8387447; Van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M., Gouka R.J., Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A., Selten G.C.M., Veenstra A.E., van Gorcom R.F.M., van den Hondel C.A.M.J.J.;
                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                      DB 1; Length 467;
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118E828A5D7EC661 CRC64;
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51075 MW;
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467 AA;
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this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Cloning, characterization and overexpression of the phytase-encoding gene (phyA) of Aspergillus niger."; Gene 127:87-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-MYO-INOSITOL 1,2,4,5,6-PENTAKISHOSPRATE + ORTHOPHOSPHATE.
BIOTECHNOLOGY: IS USED AS A FOOD AND FEED ADDITIVE. IT CAN
FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
USED AS FOOD FOR MONOGASTRIC ANIMALS. SOLD BY NOVO NORDISK UNDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=97307250; PubMed=9164457;
Rostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell D.,
Van Loon A.P.;
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                                                                                                                                                                                        Ullah A.H.J., Dischinger H.C. Jr.; "Aspergillus ficuum phytase: complete primary structure elucidation by chemical sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Struct. Biol. 4:185-190(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Aspergillus' ficuum phytase: partial primary structure, substrate selectivity, and kinetic characterization."; Prep. Biochem. 18:459-471(1988).
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                                                                                                                                                                                                                                                                                                                                   Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.; "Cyclohexanedione modification of arginine at the active site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure of phytase from Aspergillus ficuum at 2.5-A resolution.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O
                                                                                                            Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 192:747-753(1993).
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION, AND PARTIAL SEQUENCE.
STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE-89160685; Pubmed-2852807;
                                                                                                                                                SEQUENCE OF 24-464.
STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE-93249451; PubMed=8387289;
                                                                                                                                                                                                                                                                                                      STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=91298982; PubMed=1648914;
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InterPro; IPR000560;
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PIR; PN0023; PN0023.
PIR; JN0656; JN0656.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXAKISPHOSPHATE
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Eukaryota: Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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88FE8F3584341D6D CRC64;
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PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                "Cloning of the phytases from Emericella nidulans and the thermophilic fungus Talaromyces thermophilus."; Blochim. Biophys. Acta 1353:217-223(1997).
                                                                                                                                              -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
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van Loon A.P.;
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PPAB_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mannhaupt G., Stucka R.; Ehnle S., Vetter I., Feldmann H.; "Analysis of a 70 kb region on the right arm of yeast chromosome II."; Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-87064474; PubMed-3537710;
Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott Q.D.,
Bostian S.J., Thill G.P., Rogers_D.T., Bostian K.A.;
"Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene
"Luster within the acid phosphatase multigene family of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                SEGUENCE FROM N.A., AND SEQUENCE OF 18-26.
MEDLINE-83168913; PubMed-6300772;
Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.;
"The nucleofide sequence of the yeast PHO5 gene: a putative precursor of repressible acid phosphatase contains a signal peptide.";
Nucleic Acids Res. 11:1657-1672(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 18-45.
MEDLINE-85037940; PubMed-6093051;
Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.;
Structural analysis of the two tandemly repeated acid phosphatase denes in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell. Biol. 6:1855-1865(1986).
CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: SECRETED.
INDUCTION: REPRESSED BY INORGANIC PHOSPHATE.
PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                              01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (P60)
421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECF 466
                      416 LYRVLVNDRVVPLHGCAVDKFGRCTLDDWVFGLNFARSGGNWKTCF 461
                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                     467 AA
                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 12:7721-7739(1984).
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                                                                                                                                                                        (Rel. 01, Created)
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PIR; B25241; B25241.
HSSP; P34752; 11HP.
SGD; S0000297; PHO5.
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P00635;
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59 DLPEGCEMKOLOMVGRHGERYPTVSLAKTIKSTWYKLSNYTROFNGSLSFLNDDYEFFIR 118
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                                                                    REPRESSIBLE ACID PHOSPHATASE.
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DC3C9504BC2D3D0C CRC64;
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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 Pfam; PF00128; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
SIGNAL
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D -> Y (IN REF. 1)
A -> G (IN REF. 1)
H -> G (IN REF. 1)
S -> V (IN REF. 1)
                                                                                                      N-LINKED (GLCNAC
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InterPro; IPR000560;
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                                                                                                                                                                                                                                                                                                                                                                                                                        -!- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
-!- PIM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                   STRAIN=S288C / AB972;
MEDLINE=95249563; PubMed=7731988;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Chen J.Y., Gong Y.I., Ao S.Z.;

The primary structure of acid phosphatase gene PHO11 in S.

Cerevisiae and comparison with other gene families.";

Acta Biochim. Biophys. Sin. 21:437-444(1989).

-I. CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN

ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                    Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                              nucleotide sequence of chromosome I from Saccharomyces
                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACID PHOSPHATASE PHO11 PRECURSOR (EC 3.1.3.2) (P56).
                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces
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(GLCNAC...)
(GLCNAC...)
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
SIGNAL 17 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A -> L (IN REF. 2).
VS -> AR (IN REF. 2)
R -> H (IN REF. 2).
K -> Q (IN REF. 2).
D -> G (IN REF. 2).
         467 AA.
                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
N-LINKED
         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L28920; AAC09508.1; -.
EMBL; U19789; AAA73479.1; -.
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   STANDARD;
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75
337
97
162
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InterPro; IPR000560;
                                                                                                                                                                        SEQUENCE FROM N.A.
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354
423
467 AA;
                                                                                    PHO11 OR YAR071W
                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445
                                                                                                                                                                                                                                                Storms R.K.;
   PPAB YEAST
                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                               cerevisiae.
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CARBOHYD
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                                                                                                                                                            84 ARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLK-----TYNYTL-----GADDL 128
                                                                                                                                                                                                    77 ERYPTVSKAKSIMTTWYKLSNYTGQFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
                                                                                                                                                                                                                                            129 TPF-GEQQMVNSGIKFYRRYKALARKIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPG 186
                                                                                                                                                                                                                                                                                                                                                          191 -----FNISLQTISEAESAGANTLSAHHSCPAWDD-DVNDDILKKYDTKYLSGIAK 240
                                                                                                                                                                                                                                                                             187 ANPHQASPVINVII-----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 RLNKENKGLNLTSSDANTFFAWCAYEINAR-----GYSDICNIFTKDELVRFSYGQDLET 295
                                       63; Mismatches 203; Indels 76; Gaps
                                                                             24 PRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHG 83
                                                                                                                                                                                                                                                                                                                                                                                                               242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 YYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSH 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 YYQTGPGYDVVRSVGANLFNASVKLLKESEVQDQ-------KVQTGFTH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 DNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 DIDILNYLITIGIIDDKNNLTAEHVPFMENT--FHRSWYVPQGARVYTEKFQC--SNDTY 393
                                                                                                          21 PLGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDL,PESCEMKQVQMVGRHG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - I- CATALYTIC ACTIVATOR TO THE CONTROL OF ACTD PHOSPHATASE: ONE IS ACCOUNTING THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
- INDUCTION: S.CEREVISIBLE HAS 2 TYPES OF ACTD PHOSPHATASE: ONE IS CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
- I- PIM: GLYCOSYLAYED DURING SECRETION ACROSS THE MEMBRANE.
- I- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Marri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces
16.2%; Score 399; DB 1; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 VRVLVNDRVVPLHGCGVDKLGRCKRDDF-----VEGLSFAR 457
                   Pred. No. 1e-24;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
ACID PHOSPHATASE PHO12 PRECURSOR (EC 3.1.3.2)
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MEDLINE=94378003; PubMed=8091229;
                      26.18;
               Best_Local Similarity 26.1%
Matches 121; Conservative
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P38693;
Query Match
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 NPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSNRCHDTAQYFIDG-----LGDK- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 ANPHQASFVINVII-----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLK------TYNYTL------GADDL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 ERYPTVSKAKSIMTTWYKLSNYTGOFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 PLGKLSDIDKIGTQTEIFPFL----GGSCPYYSFPGDYGISRDLPESCEMKQVOMVGRHG 76
                                                                                                                                                                                                                                                 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                . . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 467;
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26.1%; Pred. No. 1e-24;
tive 63; Mismatches 203; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (PC
BEC606CDF39B845B CRC64;
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                                                                                                                                                              Interior inconstant 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.

Flydrolase; Glycoprotein; Signal; Multigene family.

SIGNAL 18 467

ACID PHOSPHATASE PHOL2.
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                   52699 MW;
                                                                                            EMBL; U00029; AAB69729.1; -.
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75
337
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192
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SGD; S0001258; PHO12.
InterPro; IPR000560;
                                                                                                             S48996; S48996.
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1192
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CARBOHYD
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467 AA.

STANDARD;

PPA3\_YEAST P24031;

A D

PPA3\_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 GGAGPYFSFPGDYGISRDLPEGCEMKQLQMLARHGERYPTYSKGAFIMKTWYKLSNYTRQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.; "Analysis of a 70 kb region on the right arm of yeast chromosome II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A. BEDDILLE SEQUENCE FROM N.A. Hinnen A.; Bajva W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.; Bajva W., Meyhack B., Rudolph H., Schweingruber a.-M., Finnen A.; "Structural analysis of the two tandemly repeated acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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N-LINKED (GLCNAC. . .) (POTEN
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(GLCNAC. . .)
(GLCNAC. . .)
01-WAR-1992 (Rel. 21, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CONSTITUTIVE ACID PHOSPHAŢASE PRECURSOR (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .)
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SGD; S0000296; PH03.
InterPro; IPR000560; Ph03.
Ppfam; PP00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 12:7721-7739(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95208357; PubMed=7900426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 D
52776 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X01080; CAA2557.1; -. EMBL, X78993; CAA55597.1; -. EMBL, Z35961; CAA85045.1; -.
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                                                                                               PHO3 OR YBR092C OR YBR0813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast 10:1363-1381(1994)
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Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                     qenes in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-S288C
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15.0%; Score 370; DB 1; Length 468; 25.1%; Pred. No. 2.2e-22; tive 62; Mismatches 174; Indels 110; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 FKGKYAFLKT-YNYTL------GADDLTPF-GEQOMVNSGIKFYRRYKALAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 YEGSLSFLNNGYEFFIPDESLLEMETTLONSIDVLNPYTGEMNAKRHAREFLAKYGKLME 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 KIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 NCTNFPIFTTNSKRIYDTAQYFAEAL------GDGFNISLQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 ----TLSENSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLENISDRLNDENKGLNLS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 DEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 AQGVGFVN---ELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFF 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 ALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRV 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXARISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
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                      · ) (POTENTIAL)
                                               (POTENTIAL)
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MEDLINE-93371452; Pubmed-7916610;
        | N-LINKED (GLCNAC. . . ) (POT. |
| N-LINKED (GLCNAC. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431 VPLHGCGVDKLGRCKRDDFVE-----GLSFARSGGNWEEC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus niger (ficuum).";
Blochem. Blophys. Res. Commun. 195:53-57(1993).
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53076 MW,
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Matches 116; Conservative
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P34754;
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                                                                          this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFFALGLY--NGTKP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 LSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-----DRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDKGTYVRLVLNEAVLPFNDC 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 SESEVMGADSLIPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLIV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 MCPFDTVARTSDATQĽSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 MASFELNAR-----PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKY-SALIEAIQKNAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 GPYSERVSY----GIARDPPIGCEVDQVINVKRHGERYPSPSAGKSIEEALAKVYSINIT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GEQQMVNSGIKFYRRYKAL--ARKIVPF 157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 VRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 F-SSGYGRVIETARKFGEGF------FG7NYSTNAALNII 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91; Gaps
                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 SLTLLNQGP-----KEAGP------KEAGP------LFFNFAHDTNITPILAALGVLIPNEDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 EYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPF
  FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                        -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 352.5; DB 1; Length 479; 27.9%; Pred. No. 5.9e-21; tive 54; Mismatches 158; Indels 91;
                                                                                                                                                                                                                                                                                      REQUIRED FOR BINDING SUBSTRATE
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . . .)
                                                                                                                                                                                                            Pfan: PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                             3-PHYTASE B.
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52611 MW;
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Matches 117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 DYFVSDAAWYEQETTKGFYSGLNTAFDFGTTLRERYDHLINTSEEGKKL--SVWAGSQER 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 VIASAEKFIEGFOSAKLADPGANPHQASPVINVIIPE---GAGYNNTLDHGLCT----A 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VVDTAKYFAQGFMKSNYTD------MVEVVALEEEKSQGLNSLTARISCPNYNSHI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 FEESELGDDV---EANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 YKDGDFPNDIAERERAD------RLNTLSPGFNITADDIFTIALYGGFELNVRGE- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIE-AIQKNATAFKGKYAFLKTY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 SEI-----ESCTIDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVEVPTGPLSFFQDY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 IILALATLOSVFAVELOHVLGVNDRPYPORT-DDOYNILRHEGGL-GPYIGYNGWGIAAE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -;- CATALYTIC ÀCTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- INDUCTION: BY PHOSPHATE STARVATION.
-:- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GECNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                     MEDLINE-96001238; PubMed-7557473;
Payne W.E., Gannon P.M., Kalser C.A.;
RAn inducible acid phosphatase from the yeast Pichia pastoris:
characterization of the gene and its product.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.2%; Score 350; DB 1; Length 468; 25.4%; Pred. No. 9.1e-21; Live 79; Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE555B8E27718C2C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam: PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
SIGNAL
                              Last sequence update)
Last annotation update)
PRECURSOR (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52690 MW;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
01-0CT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U28658; AAA85503.1; -.
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Matches 125; Conservative
                                                                                                                                                    Pichia pastoris (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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                                                                                       ACID PHOSPHATASE PHO1
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468 AA;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=4922;
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STANDARD;

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275 ATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQD 334
                      279 ----SSFCDVLSREALLYTAYLRDLGWYYNVGNGNPLGKTIGYVXAN----- 321
                                                                  335 HISTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTK-PLSTTSVESIEETD 393
                                                                                                 322 --ATRQLLENTEAD-PRDYPLYFSFSHDTDLLQVFTSLGLFNVTDLPL----DQIQFQT 373
                                                                                                                                                          394 GYAASWTVPFAARAYVEMMQC--EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A., Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.; "The cloning and sequencing of the genes encoding phytase (phy) and PH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-KAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE=99264417; PubMed-10329192;
Kostrewa D., Wyss M., D'Arcy A., van Loon A.P.;
"Crystal structure of Aspergillus niger PH 2.5 acid phosphatase at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.4-A resolution.";
J. Mol. Biol. 288:965-974(1999).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE B) (PH 2.5 OFTIMUM ACID PHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase, Glycoprotein; Signal; 3D-structure.
SIGNAL 1 19 19 V CIMILATION
                                                                                                                                                                                                                                                                                                                                      479 AA.
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                         452 GLSFARSGGNWEE 464
                                                                                                                                                                                                                                          434 RLEALNEDSDFAE 446
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PDB, 1QFX, 19-APR-00.
InterPro, IPR000560, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 133:55-62(1993);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus awamori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=105351;
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P34755:
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                                                                                                                                                                                                                                                                             53 GPYSERVSY----GIARDPPTSCEVDGVIMVKRHGERYPSPSAGKDIEEALAKVYSINTT 108
                                                                                                                                                                                                                                                                                                                  108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GEQQMVNSGIKFYRRYKAL--ARKIVPF 157
                                                                                                                                                                                                                                                                                                                                              109 EYKGDLAFLNDWTYYVPNECYYNAETTSGPYACLLDAYNHGNDYKARYGHLWNGETVVPF 168
                                                                                                                                                                                                                                                                                                                                                                           158 VRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
                                                                                                                                                                                                                                                                                                                                                                                              218 FEESELG------DDVEANFTAVFAPPIR---ARLEAHLPGVNLTDEDVVNLMD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 MASFELNAR-----PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVANA 316
                                                                                                                                                                                                                                    Mismatches 160; Indels 91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 SESEVMGADSLIPTCDIDNDQTITCDNLIYQLPQFKVAAARLNSQNPGMNLIASDVYNLMV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMYSIFFALGLY--NGTKP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 SLTLLNQGPKE------------AGSLFFNFAHDTNITPILAALGVLIPNEDLP 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 L-----DRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 LSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perminan E.;
Thesis (1995), University of Salamanca, Spain.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE (BY SIMILARITY).
-!- PIM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyceties;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                             DB 1; Length 479;
                                                                                                                                                                4F8E0F3778CC3B08 CRC64;
                                                                                                                   N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
                    NUCLEOPHILIC ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
                                                                                                                                                                                                      14.0%; Score 346.5; DB 27.4%; Pred. No. 1.8e-20
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                                     PROTON DONOR.
      3-PHYTASE B.
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                                                                                                                                                             52678 MW;
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298
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   479
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337
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                                                                                                                                                                                                                              Matches 115;
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P52289;
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Best Local s
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453 AA

STANDARD;

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 N-----VTEYSLDQVDFQN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 IQQLSWVTPMGGRIFTEKLKC--GNASYVRYIINDVIIPVPGCTSGPGFSCPIEDFDDYI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 LFSDSNPVFTSSSGRVH--QTAKYVVSSLEEELDIQLDLQIIQENETSGANSLTPADSCM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLT--DEDVVNLMDMCPFDTVARTSD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 TY-NGDLGDEYFENATLPYLTDIKNRWMKKNSNLNLTLEHDDIELLVDWCAFETNVKGSS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 ATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGYGFVNELIARLTHSPVQD 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 YNYTLGADDLTPFGEQOMVNSGIKFYRRY------KALARKIVPFVR---- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 -----NDPLEVFNDYEFFVSNTKYFDQLTNSTDVDFSNPYAGAKTAQHLGKYLAYNYGD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 DESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCF-----PEISHLWGQYSPFFSLA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLSILLGLLSLSGTHAAPISK-----DNGTVCYALNNSTTDESIFSLLNGQGPHYDYP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 GYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF----
                                                                                                                                                                                                                          NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
13.8%; Score 340.5; DB 1; Length 469;
Best Local Similarity 24.6%; Pred. No. 5.3e-20;
Matches 121; Conservative 71; Mismatches 207; Indels 93;
                                                                                                                                                                                                              REPRESSIBLE ACID PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                        863B528D0740AA7E CRC64;
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                                                                                                                                            pfam. PF00328; acid_phosphat; 1.
PROSITE; PS00516; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; wultigene family.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 YSALIEAIQK-----NATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                             "Isolation and characterization of the structural gene for secreted acid phosphatase from Schizosaccharomyces pombe."; J. Biol. Chem. 261:2936-2941(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-86140050; PubMed-3005272;
Elliott S., Chang C., Schweingruber M.E., Schaller J., Rickli E.E.
                                                                                                                                                                                                                                                                                                                                    Rieger M., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
                                                                                                                                                                                                                                                                                                                                                                                                 -: SUBCELLULAR LOCATION: CELL WALL.
-: INDUCTION: REPRESSED BY PHOSPHATE AND WEAKLY BY "THIAMINE.
-: SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 326; DB 1; Length 453; 24.8%; Pred. No. 7.5e-19;
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                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Pungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACID PHOSPHATASE
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                                                     01-OCT-2000 (Rel. 40, Last annotation update)
ACID PHOSPHATASE PREGURSOR (EC 3.1.3.2).
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PROSITE; PS00616; HIS_ACID_PHOSPHAL_2; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAL_2; 1.
HYDROJES; GIYCOPIOTETH, Cell wall; Signal.
                                         Last sequence update)
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                         (Rel. 08, Created)
(Rel. 08, Last sequ
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                                                                                                                                                    Schizosaccharomyces.
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                                                                                                                                                                 NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                  STRAIN=972;
                             01-AUG-1988
                                             01-AUG-1988
PPA1_SCHPO
P08091;
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RESULT 13 PPA1\_SCHPO

| 82<br>143<br>142 | 203 GAGXNNTLDHGLCTAFEESELGDDVEANFTA 195 H           195 TAGSNSLSSYNACPASBADDFTTPALEAWRN 263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQY. : | 255 ICSYEIALQDYSEFCKLFNSVDFLNFEYEGDLSFSYGMGNSVKWGSIFGGAYANS 30 323 LIARLTHSPVQDHTSTNHTLDSNPATFPINATIYADFGHDNTWYGTEGRICTUNGTTTANG | 310 | Y 383 TISVESIEETDGXAASWIVPFAARAYVEMMOCEAEKEPLURVLUNDRVVPLHGCG 437 | PPA2_SCHPO PPA2_SCHPO STANDARD; PRT; 463 AA. | 01-JUL-1993 (Rel. 26, Created)<br>01-JUL-1993 (Rel. 26, Last sequence up |    |       |                | Yang J., Schweingruber M.E.; "The structural gene coding for in Schizosaccharomyces pombe."; |    | Strains 9.72. Lyne M., Rajandream M.A., Barrell B.G., Baker S., Mungall K.; Submitted (Nov-1998) to the EMBL/GenBank/DDBJ dtabases. | -!- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHO<br>-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MOI<br>ALCOHOL: + OPWHODHOGENIAME | -1- SUBJECTION: REPRESSED BY THIAMINE1- SIMILARITY: REPRESSED BY THIAMINE. | This SWISS-PROT entry is converted to the state of the st | between the Swiss Institute of Bioinformatics and the EMBL outstatio the European Bioinformatics Institute of Institute or Institute or Ambar 2000 and the EMBL outstation |       | or send an email to license@isb-sib.ch). | EMBL; X56<br>EMBL; ALC<br>PIR; S141 | InterPro): IPR000560;<br>Pfant: PP00328; acid_phosphat; 1.<br>PROSITE; PS00616; HTS_ACID_PHOSPHAT_1; 1. | PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.<br>Hydrolase; Glycoprotein; Cell wall; Signal. |
|------------------|--|--|-----|---|--|--|----|-------|----------------|--|----|---|--|--|--|--|-------|--|-------------------------------------|---|--|
| Db<br>Qy<br>Db   | Oy<br>Oy   | Db<br>Qy   | qq  | QQ<br>Qp  | PPP.   | 222  | OE | 88888 | RN<br>RY<br>XX | RT<br>RT   | RR | R R B   | 388  | 8888   | ខ្លួ   | ខ្លួ   | ខ្លួន | ပ္ပင္ပ                                   | DR<br>DR                            |   | KW<br>KW   |

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                                                                                                                                                                                                                                                                                                                           51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSS-----KSKKYSALIE---- 100
                                                                                                                                                                                                                                                            Query Match
12.2%; Score 301; DB 1; Length 463;
Best Local Similarity 25.4%; Pred. No. 8.1e-17;
Matches 105; Conservative 66; Mismatches 185; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         101 --AIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRRYKALARKIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                156 PFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPE--GAGYNNTLDHG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 YDINTAAQEKVVDSAEWFSYGM----FGDDMQNKTNF----IVLPEDDSAGANSLAMYY 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 LCTAFEESELGDD-VEANFTA---VFAPPIRARLEAHL-PGVNLTDEDVVNLMDMCPFDT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 VARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGYGFVNELIARLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 ALRDN-----SDFCSLFTPSEFLNFEYDSDLDYAYWGGPASEWASTLGGAYVNNLANNL- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 -----RKGVNNASDRK------VFLAFTHDSQIIPVEAALGFFPDIIPEHPLPTDK 367
                                                                                                                                                                                                                                                                                                                                                NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
                                                               N-LINKED (GLCNAC...) (POTEWITAL).
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Rhabditidae; Peloderinae; Caenorhabditis.
                        THIAMINE-REPRESSIBLE ACID PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matthews P., Lloyd C.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 NIFTYSLKTSSFVPFAGNLITELFLC-SDNKYYVRHLVNQQVYPLTDGGYGFSG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPAX_CAREL STANDARD; PRT; 755 AA. 009549; 017843; 01-NOV-1995 (Rel. 32, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 LADESAISPDVPKGCRVTFVQVLSRHGAR-----YPTSSKSKKYSALIEAIQKNATAFK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 LIDEDVVNLMDMCPFDTVARTSDA--TQLSPFCD-LFTHDEWLQYDYLQSLGKYYG---- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 ---YGAGNP------LGPAQGVGFVNELIARLTHSPVQDHTSTNHTLD-SNPA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GKYAFLKTYNYTLGA---DDLTPFGEQQMVNSGIKFYRRY------KALARKIVPFV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|| :|| :| :| :| :| 372 ------NWTFGGGGLGELTPMGMSEMNNLGTIFRRRXYEDOOFLSHRYAAKBI--YI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 RASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD----- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 RSTNLNRTIISAMSLLYG-----MFPPGA------WNI---QGVDYPNDVDWQQGFTF 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 ----HGL------CTAFEE----SELGDDVEANFTAVFAPPIRARLEAHLPGVN 251
                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
5.4%; Score 134; DB 1; Length 755;
Best Local Similarity 21.9%; Pred. No. 0.0049;
Matches 91; Conservative 56; Mismatches 123; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 TFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPF 403
                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                     E7F3050115A235EB CRC64;
                                                                                                                                                                                                                           Pfam: PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                             EMBL; 247072; CAA87370.1; -
EMBL; 254342; CAA87370.1; JOINED.
EMBL; 254342; CAA91156.1; -
EMBL; 27072; CAA91156.1; JOINED.
WORMPEP; F26C11.1; CE05732.
InterPro; IPR000560; -
                                                                                                                                                                                                                                                                              protein; Hydrolase.
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702 708 B
755 AA; 87783 MW;
                                                                                                                                                                                                                                                                                Hypothetical
ACT_SITE 3
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DISULFID
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Search completed: October 26, 2001, 15:18:02 Job time: 448 sec

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October 26, 2001, 15:18:09; Search time 32.57 Seconds (without alignments) 295.232 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                           1 MGVFVVLLSIATLFGSTSGT......DFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                               197339
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/AA_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/AB_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                197339 seqs, 20590346 residues
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                              Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                Run on:
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|-------------------------------|--|---|
| f                             | Sequence 1, Appli<br>Sequence 2, Appli<br>Sequence 8, Appli<br>Sequence 2, Appli<br>Sequence 20, Appli<br>Sequence 20, Appli<br>Sequence 32, Appli<br>Sequence 32, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 24, Appli<br>Sequence 24, Appli<br>Sequence 24, Appli<br>Sequence 28, Appli<br>Sequence 27, Appli<br>Sequence 28, Appli<br>Sequence 28, Appli<br>Sequence 28, Appli   |   |
| SUMMARIES<br>B ID             | SO CONTRACTOR OF THE CONTRACTO |   |
| %<br>Query<br>Match Length DB | 4410<br>4420<br>4420<br>4420<br>4420<br>4420<br>4420<br>4430<br>4440<br>444  |   |
| %<br>Query<br>Match           | 888 0 7 75 5 5 5 6 7 8 8 8 8 9 9 7 7 5 5 5 5 7 7 7 5 5 5 7 7 7 7 7 7   |   |
| Score                         | 2185<br>2173<br>1866<br>1866<br>1862<br>1862<br>1862<br>1862<br>1862<br>1873<br>1813<br>1395<br>1395<br>1395<br>1395<br>1395<br>1395<br>1395<br>13   |   |
| Result<br>No.                 | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  |   |

|   | ŧ                  | Sequence 4, Appli  | Sequence 32, Appl | Sequence 7, Appli | Sequence 8, Appli | æ                   | 32,                | 10                 | Sequence 10, Appl | 1, 7               | 48,             |                   | 2, 4               | ď               | Sequence 2, Appli | 'n              | 'n.             | Sequence 1, Appli |
|---|--------------------|--------------------|-------------------|-------------------|-------------------|---------------------|--------------------|--------------------|-------------------|--------------------|-----------------|-------------------|--------------------|-----------------|-------------------|-----------------|-----------------|-------------------|
|   | 2 US-08-374-652C-4 | 3 US-08-993-359-32 | 3 US-08-680-506-7 | 3 US-08-680-506-3 | 2 US-08-241-853-8 | 2 US-08-374-6520-22 | 1 US-08-241-853-10 | 2 US-08-850-917-10 | 1 US-08-758-213-1 | 2 US-08-692-787-48 | 4 US-09-040-140 | 2 US-09-146-283-2 | 3 US-08-579-8234-2 | US-09-344-195-2 | US-08-151-574-2   | US-08-419-448-2 | US-09-171-878-1 | H                 |
|   | 479                | 92                 | 44 9<br>9 1 9     | 113               | 113               | 24                  | 113                | 113                | 386               | 386                | 386 4           | 515 2             | 515 3              | 515 4           | . 35 1            | 35 2            | 675 4           |                   |
|   | 14.0               | 7.5                | 70                | 6.4               | 4.9               | 4.7                 | 4.5                | 4.5                | 4.0               | 4.0                | 4.0             | 4.0               | 4.0                | 4.0             | m (               | ω (<br>Ο (      | 3.8             |                   |
| • | 346.5              | 170                | 121.5             | 121               | 121               | 115                 | 110                | 110                | χ, α<br>Σ α       | 20 G               | æ 6             | 800               | 30 c               | y (             | 7 0               | 760             | 0.06            |                   |
|   | 28                 | 3.0                | 31                | 32                | e e               | 4.0                 | 0 0                | 37                 | 200               | 0 0                | n <             | 4 <b>*</b>        | T (                | 7 6             | 7 4               | * V             | 7               |                   |
|   |                    |                    |                   |                   |                   |                     |                    |                    |                   |                    |                 |                   |                    |                 |                   |                 |                 |                   |

# ALIGNMENTS

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                                                  US-07-923-724-8
                                                                                                                                                                                                                                                                                                                                                    STATE:
                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 FCDLFTHDEWIOYDYLOSLGKYYGYGAGNPLGPAQGYGFVNELIARLTHSPYQDHTSTNH 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDWCPFDTVARTSDATQLSP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 KLADPGANPHQASPVIN----------VIIPEGAGYNNTLDHGLCTAFEE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YTLGADDLTPFGEQQWVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SAISPDVPKGGRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.0%; Score 2173; DB 4; Length 467; Best Local Similarity 85.2%; Pred. No. 7.3e-221; Matches 415; Conservative 13; Mismatches 19; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGVEVVLLSIATLEGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGGYSPFFSLADE 60
                             301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:consensus OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                           FILE REFERENCE: consensus phytases 13239
FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER PLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lehmann, Martin
TITLE OF INVENTION: CONSENSUS Phytases
                                                                                                                                                                                                        ; Sequence 2, Application US/09121425
; Patent No. 6153418
                                                                                                                  447 DDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 467
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1 MGVSAVLLPDYLLAGVTSGLAVPASRNOSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.5%; Score 1866; DB 1; Length 467; 74.5%; Pred. No. 1.9e-188; tive 44; Mismatches 75; Indels (
                                                                                                APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Rambosek, John A.
APPLICANT: Remnosek, John A.
APPLICANT: Pagerstr m, Richard B.
APPLICANT: Pagerstr m, Richard B.
APPLICANT: Pagerstr m, Fichard B.
APPLICANT: Pagerstr m, Trichoderma
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                           E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1050.0240004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION NUMBER: UK 8610600
APPLICATION NUMBER: UK 8610600
                                                          APPLICANT: Nevalainen, Helena K.M. APPLICANT: Paloheimo, Marja T. APPLICANT: Miettinen-Oinonen, Arja S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
Sequence 8, Application US/07923724
Patent No. 5780292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cimbala, Michele A. REGISTRATION NUMBER: 33,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 348; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                               GENERAL INFORMATION:
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P-41,264 ER: 1050.0080001

REGISTRATION NUMBER:

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121 YTLGADDLTPFGEGOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFOSA 180
                  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                             241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                        301 KYYGYGAGNPLGPAQĞVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                    361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAVVEMMQCEAEKEP 420
                                                                                                                                                                                                                                                               APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Paldington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Fagerstr M. Richard B.
APPLICANT: Fagerstr M. Richard B.
APPLICANT: Prostor, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes NUMBER OF SEQUENCES:
ADDRESSED.
ADDRESSES:
ADDRESSES.
                                                                                                                                                                                                                                                                                                        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NDATA:
FILING DATE: 01-MAR-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/923,724 FILING DATE: 31-JUL-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/044,077
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08609426A
Patent No. 5830733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UK 8610600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-MAR-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reed, Grant E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Patent No.
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APPLICANT: NEVALAINEN, HELENA K M.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: MIETTINEN-OINONEN, ARJA S.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: BECYDES IN DESIRED RATIOS
CORRESPONDENCES: 94
CORRESPONDENCES: 94
CORRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                              61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                  121 YTLGADDLIPFGEDOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFOSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                            1 MGVSAVLLPLYLLAGVISGLAVPASRNOSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 KYYGYGAGNPLGPAQGYGFVNELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
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                                                                                                                                                                                                                                  Length 467;
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Best Local Similarity 74.5%; Pred. No. 1.9e-188;
Matches 348; Conservative 44; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
REFERENCE/DOCKET NUMBER: 1050
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ IDD NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08374652C
Patent No. 5834286
                                                                                                                                                 , MOLECULE TYPE: protein US-08-609-426A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WASHINGTON
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STREET: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 KYYGYGAGNPLGPAQGYGEVNELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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15.5%; Score 1866; DB 2;
Best Local Similarity 74.5%; Pred. No. 1.9e-188;
Matches 348; Conservative 44; Mismatches 75;
                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1050.071001
                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILLING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                  APPLICATION NUMBER: US/08/374,652C FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                APPLICATION WUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 467 amino acids
                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
USA
                                                                                                                                           FILING DATE:
             20005
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241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATGLSPFCDLFTHDEWIQYDYLGSLG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.4%; Score 1862; DB 1; Length 467; Best Local Similarity 74.5%; Pred. No. 5.2e-188; Matches 348; Conservative 44; Mismatches 75; Indels (
                                                                                                                                               Cloning and Expression of Microbial Phytase
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24615-20026.00
                                                                                                                                                                                                                        ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
                                                     APPLICANT: ROBERT F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORREY-AGENT INFORMATION:
        Sequence 32, Application US/08151574; Patent No. 5436156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 246
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,959
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Murashige, Kate H
REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-151-574-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                               TITLE OF INVENTION: CLC TITLE OF INVENTION: Phy NUMBER OF SEQUENCES: 5: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                               Menlo Park
                                                                                                                                                                                                                                                                                                             94025-3471
                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                COUNTRY:
US-08-151-574-32
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301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                     361 HDNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYYEMMQCEAEKEP 420
                                                                                     61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YTLGADDLTPFGEDQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFGSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLMGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Pest Local Similarity 74.5%; Pred. No. 5.2e-188;
Matches 348; Conservative 44; Mismatches 75; Indels
                                                                                                                               421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: VAN OOLJEN, ALBERT J. j.
APPLICANT: RETYPELD, KRIJN
APPLICANT: PEN, JAN
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/146,424
GIASCHERON DATE: US/08/146,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44615-20011.24
                                                                                                                                                                                                                                               Sequence 20, Application US/08146424
Patent No. 5593963
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: KENNEDY, BILL
REGESTRATION NUMBER: 33,407
REFRENCE/CDCKET NUMBER: 4461:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
mptry. 7,615) 494-0792
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INFORMATION FOR SEQ ID NO: 20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1018
COMPUTER READABLE FORM:
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California
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181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                           241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLOSLG 300
                                                                                                               301 KYYGYGAGNPLGPAQGYGFVNELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLXADFS 360
                                                                                                                                                                      361 HDNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                            421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                   APPLICANT: PEN JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
APPLICATION DATA:
APPLICATION NUMBER: US/08/693,709
FILING DATE: 07-AUG-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24615-20011.10
                                                                                                                                                                                                                                                                                                                                                                                                                VAN OOLJEN, ALBERT J.J. RIETVELD, KRIJN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08693709
Patent No. 5770413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 2461:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                            HOEKEMA, ANDREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 amino acids
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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internal
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palo Alto
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MOLECULE TYPE:
FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
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Sequence 32, Application US/08419448
Sequence 32, Application US/08419448
Sequence 32, Application US/08419448
SEQUENCE OF US O
                                                                                                                                         75.4%; Score 1862; DB 1; Length 467; 74.5%; Pred. No. 5.2e-188; Indels (tive 44; Mismatches 75; Indels (
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2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
NAME/KEY: Signal Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                       Best Local Similarity 74.5%
Matches 348; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                         LOCATION: 1 ...23
CTHER INFORMATION:
US-08-693-709-2
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ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
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                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                           Query Match 75.4%; Score 1862; DB 2; Length 467; Best Local Similarity 74.5%; Pred No. 5.2e-188; Matches 348; Conservative 44; Mismatches 75; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Rly, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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; Patent No. 5866118
                       ATTORNEY/AGENT INFORMATION:
NAME: MURAShigo, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24f
TELECOMMUNICATION INFORMATION:
                                                                                                           TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
FILING DATE: 10-APR-1995
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
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10174-6401
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                                                                                                                                                                                               Linear
               CLASSIFICATION:
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                                                                                                                                                                                             TOPOLOGY:
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single
                                                           : New York
RY: U.S.A.
10174-6401
                                                                                                                                       OPERATING SYSTEM:
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                                 STREET: 405 Le,
CITY: New York
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                      ADDRESSEE:
                                                                                                                          COMPUTER:
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                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.4%; Score 1862; DB 2; Length 467; 74.5%; Pred. No. 5.2e-188; ative 44; Mismatches 75; Indels
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APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825

FILING DATE: 18-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INCORMATION:
REGISTRATION NUMBER: 33,728
                                                                                                                                                4758.200-US
                                                                                                                                  REFERENCE/DOCKET NUMBER: 475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPAX: 212 867 0298
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Patent No. 6221644
GENERAL INFORMATION:
                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3;
               IBM Compatible
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                single
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CORRESPONDENCE ADDRESS:
                COMPUTER: LEM COM
OPERATING SYSTEM:
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Best Local Similarity
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No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAVVEMMQCEAEKEP 420
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75.4%; Score 1862; DB 4; Length 467;
Best Local Similarity 74.5%; Pred. No. 5.2e-188;
Matches 348; Conservative 44; Mismatches 75; Indels (
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                                                                                                                                                   SUFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILING DATE:
              405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                              4758.200-US
                                                                                                                                                                                                                       CLASSIFICATION:
PRION APPLICATION:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18 WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 475
TELECOMMUNICATION INFORMATION: 72LEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                           467 amino acids
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-09-155-855-3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                  APPLICANT: ANAZAWA, Hideharu
APPLICANT: RANEKO, Syunichi
APPLICANT: RANEKO, Syunichi
APPLICANT: RANEKO, Syunichi
APPLICANT: NAGASHIRA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REPERENCE: 81356/124
CURRENT ELILING DATE: 1998-10-05
CURRENT FILING DATE: 1998-10-05
EARLIER PILING DATE: 1997-04-04
EARLIER PILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTHARE: PALCATION NOS: 7
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APPLICANT: ANASAHAM, Tadashi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.1%; Score 1855; DB 4; Length 467; Best Local Similarity 73.4%; Pred. No. 2.8e-187; Matches 343; Conservative 51; Mismatches 73; Indels Cartes 1865; DB 4; Length 467; Pred. No. 2.8e-187; Redels Cartes 1865; DB 4; Length 467; Pred. No. 2.8e-187; Lindels Cartes 1865; DB 4; Length 467; Pred. No. 2.8e-187; Pred. No
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Sequence 3, Application US/09155855 Patent No. 6139902
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APPLICANT: KONDO, Hidemasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Aspergillus niger
US-09-155-855-3
                                                                                GENERAL INFORMATION:
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327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
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                                                                                                                                                                                                                                                                                                                    Gaps
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APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 8136/124
CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DAME: 1998-10-05
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                               73.4%; Score 1813; DB 4; Length 443; 75.1%; Pred. No. 7.1e-183; tive 49; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER APPLICATION NUMBER: JP 084314
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
FILE REFERENCE: 81356/124
CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER PILING DATE: 1996-04-05
NUMBER: OF SEQ ID NOS: 7
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; Patent No. 6139902
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US-09-155-855-1
                                                                                                                                                                                                                                                                                                             Best Local Similarity 75.1%
Matches 331; Conservative
                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
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US-09-155-855-2
                                                                                                                                                                                          ENGTH: 443
                                                                                                                                                                                                             TYPE: PRT
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                                                                        ; OTHER INFORMATION: Xaa at positions 2 & 3 may be any amino acid or unknown
US-09-155-855-2
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                                                                                                                                                                                                                                                              90 SKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRKA 149
                                                                                                                                                                                                                                                                                150 LARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 SPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESI 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 SCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTS 89
                                                                                                                                                                                                                   Query Match
Pest Local Similarity 75.3%; Pred. No. 2.4e-182;
Matches 330; Conservative 49; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURTINARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 Lexington Avenue, Suite 6400
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Patent No. 5866118
                                          ORGANISM: Aspergillus niger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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SEQ ID NO 2
                               TYPE: PRT
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58 ADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLK 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 QSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVE-ANFTAVFA 236
                                                                                                                                                                                                                                                                                                                                                 Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 PPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDAT----QLSPFCDLFTHDEWIQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 PRVLKKITKHMPGVNLTLEDVPLFMDLCPFDTVG--SDPVLFPRQLSPFCHLFTADDWMA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 YDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLT-HSPVQDHTSTNHTLDSNPATFPL 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 EMMQC------EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSG 459
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409 ELLRCETETSSEEEEEGEDEPFVRVLVNDRVVPLHGCRVDRWGRCRRDEWIKGLTFARQG 468
                                                                                                                                                                                                                                                                                                                                                                       1 MGVF-VVLLSIATLFGSTSGTALGP--RGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSL 57
                                                                                                                                                                                                                                                                                                                                                                                                       6 LGSFLVLLLQFSALL--TASPAIPPFWRKKHPNVD-----IARHWGQYSPFFSL 52
                                                                                                                                                                                                                                                                                                 Ouery Match 56.5%; Score 1395; DB 2; 1
Best Local Similarity 58.5%; Pred. No. 1.1e-138;
Matches 285; Conservative 59; Mismatches 105;
                                                       4758.200-US
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                NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
                                              REFERENCE/DOCKET NUMBER: 475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 028
INFORMATION FOR SEQ ID NO: 2:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     475 amino acids
                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                        single
                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                         linear
                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                 LENGTH:
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OM protein - protein search, using sw model

Run on:

October 26, 2001, 15:17:29 ; Search time 57.24 Seconds

(without alignments) 494.609 Million cell updates/sec

US-09-488-265-26 2470 Title: Perfect score:

1 MGVEVVLLSIATLFGSTSGT........DFVEGLSFARSGGNWEECFA 467 Sequence:

Scoring table:

412676 seqs, 60623988 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 . Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDSI/gcgdata/geneseq/geneseqp/AA1990.DAT:
| SIDSI/gcgdata/geneseqcyeneseqp/AA1991.DAT:
| SIDSI/gcgdata/geneseqcyeneseqp/AA1991.DAT:
| SIDSI/gcgdata/geneseqcyeneseqp/AA1992.DAT:
| SIDSI/gcgdata/geneseqcyeneseqp/AA1993.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description              | Consensus phytase-Phytase-D, a cons Consensus phytase-Consensus phytase-Mutant phytase-Donsensus phytase-Consensus phytase- |
|-----------|--------------------------|---|
| SUMMARIES | ID                       | AAB20524<br>AAV69566<br>AAY63170<br>AAB20527<br>AAB20533<br>AAB20534<br>AAB20531<br>AAB20533<br>AAB20533<br>AAB20533<br>AAB20533  |
|           | DB                       | 21<br>21<br>21<br>21<br>21<br>21<br>21<br>21  |
| 8.        | Query<br>Match Length DB | 4667<br>4667<br>4667<br>4667<br>4667<br>4667<br>4667<br>461   |
| æ         | Query<br>Match           | 1000.0<br>99.1<br>99.1<br>98.9<br>98.9<br>98.6<br>95.3<br>94.9  |
|           | Score                    | 2470<br>2448<br>2448<br>2448<br>2442<br>2442<br>2343<br>2347<br>2344  |
|           | Result<br>No.            | 10<br>10<br>11<br>11  |

|         | sus phyt | phytase | phy     | isus phy | Pnytase-1, a conse | Fungal consensus p | Consensus | Changanon | 9 +   | icere conse | onsensus | nseusans | phy     | 'n   | Consensus phytase- | Phytase-7. a deriv | , 01    | Conscisses piny case |         | <u>.</u> | Phytase-11, a cons | Consensus phytase | Initial consensus |          |        | Mutant Aspergillus | A. fumigatus phyta |         | Mutant Aspergillus | Asperdillie fumica | A finiteting running | Acception program | Aspergillus rumiga | rn3     | m       | ns.  | Aspergillus fumiga |
|---------|----------|---------|---------|----------|--------------------|--------------------|-----------|-----------|-------|-------------|----------|----------|---------|------|--------------------|--------------------|---------|----------------------|---------|----------|--------------------|-------------------|-------------------|----------|--------|--------------------|--------------------|---------|--------------------|--------------------|----------------------|-------------------|--------------------|---------|---------|------|--------------------|
| AAB2052 | AAY695   | AAWG338 | AAROOS1 | AAVAGSS  | OCCOUNT A          | AAWYSSB            | AAMA3     | AAW93     | AAY39 | AAWG3       | AAWG3    | AABOORA  | CC02000 |      | 110900             | AAY6957            | AAB2052 | AAB2051              | AAB2052 | AAVAGE   | AAROOFS            | AAVAGEE           | 0000000           | AABZU335 | CECTOR | 7060144            |                    | AAB2052 | AAY6957            |                    | AAY3990              | AAY6954           | AAR205             | AAVAGES | AAROOFO | 2000 | AATOYSS            |
|         |          |         |         |          |                    |                    |           |           |       |             |          |          |         |      |                    |                    |         |                      |         |          |                    |                   |                   | 170      |        |                    |                    |         |                    |                    |                      | 21                | 21                 | 21      | 15      | 1 5  | 7                  |
| 467     | 467      | 467     | 467     | 467      | 167                | 7 7                | 407       |           |       | 467         |          |          | 167     |      |                    |                    | 467     |                      | 437     | 437      |                    | , (*              | , (               | 424      | ľ      | V                  | οv                 | ט כ     | ο ,                | 9                  | 465                  | 440               | 4                  | 4       |         | ٠,   |                    |
| 94      | 94       | 93      | 93      | 93       | 6                  | 0 0                | ח כ       | 25        | 93    | 8           | 92       | 92       | 93      | 0    | o                  | 0 0                | 9       | 88                   | 85      | 8        | 83                 | 83                | ά                 | 83.0     | 82     | c                  | , c                | 3 0     | 9 1                | : :                | •                    | •                 |                    |         |         |      |                    |
| 2342    | 2342     | 2311    | 2311    | 2311     | 2305               | 2304               | ***       | 2304      | 2301  | 2296        | 2295     | 2291     | 2291    | 2204 | 2204               | 1000               | -T077   | 2185                 | 2115    | 2115     | 2066               | 2066              | 2050.5            | 2050.5   | 2048   | 2028               | 2028               | 2028    |                    | 1907               | 5                    | 892.              | 889.               | σ.      | 884.    | 884  |                    |
| 12      | 13       | 14      | 15      | 16       | 17                 | 2                  | 9 0       | H (       | 07    | 21          | 22       | 23       | 24      | 25   | 26                 | 0 0                | 7 0     | 87                   | 29      | 30       | 31                 | 32                | 33                | 34       | 35     | 36                 | 37                 | 80      | 30                 | n c                | 04                   | 41                | 42                 | 43      | 44      | 45   |                    |

### ALIGNMENTS

AAB20524 standard; Protein; 467 AA AAB20524

AAB20524;

05-DEC-2000 (first entry)

Consensus phytase 10 SEQ ID NO:26.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure. 

Synthetic.

WO200043503-A1.

27-JUL-2000.

21-JAN-2000; 2000WO-DK00025.

99DK-0000092. 99DK-0001340. 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS.

Lehmann M;

WPI; 2000-491161/43. N-PSDB; AAA73232

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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaccutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
                                                                                                             Claim 1; Fig 5a-c; 240pp; English.
                                                             compound foods and feeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60 0; Gaps 100.0%; Score 2470; DB 21; Length 467; 100.0%; Pred. No. 3.5e-240; Live 0; Mismatches 0; Indels 0; Matches 467; Conservative Best Local Similarity

ó;

121 YTLGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180 61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120 g g φŽ g Ω

241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300 δŽ οp οy

301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360 Ωp δλ g

ŏ Db

421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467 δλ g

AAY69566 standard; protein; 467 AA. AAY69566; AAY69566 RESULT

19-APR-2000 (first entry)

Phytase-10, a consensus phytase.

phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; phytase-10. 

//note= "phytase signal peptide from Aspergillus terreus cbs16.46" /note= "Mature phytase-10 consensus" Location/Qualifiers Emericella nidulans.
Talaromyces thermophilus ATCC20186.
Myceliophthora thermophila.
Paxillus involutus NN005693. Aspergillus fumigatus ATCC32722. Aspergillus fumigatus ATCC58128. Aspergillus fumigatus ATCC56906. Aspergillus terreus cbs16.46.
Aspergillus niger var. awamori.
Aspergillus niger str. NRR13135.
Aspergillus fumigatus ATCC13073. Aspergillus fumigatus ATCC32239 terreus cbs16.46. Agrocybe pediades NN009289. Peniophora lycii NN006113. Trametes pubescens NN9343. 27 . . 467 terreus 9A1 Thermomyces lanuginosa Synthetic. Peptide Protein 

EP969089-A1

05-JAN-2000.

99EP-0111949. 23-JUN-1999; 98EP-0111960. 29-JUN-1998;

(HOFF ) HOFFMANN LA ROCHE & CO AG F.

Brugger R, Lehmann M, Wyss M;

WPI; 2000-099429/09. N-PSDB; AAZ59642. New stabilized enzyme formulation, useful for feed compositions for monogastric animals

Example 4; Fig 17; 101pp; English.

The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate formulation, comprising phytase (myo-inositol hexakisphosphate formulation) and one or more stabilising agents including to phosphohydrolase) and one or more stabilising agents including for phosphohydrolase) and social carboxymethylosing with a molecular weight of 600 cy 4000 Da, preferrably 1000 to 3550 Da; the disodium salts of malonic, to 4000 Da, preferrably carboxymethylosilulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal companies to the feed of such animals. Phytase enhances the nutritional phosphate to the feed of such animals. Phytase enhances the nutritional cy value of plant material without the need for adding additional phosphate could be considered from phytase phosphorus using the cauched by adding phytase to animal feed, as the animal can make use of thermostability and can therefore remain stable during long-term storage and may the man make use of thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents a consensus sequence, designated phytase-10, which was derived from the mature phytase sequences from a variety of fungi (AAY69544-Y69554, AAY69564) and the Basidiomycetes phytase consensus AAY69563 and additionally contains the Aspergillus terreus obsilé.46 signal peptide at the N-terminus.

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                                        Gaps
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                                                         KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
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                                                                                                                                                                                                                                                                                                                      Consensus phytase-10-thermo(3)-Q50T-K91A protein sequence.
                                       Indels
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                          DB 21;
                         100.0%; Score 2470; DB 21; 100.0%; Pred. No. 3.5e-240;
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                                       Mismatches
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467; Conservative
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18-SEP-1998;
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This sequence represents the consensus phytase-10-thermo(3)-050T-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytase) simultaneously.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2448; DB 20;
Pred. No. 5.9e-238;
2; Mismatches 3;
                                                       Example 3; Fig 10; 71pp; English
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98.9%;
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Matches 462; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -
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Pred. No. 5.9e-238;
2; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 8a-c; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.1%;
Best Local Similarity 98.9%;
Matches 462; Conservative 5
                                                                                                                                                        99DK-0000092.
99DK-0001340.
                                                                                                     21-JAN-2000; 2000WO-DK00025
                                                                                                                                                                                                                                             (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-491161/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467 AA;
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA73234.
WO200043503-A1
                                                                                                                                                        22-JAN-1999;
21-SEP-1999;
                                                     27-JUL-2000.
                                                                                                                                                                                                                                                                                                   Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Phytase signal peptide from Aspergillus terreus cbs16.46"
                                                                                                                                                                                                         Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Mature phytase-10-thermo[3]-Q50T-K91A"
Mutant phytase-10, phytase-10-thermo[3]-Q50T-K91A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         Talaromyces thermophilus ATCC20186. Myceliophthora thermophila.
                                                                                        AAY69569 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 19; 101pp; English.
                                                                                                                                                                                                                                                                                                       Aspergillus niger var. awamori.
Aspergillus niger str. NRRL3135.
Aspergillus fumigatus ATCC13073.
                                                                                                                                                                                                                                                                                                                                                  Aspergillus fumigatus ATCC32722.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC26906.
                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus fumigatus ATCC32239
Emericella nidulans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wyss M;
                                                                                                                                                                                                                                                                          Aspergillus terreus 9Al.
Aspergillus terreus cbs16.46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paxillus involutus NN005693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrocybe pediades NN009289.
Peniophora lycii NN006113.
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trametes pubescens NN9343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brugger R, Lehmann M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermomyces lanuginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monogastric animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1999;
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                                                                                                                                                   19-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                       AAY69569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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              421
                                                                          AAY69569
                                                            RESULT
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teed in the form of phytate phosphorus, monogastric animals are unable to tuilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved the inorganic phosphate liberated from phytate phosphorus using the and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents a mutant phytase-10 consensus sequence, phytase-10-thermo[3]-050T-K91A, which has a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAX69566). Its specific activity with phytate as a substrate is also strongly increased.
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467 AA; Sequence

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                                                                                                                    121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                     181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                                                                                                                                       61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                           ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                       KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                               361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE, 60
                                                                 DB 21; Length 467;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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99.1%; Score 244%; DB 21;
98.9%; Pred. No. 5.9e-238;
tive 2; Mismatches 3;
             Best Local Similarity 98.9
Matches 462; Conservative
 Query Match
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Consensus phytase 10 thermo 5 Q50T protein SEQ ID NO:95.
            AAB20533 standard; Protein; 467
                                       05-DEC-2000 (first:entry)
                         AAB20533;
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RESULT
AAB20533
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Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;

Synthetic.

food; feed; phytate; manure

421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467

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increased thermosteability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate and phytases and/or for the phytases and constitutions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
                                                                                                                                                                                                                                                        Novel phytases with improved properties such as temperature stability, \rho H stability and substrate specificity, for use in pharmaceuticals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                   The present invention describes improved phytases, preferably with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.9%; Score 2442; DB 21;
98.7%; Pred. No. 2.4e-237;
ive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 24a-c; 240pp; English,
                                                                                                                    99DK-0001340.
                                                                         21-JAN-2000; 2000WO-DK00025
                                                                                                                                                                                                                                                                                        compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461; Conservative
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                                                                                                                                                                                                            WPI; 2000-491161/43.
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              WO200043503-A1
                                                                                                                    21-SEP-1999;
                                                                                                    22-JAN-1999;
                                           27-JUL-2000
                                                                                                                                                                                Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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YILGADDLIPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180

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                                                                                                                                                                                                                                                                                                                                                                      Phytase; mutant: thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as temperature stability, for use in pharmaceuticals and
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Pred. No. 9.5e-237;
2; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                              Consensus phytase 10 thermo 5 Q50T K91A protein SEQ ID NO:97
es with improved properties and substrate specificity,
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                                                                                                                                                                          AAB20534 standard; Protein; 467
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98.5%;
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Best Local Similarity
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                                                                                                                                               AAB20534
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and evel of released phosphate. The phytases can be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       temperature stability, in pharmaceuticals and
181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                        240
                                                                                                      241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                         301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                     361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                               LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                           Consensus phytase 3 thermo 11 Q50T protein SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel phytases with improved properties such as pH stability and substrate specificity, for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 22a-c; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AAB20531 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         food; feed; phytate; manure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99DK-0001340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compound foods and feeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-491161/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA73290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB20531;
                                                                                                                                                                                                                                                                                                                                                                                       AAB20531
                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                    Db
                                                                                                                                                                                               Pp
                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                              QQ
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                                           δy
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pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower institol phosphates and/or insoitol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                                                                                                                               SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                             61 saispdvpkdcrvtfvqvlsrhgaryptsskskaysalieaiqknatafkgkyaflktyn 120
                                                                                                                                                                                                                                                                                 121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                       Gaps
                                                                                                                                                                       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE
                                                                                                                                                                                        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
                                                                                                                                                                                                                                                                                                                                                                                           241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                       95.3%; Score 2353; DB 21; Length 467; 94.9%; Pred. No. 2.2e-228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus phytase 3 thermo 11 Q50T K91A protein SEQ ID NO:93.
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB20532 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                food; feed; phytate; manure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99DK-0000092.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2000 (first entry)
                                                                                                                                              Matches 443; Conservative
                                                                                                                                 Best Local Similarity
                                                                               467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200043503-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-1999;
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                                                       invention
                                                                                Sequence
                                                                                                                      Query Match
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AAB20532
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, phymaceautical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
                                                                                                    Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFOSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 2347; DB 21; 94.6%; Pred. No. 8.9e-228; 1ve 10; Mismatches 15;
                                                                                                                      pH stability and substrate specificity, compound foods and feeds -
                                                                                                                                                                  Disclosure; Fig 23a-c; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20523 standard; Protein; 441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 94.6
Matches 442; Conservative
(NOVO ) NOVO NORDISK AS
                                                           2000-491161/43.
                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA;
                                                                           N-PSDB; AAA73291
                              Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. can be used for producing phytases with improved properties e.g. specific activity, substrate specificity, temperature profile, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -
                                                            Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 PTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 DTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes improved phytases, preferably with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 NSHSCDTVDGGYQCFPEISHLMGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 YKALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.9%; Score 2344; DB 21; Length 441; 100.0%; Pred. No. 1.6e-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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0
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                             Consensus phytase 10 (Fcp10) SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 4a-d; 240pp; English.
                                                                                                                                                                                                                                                                                                                99DK-0000092.
                                                                                                                                         food; feed; phytate; manure.
                                                                                                                                                                                                                                                                             21-JAN-2000; 2000WO-DK00025.
05-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 441; Conservative
                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-491161/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 AA;
                                                                                                                                                                                                                                                                                                                22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                21-SEP-1999;
                                                                                                                                                                                                                                              27-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                    Cehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Gaps 86

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                                                                                                                                                                                                                                                                                                         Phytase; animal feed preparation; thermostable phytase; transgenic plant;
              LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
                                                   ESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                               Consensus phytase-1-thermo(8)-050T-K91A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparing animal feed using a thermostable phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.8%; Score 2342; DB 20;
94.4%; Pred. No. 2.8e-227;
ive 10; Mismatches 16;
                                                                                                                                                                                                    AAY43169 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 9; 71pp; English.
                                                                                                         447 DDFVEGLSFARSGGNWEECFA 467
                                                                                                                       421 ddfveglsfarsggnweecfa 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98DK-0000806.
98DK-0001176.
                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-DK00154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99DK-0000093
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hes 441; Conservative
                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                         consensus sequence.
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                                                                                                                                                                                                                                                                                                                                                                             WO9948380-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1999;
                                                                                                                                                                                                                                                         06-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petersen S;
                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                             AAY43169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                      387
  327
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SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
            121 YTLGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                         240
                                                                                               300
                                                                                                                                        KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                          241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
                                                                                  KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
                                                                                                                                                                                  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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AAB20526 standard; Protein; 467 AA.

AAB20526:

(first entry) 05-DEC-2000

Consensus phytase 1 thermo 8 q50t, k91a protein SEQ ID NO:29.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

Synthetic.

WO200043503-A1.

27-JUL-2000.

21-JAN-2000; 2000WO-DK00025

99DK-0001340. 99DK-0000092 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS.

Lehmann M;

2000-491161/43. N-PSDB; AAA73233 Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and pH stablilly and compound foods and feeds

Claim 5; Fig 7a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, 

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specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce by phramecutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manuer, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus;
                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                                                                                                                                                                                                                                                                                                      SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                      61 salspdvpddcrvtfvqvlsrhgaryptssaskaysalleaiqknatafkgkyaflktyn 120
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                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                         301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
                                                                                                                                                                                                                      94.8%; Score 2342; DB 21; Length 467; 94.4%; Pred. No. 2.8e-227; Live 10; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate availibility; consensus; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
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Aspergillus niger var. awamori.
Aspergillus niger str. NRL3135,
Aspergillus fumigatus ATCC13073,
Aspergillus fumigatus ATCC13073,
Aspergillus fumigatus ATCC32722,
Aspergillus fumigatus ATCC32722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY69568 standard; protein; 467
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                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                     467 AA;
                                                                                                                                                                                                                                                       441;
                                                                                                                                       invention.
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formulation, comprising phytase (myo-inositol hexakisphosphate phospholydrolase) and one or more stabilising agents including the phospholydrolase) and one or more stabilising agents including composition to the phospholydrolase; and one or more stabilising agents including to xylitol or ribitol; polyethylene glycols with a molecular weight of 600 (cc. 4000 Da. preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and propaborus. Although a large amount of phosphate is present in animal phosphate. This form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional phosphate to the feed of such animals. Phytase enhances the nutritional cc value of plant material without the need for adding additional phosphate cc to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the caryme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence remain stable during long-term storage consensus sequence, phytase-1-thermo[8]-500T-K91A, which has a consensus copingment phytase-1 (approxes Celsius higher than that con phytase-1 (approxes Celsius higher than that
                                                                                                                                                         /note= "Phytase signal peptide from Aspergillus terreus cbs16.46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                      /note= "Mature phytase-1-thermo[8]-Q50T-K91A"
                                                                                                                                                                                                                                                                                                                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                    Location/Qualifiers
                                  Talaromyces thermophilus ATCC20186. Myceliophthora thermophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 19; 101pp; English.
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Aspergillus fumigatus ATCC32239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monogastric animals .
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                       Emericella nidulans.
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                                                                                                                                                                                                                                                                                                                                                  23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brugger R,
                                                                                  Synthetic
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                                                                                                                                              Peptide
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; 0 61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120 Gaps 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60 .; 94.8%; Score 2342; DB 21; Length 467; 94.4%; Prcd. No. 2.8e-227; ive 10; Mismatches 16; Indels 0; 441; Conservative Best Local Similarity Query Match Matches g g ŏ δŽ

467 AA;

Sequence

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This invention describes a novel process for the preparation of a consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or pharmaceutical compositions. This sequence represents the consensus phytase protein used in the method of the invention.
                                                                                                                              241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                                                                     KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                   361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                            121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical.
                                                       181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preparation of a consensus protein, especially a phytase - using programs to compare evolutionary similarity of sequences
                                                                                                                                                                                                                                                                                      421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                      Fungal phytase protein consensus DNA.
                                                                                                                                                                                                                                                                                                                                                                                        AAW93380 standard; Protein; 467 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 2; 30pp; English.
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                                                                                                                                                                                               ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
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                                          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
                             .
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       Length 467;
                            Indels
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93.1%; Pred. No. 3.8e-224;
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AAB20515 standard; Protein; 467 AA. 05-DEC-2000 (first entry) AAB20515; RESULT 15 AAB20515 ID AAB2 

Consensus phytase SEQ ID NO:16.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure

Synthetic.

WO200043503-A1.

27-JUL-2000.

21-JAN-2000; 2000WO-DK00025.

Search completed: October 26, 2001, 16:40:03

Job time: 4954 sec

99DK-0001340 99DK-0000092 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK

Lehmann M;

WPI; 2000-491161/43.

N-PSDB; AAA73231

Novel phytases with improved properties such as temperature stability,

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                                                                               The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce harmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
 pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALLEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YTLGADDLIPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.6%; Score 2311; DB 21;
Best Local Similarity 93.1%; Pred. No. 3.8e-224;
Matches 435; Conservative 13; Mismatches 19;
                                                   Example 9; Fig 2a-c; 240pp; English.
                                                                                                                                                                                                                                                                                                                                         467 AA;
                                                                                                                                                                                                                                                                                                         invention.
                                                                                                                                                                                                                                                                                                                                           Sequence
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2001, 14:11:09; Search time 75.85 Seconds (Without alignments) 814.587 Million cell updates/sec Run on:

US-09-488-265-26 2470 Title: Perfect score:

1 MGVFVVLLSIATLFGSTSGT........DFVEGLSFARSGGNWEECFA 467 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

425026 seqs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_16:\*
: sp\_archea:\*
: sp\_bacteria:\*

Sp\_fungi:\*
Sp\_human:\*

sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_vertebrate:\* sp\_virus:\* sp\_organelle:\* sp\_plant:\* sp\_rodent:\* sp\_phage:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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|-----------|--------|-----------------|-------|------------------|--------|--------|--------|--------|--------|--------|--------------------|-------|--------------------|--------|------------------|--------------------|--------------------|--------------------|---|--------------------|--------------------|--------------------|--------------------|--|
| SUMMARIES |        | ID              | 00000 | 090027           | 093838 | 09HE00 | 000100 | 000085 | 960000 | 000107 | 00VBA60            | 110   | 0/40//             | 060172 | Q9VV72           | 035217             | 096421             | 092216             |   | 7/1660             | O9UNW1             | 09UGA3             | 092170             |  |
|           |        | DB              | ٣     | m                | m      | m      | m      | m      | ~      | ~      | . ~                | ٦ (   | n (                | m      | 'n               | 11                 | Ŋ                  | -                  |   | 7"                 | 4                  | 4                  | 13                 |  |
| ٠         |        | Match Length DB | 465   | 467              | 467    | 467    | 466    | 466    | 466    | 487    | 469                |       | 7 7 7              | 463    | ·460             | 451                | 467                | 481                | 1 0   | 407                | 487                | 487                | 449                |  |
| ď         | Query  | Match           | 77.0  | 75.3             | 75.1   | 74.6   | 73.9   | 71.1   | 9.69   | 54.5   | 13.9               |       | 100                | 77.7   | 9.8              | 8 3                | 8.3                | 7.9                | 7   |                    | 6.7                | 7.8                | 7.2                |  |
|           |        | Score           | 1902  | 1861             | 1855   | 1842   | 1826   | 1756   | 1719   | 1346.5 | 343.5              | 333 5 | , ,                | TOS    | 212.5            | 204                | 204                | 196                | 105   | 0 0                | 194                | 192                | 179                |  |
|           | Result | . i             | н     | 2                | က      | 4      | 5      | 9      | 7      | 8      | 6                  | 10    | 9 -                | 7,     | 12               | 13                 | 14                 | 15                 | 16  | 7 -                | / T                | 18                 | 19                 |  |

| 096420 drosophila 09w438 drosophila 09utx1 schizosacch 004509 arabidopsis 09jid5 mus musculu 099x95 mus musculu 09yx95 mus musculu 09yx95 mus musculu 046334 commonas t 022525 caenorhabdi 047871 eubbacterium 09xx77 mus musculu 090x91 leishmania 000839 leishmania 000839 leishmania 024719 comamonas t 019709 caenorhabdi |  |
|---|--|
|   |  |
| 096420<br>09W438<br>09UTX1<br>004509<br>019076<br>09JMG5<br>040831<br>000839<br>000839  | Q20826<br>P87212<br>O34184<br>Q915U0<br>Q9U5U0<br>Q9U5TB<br>Q9U5TB<br>Q9U5TB |
| _   | v w 1 1 1 v v v v v v v v v v v v v v v                                      |
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| 176.5<br>175.5<br>167.5<br>167.5<br>128.5<br>128.5<br>119.5<br>110.5<br>110.5<br>100.5<br>100.5   | 106.5<br>103.5<br>102.5<br>101.5<br>101.5<br>101.5<br>101.5                  |
| 01000000000000000000000000000000000000  | 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                      |
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## ALIGNMENTS

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Gaps

us-09-488-265-26.rspt

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                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
MYO-INOSITOL HEXAPHOSPHATE PHOSPHOHYDROLYASE PRECURSOR (EC 3.1.3.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
                          SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                              BY SIMILARITY.
CHOTSWITCH.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Honganing W., Oi W., Jing X.; Honganing W., Oi W., Jing X.; "PCR, cloning and characterization of the phytase (phyA) gene of . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-PHYTASE A.
REQUIRED FOR BINDING SUBSTRATE (BY
                                                                                                                                                                                                                                                                             Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Indels
                                                                                                                                                                                                                                     86FC1D9058C9B2C9 CRC64;
                                                                                                                                                                                                                                                                              77.0%; Score 1902; DB 3;
77.1%; Pred. No. 2.5e-147;
trive 37; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 AA.
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Matches 360; Conserv
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262
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337
350
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81
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DISULFID
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301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                        Length 467;
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"Phytase having high-affinity for phytic acid.";
Submitted (JAN.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB092700; CAB19824.1; -.
HSSP, P34752; 11HP.
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus niger (China Strain).";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF218813; AAF25481.1; -.
HSSP; P34752; IIHP.
                                                                                                                                                SEQUENCE 467 AA; 51029 MW; F4300A8F165EBF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                         73;
                                                                                                                                                                                           75.3%; Score 1861; DB 3; 74.3%; Pred. No. 5.6e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 AA
                                                                                                                                                                                                           Best Local Similarity 74.3%; Pred. No. 5.6e
Matches 347; Conservative 47; Mismatches
                                                                         Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                     POTENTIAL
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                                                                                                                     Signal; Lyase; Hydrolase.
SIGNAL 1
                                                                                                                                                                                                                         Matches 347; Conservative
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01-MAY-1999 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000560; -.
                                                             InterPro; IPR000560;
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5058;
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0
                                                                           75.1%; Score 1855; DB 3; Length 467; 73.4%; Pred. No. 1.7e-143; ive 51; Mismatches 73; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang L., An L., Wang Y., Yuan X.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY013315; AAG40885.1; - SEQUENCE 467 A&; 51012 MW; 3F69AD543C0B565B CRC64;
PROSITE; PS00616; HIS ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SEQUENCE 467 AA: 51028 MW; 7A38AD543EDC265C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Best Local Similarity. 73.2%;
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                                                                        Query Match
Best Local Similarity 73.4%
Matches 343; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus ficuum.
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-1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
-1- SUBCELLULAR LOCATION: SECRETED.
-1- STATILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL: U60412; AABS8465.1; -
HSSP; P34752; 11HP.
YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
                                                                    241 ARLEAHLPGVNLTDEDVVNLMDMCRFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
                                                                                                                           301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                               HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=33178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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Pasamontes L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REQUIRED FOR BINDING SUBSTRATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TREMBLrel. 13, Last annotation update)
3-PHYTASE PRECURSOR (EC 3.1.3.9) (MYO-INOSITOL-HEXAPHOSPHATE
PHOSPHOHYDROLASE) (3 PHYTASE) (MYO-INOSITOL HEXARISPHOSPHATE
                                                                                                                                                                                                                                                                            LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                          Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTIFROM PHYTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfan, PF00328; acid phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broger C., van Loon A.P.;
                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000560; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHOHYDROLASE)
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DISULFID
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-i. FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE FROM PHYTATE (BY SIMILARITY).

-i. CATALYZIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SPFPLDVPDDCHITFVQVLARHGARSPTDSKTKAYAATIAAIQKNATALPGKYAFLKSYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 KRLEADLPGVQLSADDVVNLMAMCPFETVSLTDDAHTLSPFCDLFTAAEWTQYNYLLSLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                            Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L., Loon A.P.; "The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fundi Aspergillus terreus and Myceliophthora thermophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 13, Last annotation update)
31-PHYTASE A PRECURSOR (EC 3.1.3.8) (WYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE
                                               ( POTENTIAL) ( POTENTIAL) ( POTENTIAL) ( POTENTIAL) (
                            (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                            Length 466;
                                                                                                                                                                                                                                                                                                            83; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F2AECEC1AF7C22C4 CRC64;
                                                                                                                                                                                                                                               DB 3;
                         (GLCNAC. . . (GLCNAC. . . (GLCNAC. . .
                                                                                                                                                                                                                                         Query Match
73.9%; Score 1826; DB 3;
Best Local Similarity 72.7%; Pred. No. 4.1e-141
Matches 339; Conservative 44; Mismatches 83
   (GLCNAC.
                                                                                                                            (GICNAC
N-LINKED (N-LINKED (N-LINK
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                                                                                                                                                   466 AA; 51055 MW;
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   207
230
339
352
376
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      CARBOHYD
                                      CARBOHYD
                                                                   CARBOHYD
                                                                                                   CARBOHYD
                                                                                                                            CARBOHYD
                                                                                                                                                               SEQUENCE
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301 KYYGYGAGNPLGPAQGYGFVNELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
-1- SUBCELLULAR LOCATION: SECRETED.
-1- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO 7.5, WITH MAXIMAL ACTIVITY AT PH 5.5. ALSO ACCEPT 4- NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO MORE ACIDIC PH VALUES.
-1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA
                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 466;
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                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
                                                                                                                Pfan; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                      71.1%; Score 1756; DB 3; 69.7%; Pred. No. 2.2e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                54; Mismatches
                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                               POTENTIAL.
3-PHYTASE A.
                                                                                                                                                       Hydrolase; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                        MM.
                                                                             EMBL; U59805; AAB52507.1; -.
                                                                                                                                                                                                                                                                                                                                                                        51093
                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 69.79
325; Conservative
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466
82
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361
40
                                                                                                      InterPro; IPR000560;
                                                                                                                                                                                                                                                                                                                                                                        466 AA;
                                                                                           HSSP; P34752; 1IHP
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361
31
71
215
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3339
376
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82
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ACT_SITE
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DISULFID
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466

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PRELIMINARY;

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"Cloning of the phytases from Emericella nidulans and the thermophilic fungus Talaromyces thermophilus.";
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                                                                                                                                                                                                                                                                                                                INOSITOL 1,2,4,5,6-PENTAKISHOSPHATE + PHOSPHATE.
-!- MISCELLANEOUS: HAS POTENTIAL AS FOOD AND FEED ADDITIVE. IT CAN FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
3 - PHTTASE A.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1353:217-223(1997).
     01-JUL-1997 (Tremblrel. 04, Created)
01-JUL-1997 (Tremblrel. 04, Last sequence update)
01-MAR-2001 (Tremblrel. 16, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSTTOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (4 MYO-INOSTTOL HEXARISPHOSPHATE 3-PHOSPHOHYDROLASE A).
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(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                          USED AS FOOD FOR MONOGASTRIC ANIMALS.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
BEBL: US9802; AAB96873.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                 STRAIN-ATCC 20186;
MEDLINE-98007872; Pubmed-9349716;
Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
Van Loon A.P.G.M.;
                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Talaromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 466;
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                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000560: -
Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase, Glycoprotein; Signal.
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BY
BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51450 MW;
                                                                                                       Talaromyces thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461
278
440
204
269
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357
37
410
                                                                                                                                                                                                                                                                                                                                                                                                  lIHP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 AA;
                                                                                                                    Eukaryota; Fungi;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=28565;
                                                                                                                                                                                                                                                                                         FROM PHYTATE:
                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P34752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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3; 59 DESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEALQKNATAFKGKYAFLKT 118 119 YNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQ 178 SAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPP 238 Gaps 1 MGVFVVLLS--1ATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLA 58 1 MSILLIVLSGGLVALYVSRN----PHVDSHSCNTVEGGYQCRPEISHSWGQYSPPFSLA 55 . 8 Indels 91; 69.6%; Score 1719; DB 3; 69.3%; Pred. No. 2.3e-132; 45; Mismatches Matches 325; Conservative Similarity Best Local 179 176 δ g οy q Qγ q δy

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FROM PHYTATE.

-!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 12,4,5,6-PENTAKISPHOSPHATE.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- MISCELLANBOUGS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF 3.5 TO 8.5, WITH MAXIMAL ACTIVITY BETWEEN PH 5.5 AND 6.0. ALSO ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA
                                                299 LGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYAD 358
                                                                                                   FSHDNIMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEK 418
                                                                                                                 genes for two novel phytases from the fungi Aspergillus terreus and Myceliophthora thermophila.", Microbiology 143:245-252(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The phytase subfamily of histidine acid phosphatases: isolation of
            SIMILARITY).
239 IRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQS
                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
11-JUL-1997 (TrEMBLrel. 04, Last sequence update)
3-PHYAASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE PHOSPHOHYDROLASE A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHIFTED TO MORE ACIDIC PH VALUES.

-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY
EMB: U59806, AAB52508.1; -.
HSSP: P34752; 11HP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REQUIRED FOR BINDING SUBSTRATE (BY
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales: Chaetomiaceae; Thielavia.
                                                                                                                                                        467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMPROTON DONOR (BY SIMILARITY).
                                                                                                                                                  419 EPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA
                                                                                                                                                                  Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L., van Loon A.P.G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                              487 AA
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97177792; PubMed=9025298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                         Thielavia heterothallica.
                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
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270
433
75
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35
35
421
485
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=78579;
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368
26
26
64
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165
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DISULFID
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                           LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 SNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPF 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFV 450
                                                                                                                                                                                                                                                   118 TYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGF 177
                                                                                                                                                                                                                                                                                                         178 QSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEE---SELGDDVEANFTAV 234
                                                                                                    Gaps
                                                                                                                                                                                         58 ADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLK 117
                                                                                                                                                             4 LGVMVVMVGFLAIASL------QSESRPCDTPDLGFQCGTAISHFWGQYSPYFSV 52
                                                                                                                                1 MGVFVVL---LSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSL 57
                                                                                                                                                                                                                                                                                                                                                                                   Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
97D10EDC83D051DB CRC64;
                                                                                                     43;
                                                                      ; Score 1346.5; DB 3; Length 487;
; Pred. No. 7.3e-102;
58; Mismatches 128; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Vicente A., Ferminan E., Dominguez A.; "Isolation and characterization of KIPHO3 a gene encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constitutive acid phosphatse from Kluyveromyces lactis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ007502; CAB46490.1; -...
HSSP; P34755; 10FX.
InterPro: IPRO05660; -...
Pfam: PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACID PHOSPHATASE (EC 3.1.3.2).
                              487 AA; .52537 MW;
                                                                          54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 EGLSFARSGGNWEECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 ESMAFARGNGKWDLCFA 487
                                                                                                       Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 AARAYVEMMQC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=2360/7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase.
   CARBOHYD
CARBOHYD
SEQUENCE
                                                                           Query Match
                                                                                           Local
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Q9Y846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 YEFFVSNTKYFDQLTNSTDVDPSNPYAGAKTAQHLGKYIAYNYGDLFSDSNP-VFTSSSG 172
                                                                                                                                                                                                                                                                                                                                  RVIASAEKFIEGFQSAKLADPGANPHQASPVINV----IIPEG--AGYNNTLDHGLCTA 217
                                                                                                                                                                                                                                                                                                                                                                                                    275
                                                                                                                                                                                                                                                                                                                                                                                                                                   276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 TQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 V----CDLFERNDLVAYSYYANVNNFYRRGAGNPMSNPIGSVLVNASYNLLTQADELDN 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 DESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKT 118
                                                                                                                                                                                                                      Gaps
                                                                                                                                      7 LLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCF-----PEISHLWGQYSPFFSLA 58
                                                                                                                                                                  1 MLSILLSLLSLSGTHAAPISK------DNGTVCYALNSSTTDESIFPLLNGQGPHYDYP 53
                                                                                                                                                                                                                                                                                                                                                       173 RVHQTAKYVVSSLEEE------LDIQLDLQIIQENETSGANSLTPADSCMT
                                                                                                                                                                                                                                                                     119 YNY----TLGADDLT-----PF-GEQQMVNSGIKFYRRYKALARKIVPFVRASGSD
                                                                                                                                                                                                                                                                                                                                                                                                    218 FEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLT--DEDVVNLMDMCPFDTVARTSDA
                                                                                                                                                                                                                                                                                                                                                                                                                       395 YAASWIVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 TSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY-NGTKPLSTTSVESIEETDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                     91;
                                                                     Length 469;
                                                                                                     Indels
ACID PHOSPHATASE.
5C7ABF622CEA891C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P34755; 1QFX.
InterPro; IPR000560; -.
Pfam: PF00328; acid_phosphat; 1.
PR0081E; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                     DB 3;
                                                                   13.9%; Score 343.5; DB 3
25.1%; Pred. No. 7.7e-20;
tive 68; Mismatches 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appl. Microbiol. Biotechnol. 50:77-84(1998).
EMBL; AF051161; AAC62537.1; -.
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MEDLINE=98386672; PubMed=9720203;
                    52560 MW;
                                                                                                        Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 -- VEGLSFARS 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 NRLNGIDYVSS 439
      17 4
469 AA;
                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase
                    SEQUENCE
                                                                       Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          074677;
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463 AA; 52758 MW; 6C41AF422C6D624A CRC64;

SEQUENCE

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16;
                                                                                                            66 DVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQK-NATAFKGKYAFLKTYNYTLG 124
                                                                                                                              125 ADDLTPFGEQQMVNSGI----KF----YRRYKAL--ARKIVPFVRASGSDRVIASAEKFI 174
                                                                                                                                                                                              115 DSDNYELETTRGLYSGLINAFKFGTYLRERYDSLVDTSSVLPIFAAS-EDRVVDTARSFG 173
                                                                                                                                                                                                                                        175 EGFQSAKLADPGANPHQASPVINVI----IPEGAGYNNTLDHGLC----TAFEESELGDD 226
                                                                                                                                                                                                                                                                      174 RGFFGPDYA-----TSCSIOVVNETDTSKGANALTTKDN--CPTYNSSFYDYSFGDE 223
                                                                                                                                                                                                                                                                                                      227 V---EANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCD 283
                                                                                                                                                                                                                                                                                                                                                                   284 LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                   344 SNPATFPL---NATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWT 400
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 ---ATAKILQEDGKLWFSFSHDNDLLNYITALGLITDTE----LGTEDVDFHRSFKTSEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                     224 IFQREAD-----SLINELSPGFNITADDIITMGTYCAYETNVKGH----SSFCD
                                                                                                                                                                                                                                                                                                                                                                                                   268 ALSREAFIALQYNNDVTKFYQFGPGYNMSAVAGGVYAN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALCOHOL + ORTHOPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL; AL023286; CAA18863.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                     83;
                                                       Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
 442 AA; 49370 MW; 7087D91A85B05C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                   DB 3;
                                                13.5%; Score 333.5; DB 3 25.8%; Pred. No. 4.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00328: acid phosphat: 1
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTON DONOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last annotat PROBABLE ACID PHOSPHATASE (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
                                                            Best Local Similarity 25.89 Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
104
221
324
439
458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P34755; 1QFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896
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 SEQUENCE
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Gocayne R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chon L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ruttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Rather Y. J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                       99 IEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRRYKALARKIV 155
                                                                                                                                                                                                              98 NGSIPVNFSYPENPLCFIKOWTPVIDAENADQLSSRGRLELFDLGRQLYQRYYKLFDSYV 157
                                                                                                                                                                                                                                                             PFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEG--AGYNNTLDHG 213
                                                                                                                                                                                                                                                                                             269 VARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 AIXDH-----SDFCSIFTPSEFLNFEYDSDLDQAYGGGPVSEWASTLGGAYINNLADSL- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVEŚ 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 IEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGR----C 444
                                                 62; Gaps
                                                                                                                                                                                                                                                                                                                                                 214 LCTAFEESEL----GDDVEANFTAVFAPPIRARLEAHL-PGVNLTDEDVVNLMDMCPFDT 268
                                                                                                                                                                                                                                                                                                                                                                                            209 ACPVFKDNNFHKNATDAAHAVWRNIFIEPIVNRLAKYFDSSYKLTINDVRSLFYICEYEI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 NIYTYSQKTSSFVPFAGNLITELFFC-SDSKYYVRHLYNQQVYPLIDCGYGPSGTSDGLC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                   51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTS--SKSKKYSA-----L 98
                                                                                                                          43 HEPYFDGLDSA----FPETCEIQOVHLLQRHGSRNPTGDVTATDVYSSQYLNNFQEKLL 97
         Length 463;
12.2%; Score 301; DB 3; Length 46.
24.3%; Pred. No. 2.3e-16;
Live 71; Mismatches 198; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 ELQAYLNSPIRANSTSN 443
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 KRDDFVEGLSFARSGGN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIPP1 PROTEIN.
                                           Matches 106;
    Query Match
                           Sest Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09VV72
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 -TSRRWKSSLIDPFAANFVAVKYDCPADLDREKVV-FFLNQQAVQLDWCSV---GLCKWS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                               66 DVPK-----GCRVTFVQVLSRHGARYPTSS---KSKKYSALIEAIQKNATAFKGK---- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 DIDKOYLVPGCOPOKMWIFHRHGTRLPKKSMINKASRVAELRDLIINNYQVARTKPETDA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 ----YAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFV-RASGSD-- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 LCQTDLIAIKLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTVLTANYNDTY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 --RVIASAEKFIEG-FQSAKLADPGANPHQ-----ASPVINV-IIPEGAGYNNTLD 211:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 YORTTESFKAFAAGGLFGSQNAAHPVEIPKQDLLLRPYDYCSSFKNVNYKDEGSEYYK--- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 HGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPG--VNLIDEDVVNLMDMCPFDTV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 -----FHQSKLYNDTLAD-----ISTRL----GFLYTLEEADIKLMYDMCRYE-- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 ARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTH 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 NPVSPH------VVAHFGHSTGLLTLLTALGIQKDDIKLRADNYDSL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 EETDGYAASWTVPFAARAYVEMMQCEA--EKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              .8.6%; Score 212.5; DB 5; Length 460; 23.9%; Pred. No. 3.9e-09;
                                                                                                                                                                                                                                                                                                                                                          F00B25718E40807D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                        64; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-AUG-1999 (TrEMBLrel. 11, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 DFVE-----GLSFARSGG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 DVLEKYKTIADADCGEYYCRTGG 435
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00328; acid_phosphat; 1.
SEOUENCE 460 AA; 52685 MW; F
                                                                                                                                                                                                                                                                                                      EMBL; AE003527; AAF49450.1; -. FlyBase; FBgn0026061; Mippl.
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                InterPro; IPR000560; -.
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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specificity.";
J. BAGJ. Chem. 266:16499-16506(1991).
J. BAGJ. Chem. 264:16499-16506(1991).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INOSITOL 1,3,4,5-
TETRAKISPHOSPHATE TO INOSITOL 1,4,5-TRIPHOSPHATE AND INOSITOL 1,3,4,5,6-TETRAKISPHOSPHATE 1,3,4,5,6-PERRAKISPHOSPHATE TO INOSITOL 1,4,5,7-TRISPHOSPHATE. DEPHOSPHORYLATES AND THEN TO INOSITOL 1,4,5-TRISPHOSPHATE. DEPHOSPHORYLATES INOSITOL HEXAKISPHOSPHATE WITHOUT SPECIFICITY TOWARDS A PARTICULAR
                                                                                                                                                                                                                                                                                                                                                           Shears S.B.; "Purification of an inositol (1,3,4,5) tetrakisphosphate 3-phosphatase
                                                                                                                                                                                                                                                                                                                                   Nogimori K., Hughes P.J., Glennon M.C., Hodgson M.E., Putney J.W. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 ALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 OLOGILIOTRESVDGGSRVAAALDQWPLWYDD---WMDGQLVEKGRQDMRQLALRLAALFP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 --FVR------ASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 SPFFS------LADESA--ISPDVPKG-CRVTFVQVLSRHGARYPTSSKSKKYS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 SPYFGTKTRYEDVNPWLLGDPVAPRRDPELLAGTCTPVQLVALIRHGTRYPTTKQIRKLR 73
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                           SEQUENCE OF 11-451 FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                           Craxton A., Caffrey J.J., Burkhart W., Safrany S.T., Shears S.B.; "Molecular cloning and expression of a rat hepatic multiple inositol polyphosphate phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00328; acid_phosphat; 2.
PROSITE; PS00014; ER_TARGET; UNRNOWN_1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; FALSE_NEG.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; FALSE_NEG.
ACT_SITE 59 S9 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREVENT SECRETION FROM ER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-i- TISSUS SPECIFICITY: MOST ABUNDANT-IN KIDNEY AND LIVER.
-i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL; AF012714; AAC33453.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .) (POTENTIAL).
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HEPATIC MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE (EC 3.1.3.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 451;
                                                                                                                                                                                                                                                                                                                                                                                         activity from rat liver and the evaluation of its substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.3%; Score 204; DB 11; Length 45
21.5%; Pred. No. 1.9e-08;
ive 73; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (POTENTIAL) PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EB1C05512A03020B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P -> H.
S -> P (IN AAC53453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::
                                                                                                                                                                                              MEDLINE=98028656; PubMed=9359836;
                                                                                                                                                                                                                                                                                                                        MEDLINE=91358435; PubMed=1653239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 S
451 PR
51592 MW;
                                                                                                                                                                                                                                                    polyphosphate phosphatase."; Biochem. J. 328:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92; Conservative
                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000560; -. InterPro; IPR000886; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHATE GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 AA;
                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY.
                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391
412
435
447
206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                 TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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MOD_RES
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                              206 YNNTL----DHGLCTAFEESELGDDVEANFTAVF-----APPIRARLE-----AHLPG 249
                                                        185 VNDKLMRFFDH--CEKFL----TEVERNATALYHVEAFKTGPEMQTVLKKVAATLQVPV 237
                                                                                     250 VNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGN 309
                                                                                                                                            310 PLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIF 369
                                                                                                                                                                       294 AINSRSSCNLFQDIFLHLDKAVEQKQRSQ------PVSSSVILQFGHAETLLPLL 342
131 DLFCRENYGRLRLITSSKHRCVDSSAAFLQGLW--QHYHPGLPP----PDVSDMECDPPR 184
                                                                                                                238 NNLNADLIQVAFFTCSFDLAIGGVH----SPWCDVFDVDDAKVLEYLNDLKQYWKRSYGY 293
                                                                                                                                                                                                    370 FALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP----LVRVL 425
                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoftera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophillidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 DVPK-----GCRVTFVQVLSRHGARYPTSS---KSKKYSALIEAIQKNATAFKGK---- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 DIDKOYLVPGCOPOKMWIFHRHGTRLPKKSMINKASRVAELRDLIINNYQVARTKPETDA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 -----YAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFV----- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 LCQTDLIAIKLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTVLTANYNDTY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 YQFRHTDTQRTTESFKAFABGLFGSQNAAHPVEIPKQDLLLRPYDYCSSFKNVNYKDEGS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 GYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPG--VNLTDEDVVNLMD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 ---RASGSDRVIASAEKFIEG-FQSAKLADPGANPHQ------ASPVINV-IIPEGA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 EYYK-----FHQSKLYNDTLAD-----ISTRL----GFLYTLEEADIKLMYD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 MCPFDIVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N.,
Reynolds P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.3%; Score 204; DB 5; Length 467;
Best Local Similarity 22.9%; Pred. No. 2e-08;
Matches 103; Conservative 66; Mismatches 173; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF046913; AAD02436.1; -.
FlyBase; FBgn0026061; Mippl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro, IPR000560; -. Pfam; PF00328; acid_phosphat; 1. SEOUENCE 467 AA; 53602 MW; 1A0571B9958B2632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE 1.
MIPPL OR CG4123.
                                                                                                                                                                                                                                                                                                                                                                      467 AA.
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                 PRELIMIŃARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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402 LNEKVLPL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              426 VNDRVVPL 433
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20;
323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLS 382
                                                        318 LLTHLS-NPVSPH------VVXHFGHSTGLLTLTALGIXKDDIKLR 357
                                                                                                                   383 TISVESIEETDGYAASWTVPFAAR--AYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDK 440
                                                                                                                                                               358 ADNYDSL-TSRRWKSSLIDPFAANFVAVKYDLPADLDREKVV-FFLNQQAVQLDWCSV-- 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 SPDVPK------GCRVTFVQVLSRHGARYPTSSKSKKYSALIEALQKNATAFKGKYAF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.9%; Score 196; DB 11; Length 481;
Best Local Similarity 21.0%; Pred. No. 9.3e-08;
Matches 100; Conservative 71; Mismatches 194; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AALAEWPLWYGD----WMDGQLVEKGRQDMRQLALRLAALFPDLFSRENYDRLRLITSSKH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 RVIASAEKFIEGFQSAKLADPGANPHQAS-----PVINVIIPEGAGYNNTLDHGLCTAF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 RCVDSSAAFLOGLW--QHYHPGLPPPDVSDMECGPPRINDKL-----MRFFDH--CEKF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 EESELGDDVEANFTAVFAPPIRARLEAHLPG--------VNLTDEDVVNL- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 QDIFLHLDKAVEQKQRSQ-------PVSSPVILQFGHAETLLPLLSLMGYFKDKEP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 LKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVP--FVR------ASGSD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 L-----TDVERNETALY-----HVEAFKTGPEMOKVLKKVAATLOVPMNSLNADLIQVA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 MDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGYGFV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 NELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AALLSSFARCSLPGRGD------PVASVL---SPYFGTKTRYEDANPWLLV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N., Reynolds P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLAD--ESA----I 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF046908; AAD02434.1;
MGD; MGI:1336195; Minppl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00328; acid phosphat; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SEQUENCE 481 AA; 54537 MW; 7CE78356B11F4606 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 AA.
                                                                                                                                                                                                                                          441 LGRCKRDDFVE-----GLSFARSGG 460
                                                                                                                                                                                                                                                                                  414 -GLCKWSDVLEKYKTIADADCGEYYCRTGG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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InterPro; IPR000886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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QQ ÓΫ

Search completed: October 26, 2001, 15:17:24 Job time: 3975 sec

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OM protein - protein search, using sw model

2001, 15:10:27 ; Search time 48.78 Seconds (without alignments) 682.417 Million cell updates/sec October 26,

US-09-488-265-27

1 NSHSCDTVDGYQCPEISHLW......DFVEGLSFARSGGNWAECFA 437 Perfect score: Sednence:

**BLOSUM62** Scoring table:

219241 seqs, 76174552 residues Gapop 10.0., Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote histidine acid pho acid phosphatase h acid phosphatase ( acid phosphatase (acid phosphatase hacid phosphatase hacid phosphatase (3-phytase (EC 3.1 acid phosphatase (acid phosphatase (thiamin-repressibl 3-phytase (EC 3.1. 3-phytase (EC 3.1. 3-phytase (EC 3.1. hypothetical prote homoaconitate hydr secreted acid phos secreted acid phos hypothetical prote aggregation factor polymorphic membra acid phosphatase acid phosphatase phosphatase phosphatase phosphatase acid phosphatase Description acid SUMMARIES S53476 S48996 JN0482 PABYCC \$52495 T08615 S54770 T46726 T18945 JE0369 Query Match Length DB 423 1025 1081 15.3 15.3 15.2 14.4 14.4 113.2 12.8 12.3 6.6 4.8.8 337 334.5 307.5 303.5 298 149.5 125 113.5 111 111 108.5 Result Š.

| probable glucanase hypothetical prote probable membrane cysteine proteinas canalicular multis glyceraldehyde 3-p hypothetical prote adult-specific bru hypothetical prote proteinal protei |
|--|
|  |
| T39920<br>86265<br>86265<br>86265<br>76265<br>716455<br>737690<br>636793<br>60NYE<br>KIBSGM<br>A84265<br>T33135  |
| прининовриминания  |
| 419<br>407<br>556<br>556<br>1527<br>336<br>1458<br>844<br>1350<br>2290<br>357<br>357<br>357<br>357<br>455  |
| 44444444444444444444444444444444444444   |
| 100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100   |
| 33<br>33<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>30<br>3  |
|  |

## ALIGNMENTS

| N, Alternate names: myo-inositol hevskienhooming   |
|--|
| 'Olase, phyA protein   |
| C; Date: 14-Jul-1994 #sequence revision 10-Oct-100F #1   |
| inge 11-Jun-1999   |
|  |
| Gene 133, 55-62, 1993  |
|  |
| A; Reference number: JN0889; MITD: 94/04/0796  |
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| PID:9166519  |
| A; Note: part of the segments included the contract of   |
| mature protein, was con  |
| C, Genetics:   |
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| C; Keywords: extracellular protein: alvonnatein. nhochah: a: a:  |
| Afitte: The cloning and sequencing of the genes encoding phytase (phy) and statement number: JN0889; MUID:94040796 Afacession: JN0889 Afacession: JN0889 Afacession: JN0889 Afacession: JN0889 Afacession: JN0889 Afacinate type: DNA Afacession: Afacesions: 1-467 < PID. Afacession: Afacesions: 1-467 < PID. Afacesion: Afacesions: Afacesions and Afacesion |

Ä do.

C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph F;1-19/Domain: signal sequence #status predicted <SIG> F;20-467/Product: 3-phytase A #status experimental <MAT> F;27,59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) # F;81,361/Active site: Arg, His #status predicted F;82/Active site: His (phosphohistidine intermediate) #status predicted

Length 467; 72.7%; Score 1688; DB 1; 73.9%; Pred. No. 5.2e-132; tive 40; Mismatches 59; Local Similarity Matches 331; Query Match

1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESALSPDVPKGCRVTFVQVLSRHGARY 58 Gaps Indels 18; 59; Conservative

10;

59 PTSSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117 q δŏ

q

118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174 ŏλ QQ

175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233 207 ò qq

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DNA mismatch repai

T51613

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A; Accession: JN0482
A; Molecule type: protein
A; Molecule type: I-441 < William
A; Molecule type: I-441 < William
A; Molecule type: Molecule that the 9 Asn followed by Thr or Ser after an intervening resingular, and Molecule that the 9 Asn followed by Thr Or Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Molecule that the 10 Ser after an intervening resingular and Mole
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C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphortein; ph C;Keywords: extracellular protein; glycoprotein; phosphortein extracellular protein; phosphohistidine site: carbohydrate (Asn) (covalent) #sta F;59,38/Active site: Arg, His #status predicted
F;59,Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                         N.Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein C.Speciaes: Aspergillus ficuum C.Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 07-May-1999 C.Accession: JN0482; PN0023 C.Accession: JN0482; PN0023 F. H.C. R:011ah, A.H.J.; Dischinger Jr., H.C. Biochem. Biophys. Res. Commun. 192, 747-753, 1993 A;Itle: Aspergillus ficuum phytase: Complete primary structure elucidation by chemic A;Aceternoce number: JN0482; MUID:93249451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| |:||::::||||||:| |||||||:|
| BNITQTDGFSSAWTVPFASRLYVEMMQCQA------EQEPLVRVLVNDRVVPLHGCPVD 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
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                                      18;
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73.7%; Pred. No. 3.8e-130;
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                                                                                                                                              410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                         440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467
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C; Superfamily: yeast acid phosphatase
C; Superfamily: yeast acid phosphatase
C; Superfamily: phosphonistidine; phosphoprotein; phosp
C; K23/Nomain: signal sequence #status predicted <SIG>
F; 1-23/Nomain: signal sequence #status experimental <MAT>
F; 24-467/Product: 3-phytase A #status experimental <MAT>
F; 27, 59, 105, 120, 207, 230, 339, 352, 336, 388 Binding site: carbohydrate (Asn) (covalent) #states F; 81, 361/Active site: Arg, His #status predicted
F; 81, 561/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyAA; Reference number: JN0656; MUID:93252284
A; Accession: JN0656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein C;Species: Aspergillus niger C;Decies: Aspergillus niger C;Date: 03-reb-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999 C;Accession: JN0656; S28456 R;van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross_references: GB:216414; NID:92392; PIDN:CAA78904.1; PID:92393
A;Experimental source: strain NRRJ3135
A;Experimental source: northwest of the mature protein, were contained to parts of the sequence, including the amino end of the mature protein, were contained: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and C;Comment: This enzyme catalyzes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                     267 DIISTSTVDTKLSPECDLFTHDEWIHYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326
                                                                                                    y Match 72.6%; Score 1684; DB 1; Length 467; Local Similarity 73.9%; Pred. No. 1.1e-131;
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A;Gene: phyA
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A;Cross-references: EMBL:U00029; NID:g551322; PIDN:AAB69729.1; PID:g458917; MIPS:YHR2 Submitted to the EMBL Data Library, January 1995
                                                                                                                                                                                                                                      deid phosphatase (EC 3.1.3.2) PHO12 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YHR215W C;Species: Saccharomyces cerevisiae C;Species: O2-Dec.1994 #sequence_revision O2-Dec.1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-16, L',18-81, 'AR', 84-149,'H',151-467 <XUL>
A; Cross references: EMBL:U19789; NID:9847754; PIDN:AAA73479.1; PID:9847755
A; Genetics: A; Constraint and AR A; Cross references: SGD:S0001258; MIPS:YHR215W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 QK-NATFKGKYAFLK-----TYNYTL-----GADDLTPF-GENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 SNYTGQFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVLNPYTGEMNAKRHARDFLAQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 YKALARNIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 LSAHHSCPAMDDD-VNDDILKKYDTKYLSGIAKRLNKENKGLNLTSSDANTFFAWCAYEI 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 EISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 ESEVQDQ------KVWLSFTHDTDILNYLTTIGIIDDQNNLTAEHVPF 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 IETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKLG 412
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----SNDTYVRYVINDAVVPIETCSTGPGF 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, February 1994
A:Description: The sequence of S. cerevisiae cosmid 9177.
A:Reference number: $46671
A:Accession: $48996
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es 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Map position: 8R
C.Superfamily: yeast acid phosphatase
C.Keywords: phosphoric monoester hydrolase
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                                                                     415 SCEINDFYDYAEKRVAGTDFLK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 SCEINDFYGYAEKRVAGTDFLK 436
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A; Accession: S59659
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A; Residues: 1-467 <MAC>
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A.Reference number: 853458
A.Rocession: 853476
A.Rocession: 1-467 <-8052
A.Cross-references: EMBL:L28920; NID:91616966; PIDN:AAC09508.1; PID:9456155; MIPS:YAR071
A.Rocession: J.Y. Googy, Y. Ao, S.Z.
Acta Biochiu. Blophys. Sin. 21, 437-444, 1989
A.Reference number: 3C1018
A.Reference number: 3C1018
A.Rocession: JC1018
A.Rocession: JC1018
A.Rocession: JC1018
A.Rocession: JC1018
A.Rocession: JC1018
A.Rocession: JC1018
A.Rocession: Spaper is in Chinese, with an English abstract
A.Gonetics:
A.Gonetics:
A.Gonetics: SGD:S0000094; MIPS:YAR071W
A.Rocession: JC1018
A.Rocession: JC1018
A.Rocession: JC1018
A.Rocession: A.R
                                                                                                                                                                                                                                                                                       C; Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Apr-2000 C; Accession: S53476; JC1018 R; Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac Submitted to the EMBL Data Library, February 1994 A; Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Keywords: glycoprotein; phospholistidine; phosphoprotein; phosphoric monoester hydrola F:1-17/Domain: signal sequence #status predicted <SIG> F:18-46/Product: acid phosphatase #status predicted <MAT> F:74/Active site: Arg #status predicted <MAT> F:75/Active site: His (phosphohistidine intermediate) #status predicted F:75/Active site: His (phosphohistidine intermediate) #status predicted F:97,162,192,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                        acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YAR071w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Apr-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 YKALARNIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.3%; Score 356; DB 2; Length 467;
26.9%; Pred. No. 1.3e-21;
tive 63; Mismatches 190; Indels 70; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 EISHLWGOYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERI 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 IETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVDKLG 412
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A, Map position: 1R
C; Superfamily: yeast acid phosphatase
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Matches 119; Conservative
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421 FYDYAEKRVAGTDFLK 436
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A; Residues: 18-45 <BAJ2>
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A.Fitle: Structural analysis of the two tandemly repeated acid phosphatase genes in yeas A.Reference number: 805794; MUID:85037940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-218, 'MKT', 222-467 < BAJ1>
A; Residues: 1-218, 'MKT', 222-467 < BAJ1>
A; Cross-references: EMBIS: X01080; NID: 94148; PIDN: CAA25557.1; PID: 9758281
A; Cross-references: EmBIS: X01080; NID: 94148; PIDN: CABS: A sp and TAC for residue
A; Note: the authors translated the codon AAT for residue 134 as Asp and TAC
R; Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Ellitott, Q.D.; Bostian, S.J.; Thill, G
R; Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Ellitott, Q.D.; Bostian, S.J.; Thill, G
R; Title: Reciprocal requiation of the tandemly duplicated PHO5/PHO3 gene cluster within
A; Reference number: A93074; MUID: 87064474
acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (Saccharomyces cerevislae)
Nathermate names: acid phosphatase PHO3; protein YBR0813; protein YBR092c
C; Species: Saccharomyces cerevisiae
C; Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C; Accession: S48595; 845960; S05794; A25241; S44674
R; Mannhaupt. G; Stucka, R; Ehnle, S; Vetter, I; Feldmann, H..
Yeast 10, 1363-1381, 1994
A; Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476050
A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476050
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R;Feldmann, H:; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 ACPGWDEDANDDILDKYDTTYLDDIAKRLNKENKGLNLTSKDANTLFAWCAYELNAR--- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVG-FNELIARLTHSPVQD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 CTAFEDSTLGDDAEANFTAVFAPPIRARL-EALPGVNLTDEDVVNLMDMCPFDTVARTSD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 NIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLDHGL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 NQTSFPIFAASSERVHDTAQYFIDG-----LGDQFNISLQTVSEAMSAGA---NTLSAGN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 FNGSLSFLNDDYEFFIRDDDDLEMETTFANSDNVLNPYTGEMDAKRHAREFLAQYGYMFE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 GGAGPYFSFPGDYGISRDLPEGCEMKOLQMLARHGERYPTYSKGATIMKTWYKLSNYTRQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LTPF-GENQMVNSGIKFYRRYKALAR 123
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                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.8 Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S45927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-467 <FE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-44 <TAI>
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                               A; Accession: S48259
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A; restauces: 1-46/ <MAN>
A; coss-references: EMBL: X78993; NID:9476045; PIDN:CAA55598.1; PID:9476051
A; choss-references: EMBL: X78993; NID:9476045; PIDN:CAA55598.1; PID:9476051
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
B; Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
A; Reference number: S45927
A; Rocession: S45961
A; Reference number: S45927
A; Rocession: S45961
A; Rocession: S45961
A; Rocession: S45961
A; Rocession: S45962
A; Cross references: EMBL: Z35962; NID:9536364; PIDN:CAA85046.1; PID:9536365; GSPDB:GNO
A; Cross references: EMBL: Z35962; NID:9536364; PIDN:CAA85046.1; PID:9536365; GSPDB:GNO
A; Cross references: EMBL: Z35962; NID:936364; PIDN:CAA85046.1; PID:9536365; GSPDB:GNO
A; Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repr
A; Reference number: A00777; MUID:83168913
A; A; Accession: A00777; MUID:83168913
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A; Residues: 1-30, T',32-51,'S',53-75 <MEX>
A; Cross-references: EMBL:MAJ18; NID:q172156; PIDN:AAA34868.1; PID:q172157
A; Cross-references: EMBL:MAJ18; NID:q172156; PIDN:AAA34868.1; PID:q172157
B; Tail:Yamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill
R)1. Cell. Biol. 6, 1855-1865, 1986
A; Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster with
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A; Molecule type: 18-26, Xr, 28 <ARI2>
R; Mesidues: 18-26, Ys, 28 <ARI2>
R; Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinnen, A.
EMBO J. 1, 675-680, 1982
A; Title: Two yeast acid phosphatase structural genes are the result of a tandem dupli
A; Reference number: S41855; MUID:84236032
A; Accession: S41855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (Saccharomyces cerevisia mishlernate names; acid phosphatase PHO5; protein YBR0814; protein YBR093c C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 19-Febr-1984 #sequence_revision 30-Sep-1991 #text_change 12-Nov-1999 C;Date: 19-Febr-1984 #sequence_revision 30-Sep-1991 #text_change 12-Nov-1999 C;Date: 19-Febr-1984 #sequence_revision 30-Sep-1991 #text_change 12-Nov-1999 C;Date: 19-Febr-1985; B4876; S4880; S5880; S5880;
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A; Cross-references: EMBL:V01320; NID:g4158; PIDN:CAA24630.1; PID:g4159
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A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II. A;Feference number: S48255; MUID:95208357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 HKSHYVPQGARVYTEKFQC-----SNDTYVRYVINDAVVPIETCSTGPGFSCEIND 420
                                                                                                                                                                                                                                                                                                                                                                                                  359 AASWTVPFAARAYVENMQCEAGGGGGGGGGFKFLVRVLVNDRVVPLHGCGVDKLGRCKLDD 418
                                                                                                                                299 HTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIETDGY 358
                                                                                                                                                                                                                                                          -----LKVWLSFTHDTDILNYLTTAGIIDDKNNLTAEYVPFM-GNTF 369
271 --GYSDVCDIFTEDELVRYSYGQDLVSFYQDGPGYDMIRSVGANLFNATLKLLKQSETQD 328
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N;Alternate names: protein D2815
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A; Residues: 1-468 <AND>
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A;Reference number: A93074; MUID:87064474
A;Accession: B25241
A;Accession: B25241
A;Residues: 1-44 < TAI>
B;A:Bergman, L.W. < TAI>
MOI. Cell. Biol. 6, 2298-2304, 1986
A;Title: A DNA fragment containing the upstream activator sequence determines nucleosome A;Reference number: A25367; MUID:87064526
A;Accession: A25367
                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-2, Yr, 4-43, 'T', 45-51 <BER>
A; Residues: 5: Monod, M; Hinnen, A.; Haquenauer-Tsapis, R.
Mol. Cell. Biol. 7: 3306-3314, 1987
A; Title: The yeast acid phosphatase can enter the secretory pathway without its N-termin
A; Reference number: A27774; MUID:88038886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Superfamily: yeast acid phosphatase
C. Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
F.11-17/Domain: signal sequence #status predicted <SIG>
F.18-46/Fordouct: acid phosphatase, repressible #status experimental <MAT>
F.75/Active site: His (phosphohistidine intermediate) #status predicted
F.97,103,162,192,250,315,386,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 FKGKYAFLK-TYNYTLGADD------LTPF-GENQMVNSGIKFYRRYKALAR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 NIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVII-----PEGSGYNNT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 LDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARL-EALFGVNLTDEDVVNLMDMCPFDTV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 ARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVG-FNELIARLTH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 ----NAKGYSDVCDIFTKDELVHYSYYQDLHTYYHEGPGYDIIKSVGSNLFNASVKLLKQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQK-NAT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 SACNSCPAW-DYDANDDIVNEYDTTYLDDIAKRLNKENKGLNLTSTDASTLFSWCAFEV- 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKLGR 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 -GNTFHRSWYVPQGARVYTERFOC-----SNDTYVRYUNDAVVPIETCSTGPGFS 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 26.5%; Pred. No. 7.5e-21;
Matches 117; Conservative 57; Mismatches 187; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: SGD:S0000297; MIPS: YBR093c
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                                                                                                                                                                                                                                                                                                          A Accession: A27774
A Molecule type: DNA
A: Residues: 1-51,'S',53-60 <SIL>
A; Cross references: GB:M17306
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SGD:PHO5; MIPS:YBR093c
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acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)

RESULT

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A.Molecule type: DNA
A.Residues: 1-468 <URR>
A.Cross-references: EMBL:274072; NID:91430996; PIDN:CAA98583.1; PID:91430997; MIPS:YD
C; Species: Saccharomyces cerevisiae
C; Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C; Accession: 825495; 856756
R; Andre, B.; Vissers, S.; Urrestarazu, L.
Submitted to the EMBL Data Library, February 1995
A; Description: The sequence of a 42 kb segment located on the left arm of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A;Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterizati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichia pastoris)
N.Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: Z48432; NID: 9683669; PIDN: CAA88335.1; PID: 9683673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%; Score 337; DB 2; Length 46%;
26.0%; Pred. No. 5e-20;
tive 60; Mismatches 161; Indels 118; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GADDLTPF-GENQMVNSGIKFYRRYKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 TGKYEGSLSFLNNGYEFFIPDESLLEMETTLQNSIDVLNPYTGEMNAKRHAREFLAKYGK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LARNIVPE-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 HGLCTAFEDSTLG-------DDAEANFTAVFAPPIRARL-EALPGVNLT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Pichia pastoris: C.Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 LMENCTNFPIFTTNSKRIYDTAQYFAEAL-------GDGFNISLQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 ----TLSENSSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLENISDRLNDENKGLNLS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 DEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 RKDAAALFSWCAFEL----NAKGYSNICDIFSAAELIHYSYETDLISFYQNGPGYKLIK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQKNATF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 AQGVG-FN---ELIARLIHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 SIGANLFNATVKLIRQSAH--------LDQKVWLSFTHDTDILNYLT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 ALGLYNGTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGEKEPLVRV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 TAGLIDDTRNITTNHV-PFRDHSYHRSWYIPQGARVYTEKFQC-----SNDSYVRY 397
                                                                                                                                                                                                                                                                                                            A Experimental source: strain 5288C
R;Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 VVNDAVVPIESCSSGPGFSCEEGTFYEXAKDRLKGVSF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 LVNDRVVPLHGCGVDKLGRCKLDDFVE-----GLSF 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 4L
C;Superfamily: yeast acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 KGKY----AFLKT-YNYTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Experimental source: strain S288C C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S67535
A; Accession: S67556
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C; Superfamily: yeast acid phosphatase

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3-phytase (EC 3.1.3.8) B precursor - Aspergillus ficcuum
3-phytase (EC 3.1.3.8) B precursor - Aspergillus ficcuum
N.Alternate names: pH 2.5-optimum acid phosphatase
N.Alternate names: pH 2.5-optimum acid phosphatase
N.Alternate names: pH 2.5-optimum acid phosphatase
C.Species: Aspergillus ficcuum
C.Species: NoT94; PN05460
C.Accession: JN0715; PN0546; PN0460
C.Accession: Jnophys. Res. Commun. 195, 53-57, 1993
Biochem: Biophys. Res. Commun. 195, 53-57, 1993
A;Title: Identification and cloning of a second phytase gene (phyB) from Aspergillus
A;A;Reference number: JN0715; MUID:93371452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 65-66,68-93 <ULL>
C;Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Rolecule type: DNA
A.Rolecule type: DNA
A.Cross-references: GB:L20567
A.Accession: PN0594
A.Rolecule type: protein
A.Rollah, A.H.J.: Dischinger Jr., H. C. Commun. 192, 754-759, 1993
Blochem: Biophys: Res. Commun. 192, 754-759, 1993
A.Ritle: Identification of active-site residues in Aspergillus ficuum extracellular A.Reference number: PN0460; MUID:93249452
Circy or stracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; algoral sequence fitting predicted <NAT>
F:20-479/Product; 3-phytase fitting predicted <MAT>
F:31-337/Active site: Arg, His fitting predicted F:82/Active site: His (phosphohistidine intermediate) fitting predicted F:82/Active site: His (phosphohistidine intermediate) fitting predicted F:106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) fist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 NPLGPAQGVGFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 FALGLY --NGTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEREPL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 AALGVLIPNEDLPLDRVAF----GNPYSIGNIVPMGGHLTIERLSCOATALSDEG---TY 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 NYSTNAALNIISESEVMGADSLTPTCDTDNDQTTCDNLTYQL-PQFKVAAARLNSQNPGM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AGSLFFNFAHDTNITPIL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 NLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSLKYYGYGAG--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 NLTASDVYNLMVMASFELNAR----PFSNWINAFTQDEWVSFGYVEDLNYY-YCAGPGD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 NNILDHGLCTAFEDSTLGDDAEA------NFTAVFAPPIR---ARLEAL-PGV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 YSALIERIQK-NAT-FKGKYAFLKTYNYTL-----GADDLT-PF-GENQWVNSGIKFYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 IEEALAKVYSINTTEYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 RYKAL--ARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                9 DGYQCPEISHLWGQ--YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKK 66
                                                                                                                                                                                                                                                                                                                                                                                                   41 DGYSI -- LKHYGGNGPYSERVSY ---- GIARDPPTSCEVDQVIMVKRHGERYPSPSAGKD 94
                                                                                                                                                                                                                                    Length 479;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                    13.2%; Score 307.5; DB 1;
27.4%; Pred. No. 1.5e-17;
tive 55; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 RYGHLWNGETVVPFF-SSGYGRVIETARKFGEGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 KNMAAVGAVYANASLTLLNQGPKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 VRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 VRLVLNEAVLPFNDCTSGPGYSCPLANYTSILN 431
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A; Residues: 65-66, 68-93 <ULL>
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                 Best Local Similarity
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C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #sequence_revision 19-oct-1995 #text_change 11-Jun-1999
C;Accession: JN0890
C;Accession: JN0890
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; National S5-62, 1993
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optim
A;Reference number: JN0889; MUID:94040796
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A; Residues: 1-479 <PID>
A; Cross-references: GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482
A; Cross-references: Strain ALK0243
C; Comment: The highly similar enzyme from A. ficuum has been shown to have 3-phytase (EC
                                                                                                                                                                                                                                 C; Superfamily: yeast acid phosphatase
C; Superfamily: yeast acid phosphohistidine; phosphoprotein; phosphoric monoester hydrola
C; Keywords: glycoprotein; phosphohistidine; predicted <SIGO-
F;16-468/Product: acid phosphatase #status predicted <AMT>
F;16-468/Product: acid phosphohistidine intermediate) #status predicted
F;163,196,226,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;345/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 GVGFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFFALGLYN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 GTK-PLS----TTSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGEKEPLVRVL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 VTDLPLDQIQFQTSFKSTE-----IVPMGARLLTERLLCTV-----EGEEKYYVRTI 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 DVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEWQYD-YLQSLK-YYGYGAGNPLGPAQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 DIPTIALYGGFELNVRGE----SSFCDVLSREALLYTAYLRDLGWYNVGNGNPLGKTI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 SKSKKYSALIERIQKNATFK---GKYAFLKTYNYTLG-----ADDLTP---FGENQMVNS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 NVGKQLEALYQKL-LDADVEVPTGPLSFFQDYDYFVSDAAWYEQETTKGFYSGLNTAFDF 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GIKFYRRYKALARNIVP----FVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GTTLRERYDHLINTSEEGKKLSVWAGSQERVVDTAKYFAQGFMKSNYTD------MVEV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 IIPE---GSGYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEAL-PGVNLTDE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 VALEEEKSOGLNSLTARISCPNYNSHIYKD---GDFPNDIAEREADRLNTLSPGFNITAD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TVDGYQCPEISHLWGQYSPF----FSLADESAISPDVPKGCRVTFVQVLSRHGARYPTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 TDDQYNI--LRHL-GGLGPYIGYNGWGIAAESEI-----ESCTIDQAHLLMRHGERYPST 91
                                                                        A;Molecule type: DNA
A;Residues: 1.468 <PAY>
A;Cross_references: GB:U28658; NID:9881955; PIDN:AAA85503.1; PID:9881956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 LNDAVFPLSDCSSGPGFSCPLNDYVSRLEALNEDSDFAE 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.4%; Score 334.5; DB 2; Similarity 27.0%; Pred. No. 8.1e-20; 24; Conservative 65; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 VNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAE 434
                     A; Reference number: JC4285; MUID:96001238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 261/1; 300/2; 335/2
                                                                                                                                                                  A; Experimental source: GS115
                                                            A; Accession: JC4285
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                                                                                                                                                                                                               C;Genetics
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Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -463 <LYN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type:
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues:
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A;Gene: phyB
A;Introns: 261/1; 300/2; 335/2
G;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosp
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                            F;20-479/Product: 3-phytase #status experimental <MAT>
F;20-479/Product: 3-phytase #status predicted
F;81,337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riellott, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J. J. Biol. Chem. 261, 2936-2941, 1986
A/Title: Isolation and characterization of the structural gene for secreted acid phospha A; Reference number: A25326; MUID:86140050
A; Accession: A25326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid phosphatase (EC 3.1.3.2) precursor [similarity] - fission yeast (Schizosaccharomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL137099; PIDN:CAB68657.1; GSPDB:GN00067; SPDB:SPBP4G3.02
A;Experimental source: strain 972h(-); clone pl p4G3
C;Genetics:
A;Gene: pho1; SPDB:SPBP4G3.02
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YSALIERIQK-NAT-FKGKYAFLKTYNYTL-----GADDLT-PF-GENQMVNSGIKFYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A25326; T50405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 IEEALAKVYSINTTEYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYKAL--ARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 NNTLDHGLCTAFEDSTLGDDAEA------NFTAVFAPPIR---ARLEAL-PGV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 NYSTNAALNIISESEVMGADSLIPICDIDNDQTICDNLIYQL-PQFKVAAARLNSQNPGM 249
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----FGY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 NLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSLKYYGYGAG--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLTASDVYNLMVMASFELNAR----PFSNNINAFTQDEWVSFGIVEDLNYY-YCAGPGD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 NPLGPAQGVGFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 KNMAAVGAVYANASLTLLNQGP-----KEAGP-----LFFNLAHDINITPIL 345
                                                                                                                                                                                                                                                                                                                                              9 DGYQCPEISHLWGQ--YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKK 66
                                                                                                                                                                                                                                                                                                                                                                          334 FALGLY--NGTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGKEPL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 AALGVLIPNEDLPLDRVAF----GNPYSIGNIVPMGGHLTIERLSCQA---TALSDKGTY 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: DNA
A.Residues: 1-453 <ELL>
A.Cross_references: GB:M11857; NID:g173422; PIDN:AAA35321.1; PID:g173423
R.Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                       Query Match
13.1%; Score 303.5; DB 1; Length 479;
Best Local Similarity 27.4%; Pred. No. 3.1e-17;
Matches 124; Conservative 56; Mismatches 174; Indels 99,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 VRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 VRLVLNEAVLPFNDCTSGPGYSCPLANYTSILN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-453 <RIE>
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C;Species: Schizosaccharonyces pombe;
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1999
C;Accession: S14119; 740455
R;Yang, J; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990
A;Title: The Structural gene cooling for thiamin-repressible acid phosphatase in Schiz A;Accession: S14119; MUID:91064763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: ALO34382; PIDN: CAA22278.1; GSPDB:GN00067; SPDB: SPBC428.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;68/Active site: Arg #status predicted
F;69/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                        80 FKGKY-----AFLKTYNYTL---GADDLTPFGENQMVNSGIKFYRRYKALARNIVPFV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 VPIDYSVSGNPLSFVPTWTPVIEAANADALSSSGRVELFDMGRQFYERYHELFNASTYNI 157
                                                                                                                                                                                                                                                                     Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 RASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLDHGLCTAFEDS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 YTAAQQRVVDSALWYGYGM----FGEDVHNFTNYILVSENATAGSNSLSSYNACPASDAD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 TLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPF 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 CDLF-TADEWQYDYLQSLKYYGYGAGNPL--GPAQGVGFNELIARLTHSPVQDHTSTNHT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 CKLFNSVDFLNFEYEGDLS-FSYGMGNSVKWGSIFGGAYANSLANSLRS-VENNTQ---- 322
                                                                                                                                                                                                                                                                                                            23 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQK----NAT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 LDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGT---KPLSTTSVESIETDGYAASW 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 ------QVFFAFTHDANIIPVETALGFFTDNTPENPLPTS--YQVHSHSMKASE 368
                                                                                                                                                                                                                                                                                                                                                          43 HKPYF-----YGPSIDFPTTCKIKQVHTLQRHGSRNPTGGNAAFDAVGIANFQQRLLNGS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 TVPFAARAYVEMMQCEAGGGGGGGEKEPLVRVLVNDRVVPLHGCGVDKL----GRCKL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 DETTPALEAWRNVYMPPIRQRLNPYFSNYNLTNDDILNLYGICSYEIALQ-----DYSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Cross-references: GB:X56939; NID:95006; PIDN:CAA40258.1; PID:95007 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K. submitted to the EMBL Data Library, November 1998 A:Reference number: 221931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86;
                                                                                                                                                                                             12.8%; Score 298; DB 1; Length 453; 25.6%; Pred. No. 8.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%; Score 290; DB 2; Length 463; 24.3%; Pred, No. 3.9e-16; Live 70; Mismatches 183; Indels {
                                                                                                                                                                                                                                                              63; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain 972h-; cosmid c428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: yeast acid phosphatase
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.38
Matches 109; Conservative
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|                      |  | qq                | 212 VFK                         |
|----------------------|--|-------------------|---------------------------------|
|                      | 2 SKKYSALIERIOK 76   | ì                 |                                 |
| ζŏ                   |  | ΟŊ                | 239 TSD                         |
| Dp 4                 |  | qq                | 272 DH-                         |
| Oy 7                 |  | Qy                | 298 DHT                         |
| op qu                |  | Db                | 305 EWA                         |
| QY 13                |  | Qy                | 347 TTS                         |
| Db 15                | 158 YDINTAAQERVVDSAEWFSYGMFGDDWQNKTNFIVLPEDDSAGANSLAMYYSCP 211   | qq                | 365 TD-                         |
| Qy 11                |  | Qy                | 407 GVD                         |
| Dp 2                 | 212 VYEDNNIDENTTEAAHTSWRNVFLKPIANRLNKYFDSGYNLTVSDVRSLYYICVYEIALR 271   | QQ                | 415 GYG                         |
| Qy 2                 | TSDATQLSPECDLFTADEW-QYDYLQSLKYYGYGAG   | RESULT            | LT 15                           |
| Db 2                 |  | A86233            | 33                              |
| 0y 2                 |  | hypo<br>C; Sp     | hypothetical<br>C;Species: Ar   |
| Db 3                 |  | C; Da<br>C; Ac    | C; Date: U2-Ma<br>C; Accession: |
| QY 3                 | 40   | K;Theo<br>Chin,   | eologis,<br>n, C.W.;            |
| Db 3                 | 366 DKNIFTYSLKTSSFVPFAGNLITELFLCSDNKYYVRHLVNQQVYPLTDCG 415   | ansen,<br>Nature  | N . F.                          |
| Oy 4                 | 408 VDKIGRCKLDDFVEGLSFARSGGN 431   | A; Aut.<br>C.A.;  | hors:<br>Li,                    |
| Dp 4                 | 416 YGPSGASDGLCELSAYLNSSVRVNSTSN 443   | Rizzo,<br>A;Autho | Rizzo, M.; Ro<br>A;Authors: Sa  |
|                      | • `  | ker,<br>A;Ti      | ker, M.; Wu,<br>A;Title: Sequ   |
| RESULT<br>T39929     | 14 (Schimosacharomyces Dombe)  | A; Re<br>A; Ac    | A;Reference :<br>A;Accession:   |
| thiamir<br>C;Speci   | -repressible acid phospharase libsion read (common part)   | A;St<br>A;Mc      | A;Status: pro<br>A;Molecule t   |
| C; Date              | 03-Dec-1999 #sequence_revision 03-Dec-1999 #teat_cummyc_r con 2005   | A; Re             | A; Residues:                    |
| R;Lyne,<br>submitt   | Rilyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S. submitted to the EMBL Data Library, May 1998  | C; Gene<br>A; Map | C;Genetics:<br>A;Map positi     |
| A; Refe              | ence number: 2185/<br>ision: T39929  |                   |                                 |
| A; Stati<br>A; Molec | Sistem in the state of the stat | ÕÃ                | Query Matc<br>Best Local        |
| A; Resid<br>A; Cros: | lues: I-403 <liny<br>5-references: EMBL:AL023286; PIDN:CAA18863.1; GSPDB:GN00067; SPDB:SPBC21H7.03c</liny<br>  | Ř                 | tches                           |
| A; Expe.             | imental source: strain 9/2n~; cosmiu cziń/<br>lics:  | Qy                | 38 DV                           |
| A; Gene              | : SPDB:SPBC21H7.03c  | qa                | 50 NV                           |
| C; Supe              | rfamily: yeast acid phosphatase  | Qy                | 76 KN                           |
| Oner                 | Score  | qa                | 110 WK                          |
| Best Lo              | Similarity 24.9%;<br>3; Conservative 6   | QY                | 132 SG                          |
| 2                    | YSPFFSLADESAIS   | QQ                | 160 TC                          |
| Z QQ                 |  | Qy                | 192 GI                          |
| λÓ                   | 71 IERIQKNATF-KGKYAFLKTYNYTLGADDLTPFGENOMVNSGIKFYRRYKALARNIV 126   | QQ                | 199 AS                          |
| qo                   | 98 NGSIPVNFSYPENPLCFIKQWIPVIDAENADQLSSRGRLELFDLGRQLYQRYYKLFDSYV 157  | Qy                | 249 CI<br>                      |
| ò                    | SAEKFIEGFQSAKLADPAHQASPVINVIIPEG   | qq                | 259 CI                          |
| ' 원                  | : :  :  :  :  :  :  :  : ::::  :::: ::::::   | ÓΫ                | 309 N                           |
| Qy                   | 185 AFEDSTLGDDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPFDTVAR 238   | qa                | 312 -                           |
| 7                    | -  |                   |                                 |

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Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rooney, T.; Rowley, D.; Sakano, H. Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo J., Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. squence and analysis of chromosome 1 of the plant Arabidopsis.

1. A86233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Hughes, B.; Huizar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erences: GB:AE005172; NID:92160177; PIDN:AAB60740.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | protein [imported] - Arabidopsis thaliana
Arabidopsis thaliana (mouse-ear cress)
Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3DDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMC---PFDTVARTSDATQLSPF 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLFTADEWQYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQDHTSTNHTLDS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKQVALLEWT-DDLEVFLLKGY--GNSLNYKMGV---PLLEDVLHSMEEAIKAREEKLP- 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPSECTPIHLNLVARHGTRSPTKKRLRELESLAGRFKELVRDAEARKLPSDKIPGWLGQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKSPWEGK-----VKGGELIRQGEDELYQLGIRVRERFPSLFEEDYHPDVYTIRA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLDHGLCTAFEDSTL 191
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                                                                                                                                                                 TST-----NHTLDS--NPATFPLNATLYADFSHDNTMVSIFFALGLY---NGTKPLS 346
                                                                                                                                                                                                    SVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGC 406
212 VEKDNNFHKNATDAAHAVWRNIFIEPIVNRLAKYFDSSYKLTINDVRSLFYICEYEIAIK 271
                                                       DATQLSPFCDLFTADEW-QYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQ 297
                                                                                                            ----SDFCSIFTPSEFLNFEYDSDLD-QAYGGG-----PVS 304
                                                                                                                                                                                                                                                                                                                 6.6%; Score 154; DB 2; Length 468; 22.9%; Pred. No. 7.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Mismatches 184; Indels
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

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US-09-488-265-27
2321
1 NSHSCDTVDGYQCPEISHLW......DFVBGLSFARSGGNWAECFA 437 Title: Perfect score:

Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   |            | 34753 |        | 0093 | P35842 saccharomyc | P38693 saccharomyc | P24031 saccharomyc | P00635 saccharomyc | _     |       |       |             |         |      |     |       |     |       |       |       | _     | P11117 homo sapien |      |      | P42666 plasmodium |               | P09043 nicotiana t | _    |      | Q00103 ictalurid h | _     |         | 12  |            |
|-----------|---------------|------------|-------|--------|------|--------------------|--------------------|--------------------|--------------------|-------|-------|-------|-------------|---------|------|-----|-------|-----|-------|-------|-------|-------|--------------------|------|------|-------------------|---------------|--------------------|------|------|--------------------|-------|---------|-----|------------|
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|           | Length D      | 467        |       |        |      |                    |                    | 467                |                    |       |       |       |             |         |      |     |       |     |       |       |       |       | 423 I              |      |      |                   |               |                    |      | * C  |                    | 2 4 6 | 1 2 7 L | ) C | 9          |
| dР        | Query         | 72.7       | 72.6  | 72.2   | 15.3 | Ľ                  |                    | 'n                 | ٠                  | 14.4  | 13.2  | 1 (*) | 12.9        | ( )     | 1 () | ıv  | . 4   | \ a |       |       |       | . 4   | 7 4                |      | 4.2  | 4.2               | 4.2           | 4.2                | 4.2  |      | . 4                | •     |         | •   |            |
|           | Score         | 1688       | 1684  | 1676.5 | 356  | 356                | 353                | 347                | 337                | 334.5 | 307.5 | 305.5 | 300.5       | 298     | 290  | 125 | 113.5 | 111 | 108 5 | 107.5 | 104 5 | 104 5 | 102                | 86   | 98.5 | 98.5              | 97.5          | 97                 | 96.5 | 96.5 | 96.5               | , r   | 0.0     |     |            |
|           | Result<br>No. | 7          | 7     | ٣      | 4    | 5                  | 9                  | 7                  | 00                 | 6     | 10    | 11    | 12          | 13      | 14   | 15  | 16    | 17  | 8     | 19    | 20    | 21    | 22                 | 23   | 24   | 25                | 26            | 27                 | 28   | 29   | 30                 |       | 32      |     | )          |

| chlamydia t<br>butyrivibri<br>thermoanaer<br>escherichia<br>escherichia<br>mycoplasma<br>rattus norv<br>erwinia chr<br>human enter<br>escherichia<br>pediococcus<br>homo sapien |
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| 084834<br>P30269<br>P19584<br>P06995<br>P19926<br>P222<br>P15922<br>P15922<br>P15922<br>P15922<br>P15927<br>P22105  |
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| RIRL_CHLTR<br>AMY BUTFI<br>AMYB_THETU<br>NPL_ECOLI<br>AGF_ECOLI<br>MGPC_MYCGE<br>MRP3_RAT<br>PCHK_ERWCH<br>PCL_HT71B<br>QUEA_ECOLI<br>RPOC_HT71B<br>QUEA_ECOLI<br>RPOC_PEDAC    |
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                 118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASFVINVIIPEGSGY 174
                                                                                                                                                                                                                                                    59 PISSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                Indels 18; Gaps
                                                                                                                                                                                                      1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE-93252284; PubMed-8387447;
van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M.,
Gouka R.J., Suykerbuyk M.E.G., Luiten R.G.M., van Partidon P.A.,
Selten G.C.M., Veenstra A.E., van Gorcom R.F.M.,
                                                                    (POTENTIAL)
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  (POTENTIAL)
                                                                                                                                                       72.7%; Score 1688; DB 1; Length 467; 73.9%; Pred. No. 1.6e-132;
Live 40; Mismatches 59; Indels 18
                                                                                                           N-LINKED (GLCNAC. . .) (P. 118E828A5D7EC661 CRC64;
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01-FEB-1994 (Rel. 28, Last sequ
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467 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
BIOTECHNOLOGY: IS USED AS A FOOD AND FEED ADDITIVE. IT CAN
FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
USED AS FOOD FOR MONOGASTRIC ANIMALS. SOLD BY NOVO NORDISK UNDER
"Cloning, characterization and overexpression of the phytase-encoding gene (phyA) of Aspergillus niger."; Gene 127:87-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell D., van Loon A.P.;
                                                                                                                                                      STRAIN=NREL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE-93249451; PubMed=8387289;
Ullah A.H.J., Dischinger H.C. Jr.;
"Aspergillus ficuum phytase: complete primary structure elucidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i - SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ullah A.H.J.; Aspergillus ficuum phytase: partial primary structure, substrate selectivity, and kinetic characterization."; Prep. Biochem. 18:459-471(1988).
                                                                                                                                                                                                                                                                                                                           Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.; "Cyclohexanedione modification of arginine at the active site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "orystal structure of phytase from Aspergillus ficuum at 2.5-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O
                                                                                                     Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                      by chemical sequencing.";
Biochem. Biophys. Res. Commun. 192:747-753(1993).
                                                                                                                                                                                                                                                                                                                                                                 Aspergillus ficuum phytase.";
Biochem. Biophys. Res. Commun. 178:45-53(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycoprotein; Signal; 3D-structure.
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-PHYTASE A.
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MEDLINE=97307250; PubMed=9164457;
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MEDLINE=89160685; PubMed=2852807;
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                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resolution.";
Nat. struct. Biol. 4:185-190(1997).
                                                                                                                                                                                                                                                                                                       STRAIN-NRRL 3135 / VAN TIEGHEM /
MEDLINE-91298982; PubMed-1648914;
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361
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PIR; PN0023; PN0023.
PIR; JN0656; JN0656.
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InterPro; 1PR000560;
                                                                                                                                                  SEQUENCE OF 24-464.
                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
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                                                                                                                                                                                                                 18;
                                                                                                                                                                                     72.6%; Score 1684; DB 1; Length 467; 73.9%; Pred. No. 3.4e-132; ative 40; Mismatches 59; Indels 16
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Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                       88FE8F3584341D6D CRC64;
                                                                                    (GLCNAC. . .).
(GLCNAC. . .).
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(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
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                                                                                                                                                                                                       Matches 331; Conservative
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                                                                                                                                                                                              Local Similarity
                                                                                                                                                       467 AA;
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Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,

MEDLINE=98007872; PubMed=9349716;

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                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED GELCNAC...) (POTENTIAL).
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                      thermophilic fundus Talaromyces thermophilus.";
Biochim. Biophys. Acta 1353:217-223(1997).
-1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.2%; Score 1676.5; DB 1; Length 463; 73.4%; Pred. No. 1.4e-131;
                                                                                                                                                                                                                                                                                                                                                                    REQUIRED FOR BINDING SUBSTRATE
van Loon A.P.; "Cloning of the phytases from Emericella nidulans and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECC5827D1E1C82A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
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                                                                                                                                                                                                                                                                         Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                     3-PHYTASE B.
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331
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463 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALCOHOL + ORTHOHOSPHATE.

-!- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
-!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                   SIRALN=S2090. A. D. PubMed=7731988; MEDLINE=95249563; PubMed=7731988; Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N., Bussey H., Kaback D.B., Zhong T., Barton A.B., Su Y., Davies C.K., Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen J.Y., Gong Y.I., Ao S.Z.;
Chen J.Y., Gong Y.I., Ao acid phosphatase gene PHO11 in S.
"The primary structure of acid phosphatase gene families.";
cervoisiae and comparison with other gene families.";
Acta Biochim. Biophys. Sin. 21:437-444(1989).
-i- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
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(GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence of chromosome I from Saccharomyces
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                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
ACID PHOSPHATASE PHO11 PRECURSOR (EC 3.1.3.2) (P56).
                                                                                                                                                                                                                                                                                                                                                                                                cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
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                       413 RCKLDDFVEGLSFARSGGNWAECF 436
                                        438 RCTLDDWVEGLNFARSGGNWKTCF 461
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S0000094; PHO11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 VARTSDATQLSPFCDLFTADEW-QYDYLQSLK-YYGYGAGNPLGPAQGVG-FNELIARLT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 NAR-----GYSDICNIFTKDELVRFSYGQDLETYYQTGPGYDVVRSVGANLFNASVKLLK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFFALGLYNGTKPLSTTSVES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 ESEVQDQ-----KVWLSFTHDTDILNYLTTIGIIDDKNNLTAEHVPF 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 SNYTGQFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVLNPYTGEMNAKRHARDFLAQ 155
                                                                                                                                                                                               15.3%; Score 356; DB 1; Length 467;
26.9%; Pred. No. 5.2e-22;
tive 63; Mismatches 190; Indels 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    75 QK-NATFKGKYAFLK-----TYNYTL-----GADDLTPF-GENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                 15 EISHLWGQYSPPFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERI 74
                                                                                                                                                                                                                                                                                                                                  36 EIFPFLGGSGPYXSFFGDYGISRDLPESCEMKQVQMVGRHGERYPTVSKAKSIMITWYKL 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                           AECDCIC046B326C3 CRC64;
A -> L (IN REF. 2).
VS -> AR (IN REF. 2).
R -> H (IN REF. 2).
R -> Q (IN REF. 2).
D -> G (IN REF. 2).
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
ACID PHOSPHATASE PHO12 PRECURSOR (EC 3.1.3.2).
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MEDLINE-94378003; PubMed-8091229;
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Matches 119; Conservative
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STRAIN-S288C / AB972;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
               INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE. PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE. SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 YKALARNIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNN 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 EISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 ESEVQDQ------KVWLSFTHDTDILNYLTTIGIIDDQNNLTAEHVPF 364
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PROTON DONOR (BY SIMILARITY)
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                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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 ALCOHOL + ORTHOPHOSPHATE
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Matches 119; Conservative
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HSSP; P34752; 1IHP.
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                                                                                                                                                                                                                                                                                                                                                                         Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H., "Analysis of a 70 kb region on the right arm of yeast chromosome II.";
                                                                                                                                                                                                                                                   MEDLINE-85037940; PubMed-6093051; Bajva W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.; Structural analysis of the two tandemly repeated acid phosphatase genes in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
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-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
                                                                                                                                                                                                                                                                                                                                                                                                                            ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                        CONSTITUTIVE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
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05FBB80DEB41B0FF CRC64;
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N-LINKED (GLCNAC. .)
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PROSITE; PSO0616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PSO0778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
SIGNAL
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                                                                                                01-MAR-1992 (Rel. 21, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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N-LINKED (GLCNAC.
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415 SCEINDFYGYAEKRVAGTDFLK 436
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                                                                                                                                                         OR YBR092C OR YBR0813
                                                                             STANDARD;
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SGD; S0000296; PHO3.
InterPro; IPR000560; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-83168913; PubMed-6330772;
Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.;
"The nucleotide sequence of the yeast PHOS gene: a putative precursor
of repressible acid phosphatase contains a signal peptide.";
Nucleic Acids Res. 11:1657-1672(1983).
                                                                                                                                                                                                                                                                                                                                    214 ACPGWDEDANDDILDKYDTTYLDDIAKRLNKENKGLNLTSKDANTLFAWCAYELNAR--- 270
                                                                                                                                                                                                                                                                                                                                                                         242 ATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVG-FNELIARLTHSPVQD 298
                                                                                                                                                                                                                                                                                                                                                                                                           271 --GYSDVCDIFTEDELVRYSYGODLVSFYQDGPGYDMIRSVGANLFNATLKLLKQSETQD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                299 HTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIETDGY 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LKVWLSFTHDTDILNYLTTAGIIDDKNNLTAEYVPFM-GNTF 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 FKGKYAFLK-TYNYTLGADD------LTPF-GENQMVNSGIKFYRRYALAR 123
                                                                                                                                                                                                                        124 NIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLDHGL 182
                                                                                                                                                                                                                                                 Í83 CTAFEDSTLGDDAEANFTAVFAPPIRARL-EALPGVNLTDEDVVNLMDMCPFDTVARTSD 241
                                                                                                                                                                                  102 FNGSLSFLNDDYEFFIRDDDDLEMETTFANSDNVLNPYTGEMDAKRHAREFLAQYGYMFE 161
                                       70; Gaps
                                                                                                    42 GGAGPYFSFPGDYGISRDLPEGCEMKQLQMLARHGERXPTYSKGATIMKTWYKLSNYTRQ 101
                                                                        21 GQYSPFFSLADESAIŞPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQK-NAT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-85037940; PubMed-6093051;
Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.;
"Structural analysis of the two tandemly repeated acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-101-1986 (Rel. 01; Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (P60).
     Length 467;
15.2%; Score 353; DB 1; Length 46
26.8%; Pred. No. 9.3e-22;
tive 62; Mismatches 187; Indels
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                                               Matches 117; Conservative
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P00635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 FKGKYAFLK-TYNYTLGADD-----LTPF-GENQMVNSGIKFYRRYKALAR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 GGAGPYYSFPGDYGISRDLPEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQK-NAT 79
                                                                 cluster within the acid phosphatase multigene family of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
                                                                                           cerevisiae.";
Mol. Cell. Biol. 6:1855-1865(1986).
-!-CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                           -i- SUBCELLULAR LOCATION: SECRETED.
-i- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE.
-i- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                      Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott O.D., Bostian S.J., Thill G.P., Rogers D.T., Bostian K.A.; "Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOPHILIC ACCEPTOR (BY SIM
PROTON DONOR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> K (IN REF. 1).
DC3C9504BC2D3D0C CRC64;
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S -> V (IN REF. 1).
AS -> DT (IN REF. 1).
R -> K (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase, Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00328; acid phosphat; 1. proSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1. proSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
SEQUENCE OF 1-44 FROM N.A. MEDLINE-87064474; PubMed=3537710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52858 MW;
                                                                                                                                                                                                                                                                                                                                                              EMBL, X01079; CAA25555.1;
EMBL, X78993; CAA55598.1;
EMBL, Z35962; CAA85046.1;
EMBL, X01080; CAA25556.1;
                                                                                                                                                                                                                                                                                                                                                  EMBL; V01320; CAA24630.1; -.
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Matches 117; Conservative
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PIR; B25241; B25241.
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466
467 AA;
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SGD; S0000297; PHO
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97
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                               162 NQTSFAVFTSNSKRCHDTAQYFIDG-----LGDQ------FNITLQTVSEAESAGANTL 209
124 NIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVII-----PEGSGYNNT 177
                                                                178 LDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARL-EALPGVNLFDEDVVNLMDMCPFDTV 236
                                                                                                                                    237 ARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVG-FNELIARLTH 293
                                                                                                                                                                     268 ----NAKGYSDVCDIFTKDELVHYSYYQDLHTYYHEGPGYDIIKSVGSNLFNASVKLLKQ 323
                                                                                                                                                                                                        294 SPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESI 353
                                                                                                                                                                                                                                         324 SEIQDQ------KVWLSFTHDTDILNFLTTAGIIDDKNNLTAEYVPFM 365
                                                                                                   210 SACNSCPAW-DYDANDDIVNEYDTTYLDDIAKRLNKENKGLNLTSTDASTLFSWCAFEV- 267
                                                                                                                                                                                                                                                                                                  366 -GNTFHRSWYVPQGARVYTEKFQC-----SNDTYVRYUNDAVVPIETCSTGPGFS 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROBABLE ACID PHOSPHATASE YDL024C.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONGR (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                          354 ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andre B., Vissers S., Urrestarazu L.;
Submitted (FEB-1995) to the EMBL/Genbank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN ALCOHOL + ORTHOPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROBABLE ACID PHOSPHATASE YDL024C PRECURSOR (EC 3.1.3.2).
YDL024C OR D2815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00128; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
HydroLase; Glycoprotein; Signal; Multigene family.
SIGNAL

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 AA.
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                                                                                                                                                                                                                                                                                                                                              414 CKLDDF-----VEGLSFAR 427
                                                                                                                                                                                                                                                                                                                                                                               416 CEINDFYDYAEKRVAGTDFLK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z48432; CAA88335.1; -.
EMBL; Z74072; CAA98583.1; -.
SGD; S0002182; YDL024C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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P52290;
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                                                                                                                                                                                                                                                                          100 TGKYEGSLSFLNNGYEFFIPDESLLEMETTLONSIDVLNPYTGEMNAKRHAREFLAKYGK 159
                                                                                                                                                                                                                                              81 KGKY----AFLKT-YNYTL-------GADDLTPF-GENQMVNSGIKFYRYKA 120
                                                                                                                                                                                                                                                                                                      121 LARNIVPF-VRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLD 179
                                                                                                                                                                                                                                                                                                                                  160 LMENCTNFPIFTTNSKRIYDTAQYFAEAL--------GDGFNISLQ 197
                                                                                                                                                                                                                                                                                                                                                                  198 ----TLSENSSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLENISDRLNDENKGLNLS 253
                                                                                                                                                                                                                                                                                                                                                                                                                          221 DEDVYNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGP 278
                                                                                                                                                             60; Mismatches 161; Indels 118; Gaps
                                                                                                                                                                                        21 GQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQKNATF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                             309 SIGANLFNATVKLIRQSAH-----347
                                                                                                                                                                                                         279 AQGVG-FN---ELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 ALGLYNGTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGEKEPLVRV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .) (POTENTIAL).
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       .) (POTENTIAL).
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-:- INDUCTION: BY PHOSPHATE STARVATION.
-:- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Payne W.E., Gannon P.M., Kaiser C.A.;
"An inducible acid phosphatase from the yeast Pichia pastoris: characterization of the gene and its product.";
Gene 163:19-26(1995).
                                                                                                                                 14.5%; Score 337; DB 1; Length 468; 26.0%; Pred. No. 2e-20;
                                                            N-LINKED (GLCNAC. .) (PO N-LINKED (GLCNAC. .) (PO 1F07FF374DDF16ZC CRC64;
                               (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) ACID PHOSPHATASE PHO1 PRECURSOR (EC 3.1.3.2).
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 251 N-316 N-357 N-457 N-462 N-53076 MW;
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01-0CT-1996 (Rel. 34, Last sequ
01-0CT-1996 (Rel. 34, Last anno
                                                                                                                            Query Match
Best Local Similarity 26.08
Matches 119; Conservative
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                                                                    462
468 AA;
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P52291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 DVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEWQYD-YLQSLK-YYGYGAGNPLGPAQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 GVGFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 GTK-PLS----TTSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGEGEKEPLVRVL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 VIDLPLDQIQFQTSFKSTE-----IVPMGARLLTERLLCTV-----EGEEKYYVRTI 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 VALEEEKSQGLNSLTARISCPNYNSHIYKD---GDFPNDIAEREADRLNTLSPGFNITAD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GIKFYRRYKALARNIVP----FVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 IIPE---GSGYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEAL-PGVNLTDE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 SKSKKYSALIERIQKNATFK---GKYAFLKTYNYTLG-----ADDLTP---FGENOWVNS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 NVGKQLEALYQKL-LDADVEVPTGPLSFFQDYDXFVSDAAWYEQETTKGFYSGLNTAFDF 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TVDGYQCPEISHLWGQYSPF----FSLADESAISPDVPKGCRVTFVQVLSRHGARYPTS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 TDDQYNI--LRHL-GGLGPYIGYNGWGIAAESEI-----ESCTIDQAHLLMRHGERYPST 91
                                                                                                                                                                                                                                                              NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Last sequence update).
30-MAY-2000 (Rel. 39, Last annotation update).
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSTIOL-HEXAPHOSPHATE 3-PHOSPHOYPROLASE B) (PH 2.5 OPTIMUM ACID PHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%; Score 334.5; DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Mismatches 187; Indels
                                                                                                                                            InterPro; IPR000550; -...
Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                 ACID PHOSPHATASE PHO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 LNDAVFPLSDCSSGPGFSCPLNDYVSRLEALNEDSDFAE 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 VNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.2e-20;
                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequalomAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                52690 MW;
                                                                                                                EMBL; U28658; AAA85503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 124; Conservative
                                                                                                                                                                                                                                                                                                          163
196
256
                                                                                                                                                                                                                                                                                                                                                                                                                468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHYB OR APH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHYB_ASPAW
P34755;
                                                                                                                                                                                                                                                                                            ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local
                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 YSALIERIQK-NAT-FKGKYAFLKTYNYTL-----GADDLT-PF-GENQMVNSGIKFYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYKAL--ARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 IEEALAKVYSINTTEYKGDLAFLNDWTYIVPNECYYNAETTSGPYAGLLDAYNHGNDYKA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 DGYQCPEISHLWGQ--YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKK 66
                                                                                                             piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A., Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.; "The cloning and sequencing of the genes encoding phytase (phy) and ph 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 DGYSI--LKHYGGNGPYSERVSY----GIARDPPTSCEVDQVIMVKRHGERYPSPSAGKD
                                                                                                                                                                                                                                                                                                2.4.A resolution.";
J. Mol. Biol. 288:965-974(1999).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                      MEDLINE-99264417; Pubmed-10329192;
KOStrewa D., Wyss M., D'Arcy A., van Loon A.P.;
"Crystal structure of Aspergillus niger PH 2.5 acid phosphatase at
     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                   -i - SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY
                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.-i- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%; Score 307.5; Db 1,
... Pred. No. 5.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4F8E0F3778CC3B08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
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NUCLEOPHILIC ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00328; acid phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTON DONOR
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                                                                                                      MEDLINE=94040796; PubMed=8224894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52678 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L02420; AAA16897.1; -. PIR; JN0890; JN0890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 124; Conservative
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441
298
421
191
315
458
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PDB; 1QFX; 19-APR-00.
                                                                                                                                                                                                  Gene 133:55-62(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000560;
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225
413
191
315
458
479 AA;
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Best Local Similarity
Aspergillus awamori
                                         NCBI_TaxID=105351;
                                                                             SEQUENCE FROM N.A.
                                                                                          STRAIN-ALK0243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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24;
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                                                                                                                                                                                                                                                                               95 IEEALAKVYSINTTEYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKA 154
                                                                                                                                                                                                                                                                                                            117 RYKAL--ARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASFVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                    175 NNTLDHGLCTAFEDSTLGDDAEA------NFTAVFAPPIR---ARLEAL-PGV 217
                                                                                                                                                                                                                                                                                                                                                                                              191 NYSTNAALNIISESEVMGADSLIPTCDTDNDQTTCDNLTYQL-PQFKVAAARLNSQNPGM 249
                                                                                                                                                                                                                                                                                                                                                                                                                          218 NLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSLKYYGYGAG--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                            99; Gaps
                                                                                                                                                                                               9 DGYQCPEISHLWGQ--YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKK 66
                                                                                                                                                                                                                  274 NPLGPÄQGVGFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 KNMAAVGAVYANASLTLLNGGP-----KEAGP-----LFFNFAHDTNITPIL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 FALGLY--NOTKPLSTTSVESIETDGYAASWTVPFAARAYVENMQCEAGGGGGGGEKEPL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 AALGVLIPNEDLPLDRVAF----GNPYSIGNIVPMGGHLTIERLSCOA---TALSDKGTY 398
  N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                          Query Match 13.2%; Score 305.5; DB 1; Length 479; Best Local Similarity 27.4%; Pred. No. 8.4e-18; Matches 124; Conservative 57; Mismatches 173; Indels 99
                                                                                               395D4DA2B50FDFC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 VRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 VRLVLNEAVLPFNDCTSGPGYSCPLANYTSILN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                  52611 MW;
    191
227
250
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425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferminan E.;
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CARBOHYD
CARBOHYD
                            CARBOHYD
                                           CARBOHYD
                                                                    CARBOHYD
                                                        CARBOHYD
                                                                                                  SEQUENCE
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21;
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 ETSGANSLIPPADSCMTY-NGDLGDEYFENATLPYLTDIKNRWMKKNSNLNLTLEHDDIEL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 IMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPL-GPAQGVG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 LVDWCAFETNVKGSSAV-----CDLFERNDLVAYSYYANVNNFYRRGAGNPMSNPIGSVL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 FNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY-NGT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 VNASYNLLTQADELDN-----KVWLSFSHDTDIQQFISALGLIDNGV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 KPLSTTSV--ESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGEKEPLVRVLVNDRV 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 TEYSLDQVDFQNIQ----QLSWVTPMGGRIFTEKLKC------GNASYVRYIINDVI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 --SGYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRAR-LEALPGVNLT--DEDVVN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 ---FQGQY-----NDPLEVFNDYEFFVSNTKYFDQLTNSTDVDPSNPYAGAKTA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 ----KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINV---IIPEG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 QHLGKYIAYNYGDLF--SDSNPVFTSSSGRVH--QTAKYVVSSLEEELDIQLDLQIIQEN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 SHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 SLLNGQ-GPHYDYPQSFGIPVEVPDQCTVEHVOMLARHGERYPTASKGKLMIALWDKLKE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                               REPRESSIBLE ACID PHOSPHATASE.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%; Score 300.5; DB 1; Length 469; 25.9%; Pred. No. 2.1e-17; tive 66; Mismatches 172; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              863B528D0740AA7E CRC64;
                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC...) (
                                                                                                                                                          Interto: Interval, Interval, Interto: pro0328; acid_phosphat; 1.
pro031E; ps00616; HIS_ACID_PHOSPHAT_1; 1.
pro05ITE; ps00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprofein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 NATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 VPLHGCGVDKLGRCKLDDF-----VEGLSFARS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 IPVPGCTSGPGFSCPIEDFDDYITNRLNGIDYVSS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC
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01-AUG-1988 (Rel. 08, Last sequence update)
                                                                                          or send an email to license@isb-sib.ch).
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Matches 118; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                 "Isolation and characterization of the structural gene for secreted acid phosphatase from Schizosaccharomyces pombe."; J. Biol. Chem. 261:2936-2941(1986).
                                                                                                                                                                   Elliott S., Chang C., Schweingruber M.E., Schaller J., Rickli E.E.,
                                                                                                                                                                                                                                                                                         Rieger M., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
ALCOHOL + ORTHOPHOSPHATE.
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-i - INDUCTION: REPRESSED BY PHOSPHATE AND WEAKLY BY THIAMINE.
-i - SIMILARITY: BELONGS TO THE HISTIDINE ACID PHÖSPHATASE FAMILY.
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                                                           Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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01-OCT-2000 (Rel. 40, Last annotation update) ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
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PR05ITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PR0SITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Cell wall; Signal.
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                                              Schizosaccharomyces pombe (Fission yeast).
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Matches 107; Conservative
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PIR; A25326; A25326.
HSSP; P34752; 11HP.
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453 AA;
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                                  PHO1 OR SPBP4G3.02.
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                                                                                                               NCBI_TaxID=4896
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                                                                                          190 TLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPF 248
                                                                                                                                                         214 DFTTPALEAWRNVYMPPIRQRLNPYFSNYNLTNDDILNLYGICSYEIALQ-----DYSEF 268
                                                                                                                                                                                                                           249 CDLF-TADEWQYDYLQSLKYYGYGAGNPL--GPAQGVGFNELIARLTHSPVQDHTSTNHT 305
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"The structural gene coding for thiamin-repressible acid phosphatase
in Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 TVPFAARAYVEMMQCEAGGGGGGGEKEPLVRVLVNDRVVPLHGCGVDKL----GRCKL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THIAMINE-REPRESSIBLE ACID PHOSPHATASE. NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
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Submitted (NOV-1998) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 - AN
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--- SUBCELLULAR LOCATION: CELL WALL.
--- INDUCTION: REPRESSED BY THIAMINE.
--- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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01-007-2000 (Rel. 40, Last annotation update)
THIAMINE REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
PHO4 OR SPBC428-03C.
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Cell wall; Signal.
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01-JUL-1993 (Rel. 26, Last seq
01-OCT-2000 (Rel. 40, Last anno
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PPA2_SCHPO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                     98 NGSIPVNFSYPENPLYFVKHWTPVIKAENADQLSSSGRIELFDLGRQVFERYYELFDTDV 157
                                                                                                                                                                                                            86; Gaps
                                                                                                                                                                                                                                                                                                                                                127 PFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPE--GSGYNNTLDHGLCT 184
                                                                                                                                                                                                                                                                                                                                                                            158 YDINTAAQERVVDSAEWFSYGMFGDDMQNKTN-----FIVLPEDDSAGANSLAMYYSCP 211
                                                                                                                                                                                                                                                                                                                                                                                                         185 AFEDSTLGDD----AEANFTAVFAPPIRARLEAL--PGVNLTDEDVVNLMDMCPFDTVAR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 TSDATQLSPFCDLFTADEW-QYDYLQSLKYYGYGAGNPLGPAQ------GVGFNELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY---NGTKPLST 347
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                                                                                                                                                                                                                                23 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSS-----KSKKYSALIERIQK 76
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                                                                                                                                                                                                                                                            43 HEPYF-----NGPTTSFPESCAIKQVHLLQRHGSRNPTGDDTATDVSSAQYIDIFQNKLL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
Matthews P., Lloyd C.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN ALCOHOL + ORTHOPHOSPHATE.
                                                                                            (POTENTIAL).
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                                                                                                                                                                         12.5%; Score 290; DB 1; Length 463; 24.3%; Pred. No. 1.5e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 KYAFLKTYNYTLGADDLIPFGENQMVNSGIKFYRRY------KALARNIVPFVRASG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 SDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIP-----EGSGYNNTLD----- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 ----HGL-------CTAFED-----STLGDDAEANFTAVFAPPIRARLEALPGVNLT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
5.4%; Score 125; DB 1; Length 755;
Best Local Similarity 20.5%; Pred. No. 0.015;
Matches 90; Conservative 58; Mismatches 122; Indels 170; Gaps
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PROTON DONOR (BY SIMILARITY).
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702 708 B
755 AA; 87783 MW;
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Search completed: October 26, 2001, 15:18:03 Job time: 449 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 26, 2001, 15:17:24; Search time 75.85 Seconds (without alignments) 762.258 Million cell updates/sec

US-09-488-265-27 Perfect score:

1 NSHSCDTVDGYQCPEISHLW.......DFVEGLSFARSGGNWAECFA 437 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

425026 segs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_archea:\*
sp\_bacteria:\*
sp\_fung1:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_rodent:\*
sp\_unclassified:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\* SPTREMBL\_16:\* sp\_mhc:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_vertebrate:\*

sp\_varus:\*

SUMMARIES

|   | Description              |        | 000092 aspergillus | Q9uuz7 aspergillus | 093838 aspergillus | Oghed asperdilus |        |        |        | -      | 000107 thielavia h |        |        |       |           | Q9vv72 drosophila | 096421 droeonbila |        |        | Q9w438 drosophila | Q9uga3 homo sapien | 035217 rat + 132 none | Object Lateus norv | Cannal nomo sapien | OUST 72 HOMO CELEVISION |
|---|--------------------------|--------|--------------------|--------------------|--------------------|------------------|--------|--------|--------|--------|--------------------|--------|--------|-------|-----------|-------------------|-------------------|--------|--------|-------------------|--------------------|-----------------------|--------------------|--------------------|-------------------------|
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|   | Query<br>Match Length DB | 165    | 767                |                    | 404                | 40/              | 466    | . 466  | 466    | 201    |                    | 442    | 469    | 463   |           | 7 .               | 404               | 453    | 453    | 707               |                    | 4 5 T                 | 487                | 487                | ,                       |
| ф | Query<br>Match           | 75.9   | 72.5               |                    | 7.6                | 0.17             | 8.80   | 68.4   | 67.3   | ייי    |                    | 13./   | 12.9   | 12.3  | )<br>  01 |                   | 0                 | 8.3    | 8,3    | 7 6               | . 1                | ٥./                   | 7.5                | 7.5                |                         |
|   | Score                    | 1762.5 | 1683               | 1672               | 101                | 1000             | 1086.5 | 1588   | 1562.5 | 1275.5 | 217 5              | 0.710  | 2.88.2 | 285   | 207 5     | 106               | 100               | 192.5  | 191.5  | 176               | 175                | C / T                 | 174                | 173                |                         |
|   | Result<br>No.            | -      | 7                  | m                  | > <                | * 4              | יח     | ٥      | .7     | 80     | σ                  | ,      | 7      | 11    | 12        | 13                |                   | T-4    | 15     | 16                | 17                 | - C                   | 18                 | 19                 |                         |

| Q92216 mus musculu 092170 gallus gall 004509 arabidopsis Q91x1 schloseacch 09195 mus musculu 09195 mus musculu 09195 mus musculu 09195 mus musculu 000838 leishmania 000839 leishmania Q91559 drosophila Q91559 drosophila 09187 drosophila 09147 drosophila 091574 drosophila 091574 drosophila 091574 drosophila 091574 drosophila 091573 leishmania 02533 leishmania 02533 leishmania 02533 drosophila 02533 leishmania 02533 drosophila   | Ogusta drosophila |
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| Q922L6<br>Q92170<br>004509<br>Q9UXI<br>Q9UXI<br>Q9OXG5<br>Q9OXG5<br>Q9US39<br>Q9US39<br>Q9US18<br>Q9US18<br>Q9TW17<br>Q9TW17<br>Q9TW17<br>Q9TW17<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW10<br>Q9TW  | 2905T3            |
| 111<br>111<br>111<br>111<br>111<br>111<br>111<br>111<br>111<br>11   | D.                |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4   | 447               |
| L C C C C C C C C C C C C C C C C C   | 4.5               |
| 172<br>166<br>1133<br>128:5<br>128:5<br>128:5<br>109:5<br>106:5<br>106:5<br>106:5<br>106:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5<br>105:5 | 104.5             |
| 244440074444444444444444444444444444444   | 4 5               |
|   |                   |

## ALIGNMENTS

|          |        | 0092 PRELIMINARY: DRT. AGE AN | 1777    | 01-JUL-1997 (TrEMBLrel, 04. Created) | 01-JUL-1997 (Tremblre). 04. Tack sequence and the | 01-MAY-2000 (TrEMBLrel, 13, Last perduence update) | 3-PHYTASE A PRECURSOR (FC 31 3 0) ///OCTING THOSE THOS | OSPHOHYDROLASE A) (3 PHYTASE A) (MAYOTTHOSTHOL HEXAPPOSPHATE | PHOSPHOHYDROLASE A) | ra.   | Asperdillus fumidatus (Cartorus fumicata) |   |
|----------|--------|-------------------------------|---------|--------------------------------------|---|--|--|--|---------------------|-------|---|---|
| RESULT 1 | 92     | 000092                        | 000092; | 01-JU                                | 01-JU   | 01-MA  | 3-PHY  | PHOSP  | PHOSP               | PHYA. | Asper                                     | 1 |
| RESI     | 000092 | ID                            | AC      | DŢ                                   | DŢ  | DŢ   | DE   | DE   | DE                  | GN    | SO  |   |
|          |        |                               |         |                                      |   |  |  |  |                     |       |   |   |

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. NCBL\_TaxID=5085;

SEQUENCE FROM N.A., AND SEQUENCE OF 27-37.

STRAIN-AICC 34625;
MEDLINE-97288063; PubMed-9143104;
Pasamontes L., Harker M., Wyss M., Tessier M., van Loon A.P.G.M.;
Pasamontes L., Harker M., Myss M., Tessier M., van Loon A.P.G.M.;
Gene cloning, purification, and characterization of a heat-stable
phytase from the fungus Aspergillus funiqatus.";
Appl. Environ. Microbiol. 63:1696-1700(1997).
I- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE. 

-1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 12,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
-1- SUBCELLULAR LOCATION: SECRETED.
-1- MISCELLANEOUS: SHOWS HIGH ACTIVITY WITH 4-NITROPHENYL PHOSPHATE AT A PH RANGE OF 3 TO 5 AND WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO CELSIUS OVER A PERIOD OF 20 MIN HENDERSTURES UP TO 100 DEGREES CELSIUS OVER A PERIOD OF 20 MIN, WITH A LOSS OF ONLY 10% OF THE INTITAL ENZYMATIC ACTIVITY.

-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY. EMBL; U59804; AAB96872.1; - HSSP; P34752; 11HP. Pfam; PF00328; acid\_phosphat; 1.
PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.
PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN\_1.
Hydrolase; Glycoprotein; Signal. InterPro; IPR000560; -

Q9uga3 homo sapien 035217 rattus norv Q9unw1 homo sapien 095172 homo sapien

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10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 I-ETDGYAASWIVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVDKL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 ILDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
                                                                                                                                                                                                                                                                                                                                                             60 TSSKSKKYSALJERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-0CT-2000 (TIEMBLrel. 15, Last annotation update)
MYO-INOSITOL HEXAPHOSPHATE PHOSPHOHYDROLYASE PRECURSOR (EC 3.1.3.8).
                                                                                                                                                                                                                                                                                   48; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
                                                                                                                                                                                                                                                                                                                           27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLYQVLSRHGARYP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                        BY SIMILARITY.
COUNTRY OF POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                        SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Honghing W., Qi W., Jing X.; Honghing W., Qi W., Jing A.; "PCR, cloning and characterization of the phytase (phyA) gene of
         REQUIRED FOR BINDING SUBSTRATE (BY
                                                                                                                                                                                                                                                           DB 3; Length 465;
                                                                                                                                                                                                                                                         75.9%; Score 1762.5; DB 3; 77.4%; Pred. No. 7.7e-136; Live 36; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 AA.
3-PHYTASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 GRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                         50836 MW;
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                        463
280
442
104
1119
205
                                                                                                                                                                                             350
374
465 AA;
                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                        213
262
434
104
1119
205
228
                                                                                                                                                                                                                                                                                          Matches 345;
                                                                                                                                                                                                 CARBOHYD
                                        ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                 Query Match
               ACT_SITE
                                                                                                                     DISULFID
                                                                                                                                                            CARBOHYD
                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                           SEQUENCE
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                                                                              DISULFID
                                                                                           DISULFID
                                                                                                                                   CARBOHYD
                                                                                                                                                                                     CARBOHYD
                                                                                                         DISULFID
                                                                                                                                              CARBOHYD
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Q9UUZ7
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175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                      Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SK-57;
Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
"Phytase having high-affinity for phytic acid.";
Submitted (AAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022700; CAB19824.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
Aspergillus niger (China Strain).";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF218813; AAF25481.1; -.
HSSP; P34752; 11HP.
                                                                                                                                                                                                                                                                                             467 AA; 51029 MW; F4300A8F165EBF92 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                72.5%; Score 1683; DB 3; 73.7%; Pred. No. 2.4e-129; tive 43; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA
                                                                                                                             Interpro; IPR000560; -.
Program, PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                              POTENTIAL
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01-MAY-1999 (TrEMBLrel. 10, Last sequ
01-MAY-2000 (TrEMBLrel. 13, Last anno
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                                                                                                                                                                                                                                   Signal; Lyase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 73.78 Matches 330; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P34752; 1IHP
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                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                     59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENOMVNSGIKFYRR 117
                                                                                                                                                                                                   118 YKALARNIVPEVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                       DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                            291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEFLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESALSPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                         27 NQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANKSALSPDVPAGCHVTFAQVLSRHGARY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Indels 18; Gaps
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                                                                                                                                                                                                                                                                                               175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                               18;
                                                                              72.0%; Score 1672; DB 3; Length 467; 72.8%; Pred. No. 1.9e-128; Ive 46; Mismatches 58; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.6%; Score 1662; DB 3; Length 467; 72.8%; Pred. No. 1.3e-127; 1ve 46; Mismatches 58; Indels 18
                    PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SEQUENCE 467 AA; 51028 MW; 7A38AD543EDC265C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang L., An L., Wang Y., Yuan X.,
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AY013315, AAG40885.1; -.
SEQUENCE 467 AA; .51012 MW; 3F69AD543COB565B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA; 51012 MW; 3F69AD543C0B565B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 AA.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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(TrEMBLrel. 16, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16,
                                                                                     Best Local Similarity, 72.88
Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus ficuum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001
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                                                                            Query Match
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SEQUENCE FROM N.A.
STRAIN-ATCC 20186;
MEDLINE-980672; PubMed-9349716;
Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
van Loon A.P.G.M.;
"Cloning of the phytases from Emericella nidulans and the thermophilic
             NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
                                                                234 DTVARTSDATQLSPFCDLFTADEW-OYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                               291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                 -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
-!- MISCELLANEOUS: HAS POTEWITAL AS FOOD AND FEED ADDITIVE. IT CAN USED AS FOOD FOR MONOGASTRIC APPTIN IN SOYBEAN AND OTHER SEEDS -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
HSSP: P34752; 11HP.
                                                                                                                                                                                                   ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                   fungus Talaromyces thermophilus.";
Biochim. Biophys. Acta 1353:217-223(1997).
-1- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
3-PHYTASE A.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Talaromyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HTS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HTS_ACID_PHOSPHAT_2; UNKNOWN_1.
Hydrolase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                  466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
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                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Talaromyces thermophilus.
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357
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410
461
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOHYDROLASE A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=28565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM PHYTATE.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESI-ETDGYAASWIVPFAARAYVEMMQCEAGGGGGGGGFKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 KSIEETDGYSAAWTVPFGGRAYIEMMQC------DDSDEPVVRVLVNDRVVPLHGCEVD 435
                                                                                                                                                                                                                                                                                                                                                                                                  234 DTVARTSDATQLSPFCDLFTADEWQ-YDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                               175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARL-EALPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                  59 PTSSKSKKYSALIERLQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                       144 YKSLARNAVPEVRCSGSDRVIASGRLFIEGFQSAKVLDPHSDKHDAPPTINVIIEEGPSY 203
                                                                                                                                                                                                                                                                                                                                                             STRAIN=CBS 116.46;
Pasamontes L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.B. Broger C., Van Loon A.P.;
Broger C., Van Loon A.P.;
submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
i- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                  76; Indels 19; Gaps
                                                                                                                                                                           1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                             24 DSHSCNIVEGGYQCRPEISHSWGQYSPFFSLADQSEISPDVPQNCKITFVQLLSRHGARY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus terreus.
Buraryora: Fundi Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Fundi Ascomaceae; mitosporic Trichocomaceae; Aspergillus. NCHI_TAXID=33178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 MIHSPVQDYTTVNHTLDSNPATFPLNATLYADFSHDNTMTSIFAALGLYNGTAKLSTTEI
BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

"TINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                     Score 1596.5; DB 3; Length 466; Pred. No. 2.9e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TIEMBLIEL 04, Last sequence update)
01-JUL-1997 (TIEMBLIEL 13, Last annotation update)
3-PHYTASE PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE PHOSPHOYDROLASE) (3 PHYTASE) (MYO-INOSITOL HEXAKISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (PC
FC4575B521A5C929 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 AA.
                                                                                                                                                     36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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  440 BY 204 N-269 N-335 N-372 N-51450 MW;
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Similarity 70.8%;
                                                                                                                                                        Matches 317; Conservative
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                                                                                     466 AA;
                                            335
348
372
                                              CARBOHYD
CARBOHYD
     DISULFID
                                CARBOHYD
                                                                          CARBOHYD
                                                                                        SEQUENCE
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                                                                                                                                                                                                        SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-
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F2AECECIAF7C22C4 CRC64;
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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N-LINKED (GLCNAC. ..)
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69.6%; Pred. No. 1.4e-121;
tive 46; Mismatches 72;
  Interpro; IPR000560; -. pfan; PF00328; acid_phosphat; 1. PR051TE; PS00616; HIS_ACID_PH0SPHAT_1; 1. PR05ITE; PS00778; HIS_ACID_PH0SPHAT_2; UNKNOWN_1. Hydrolase; Glycoprotein; Signal.
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HSSP; P34752; 11HP
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       SET THE FIT TH
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MIGTOBLOLOGY 143:445-252(1997).

-! FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE FROM PHYTRATE (BY SIMILARITY).

-! CATALYTIC ACTYLYT: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.

-! SUBCELLULAR LOCATION: SECRETED.

-! MIGCELLANEOUS: SHOWS ACTIVITY WITH HYTIC ACID AT A PH RANGE OF NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH 5.5. ALSO ACCEPT 4-MORE ACIDIC PH VALLES.

-! SIMILARITY: BLEONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.

EMBL. 159805; AAB52507.1; -.
                                                                                                                                           Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L., Loon A.P.; "The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fungi Aspergillus terreus and Myceliophthora thermophila.";
                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
  PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE PHOSPHOHYDROLASE A).
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000560;
                                      Aspergillus terreus.
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376
466 AA;
                                                                                                      SEQUENCE FROM N.A.
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11; 60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118 119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLAD---PAHQASPVINVIIPEGSGYN 175 176 NTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFD 234 19; Gaps 3 HS-CDIVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59 67.3%; Score 1562.5; DB 3; Length 466; 69.3%; Pred. No. 1.7e-119; tive 51; Mismatches 67; Indels 19; Query Match Best Local Similarity 69.3% Matches 309; Conservative δ q δλ Ω δλ

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235 TVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARL 291
               292 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE 351
                                                                  352 SI-ETDGYAASWIVPFFAARAYVEMMQCEAGGGGGGGEKEPLVRVLVNDRVVPLHGCGVDK 410
                                                                                                                     -!- CATALITIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE + H(2)0 = D-MYO-I-SUBCELLOLAR LOCATION: SECRETED.
-!- SUBCELLOLAR LOCATION: SECRETED.
-!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OFFIMA SHIFTED TO MORE ACIDIC PH VALUES.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL: U59806; AAB52508.1; -- HSTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitchell D.B., Vogel K., Welmann B.J., Pasamontes L., van Loon A.P.G.M.; "The phytase subfamily of histidine acid phosphatases: isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes for two novel phytases from the fungi Aspergillus terreus and Mycellophthora thermophila.";
Microbiology 143:245-252(1997).
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PROTON DONOR (BY SIMILARITY).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Chaetomiaceae; Thielavia.
NCBI_TaxID=78579;
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                           487 AA.
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MEDLINE-9717792; PubMed=9025298;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                            Thielavia heterothallica.
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                                                                                                                                                                                                                            RESULT
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Length 442;

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Query Match
Best Local Similarity 25.8%; Pred. No. 8.7e-18;
Matches 105; Conservative 67; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52560 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACID PHOSPHATASE (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kluyveromyces lactis (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 26.2
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P34755; 1QFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 TQGVGFVNELLARLAGVPVRDGTSTNRTLDGDPRTFPLGRPLYADFSHDNDMMGVLGALG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 LYNGTKPLSTTS-VESIETDGYAASWTVPFAARAYVEMMQCBAGGGGGGG-----EKEP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381 AYDGVPPLDKTARRDPEELGGYAASWAVPFAARIYVEKMRCSGGGGGGGGGGGCROEKDEE 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFDTVARTS------DATQLSPFCDLFTADEWQ-YDYLQSL-KYYGYGAGNPLGP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 AQGVGF-NELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALG 337
                                                                                                                                                                                                                                                                                                                                                    176 NTLDHGLCTAFED---STLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMC 231
                                                                                                                                                                                                                                                                                                                        60 TSSKSKKYSALIERIQKNATFKGK-YAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
                                                                                                                                                                                                                                                                                                                                                                                                                    119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVI---NVIIPEGSGYN 175
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                             2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
                                                                                                                                                                                                                                                                            23 SRPCDTPDLGFQCGTAISHFWGQYSPYFSVPSE--LDASIPDDCEVTFAQVLSRHGARAP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
              247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
346 346. N-LINKED (GLCNAC. . .) (POTENTIAL).
487 AA; 52537 MW; 97D10EDC83D031DB CRC64;
                                                                                                                                                                                      33;
                                                                                                                                         DB 3; Length 487;
                                                                                                                                     Ouery Match
Best Local Similarity 56.3%; Pred. No. 5.2e-96;
Matches 263; Conservative 52; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 LVRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 AA; 49370 MW; 7087D91A85B05C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia angusta (Yeast) (Hansenula polymorpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiol, Biotechnol, 50:77-84(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPRESSIBLE ACID PHOSPHATASE (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC34438;
MEDLINE=98386672; PubMed=9720203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00328; acid_phosphat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF051161; AAC62537.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000560; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-4905;
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SEQUENCE
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                                                                                 SEQUENCE
                                         CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 KGKY------AFLKTYNYTLGADDLTP----FGENQMVNSGIKFYRRYRALA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GQYSPFFSLADESALSPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQKNATF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 IALOYNN-DVTKFYQFGPGYNMSAVAGGVYANATAKLLQE------313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 LNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIETDGYAASWTVPFAARAYVEM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 ADDLTPFGENQMVNSGI----KF----YRRYKAL--ARNIVPFVRASGSDRVIASAEKFI 145
                                                                                                                                                                                                                                                                                                                                                                                                198 NFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW 257
                                                                                                                                                                                                                                                                                                                                                                                                                                        224 ----IFQREADRLNELSPGFNITADDIITMGTYCAYETNVKGH-----SSFCDALSREAF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 ---QYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQDHTSTNHTLDSNPATFP 314
                                                                                                                                                                                                                        115 DSDNYELETTRGLYSGLLNAFKFGTYLRERYDSLVDTSSVLPIFAAS-EDRVVDTARSFG 173
                                                                                                                                                                                                                                                                               146 EGFQSAKLADPAHQASPVINVI----IPEGSGYNNTLDHGLC----TAFEDSTLGDDAEA 197
                                                                                                                                                                                                                                                                                                                                         174 RGF-----FGPDYATSCSIQVVNETDTSKGANALITKDN--CPTYNSSFYDYSFGDE--- 223
                                                                                        55 DTPPHCEIEQAQLFMRHGERFPTKSSGRQYKKFYDKLKKANITDYRGPLAFIEDLEYFVP 114
   77; Gaps
                                                38 DVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQK-NAT-FKGKYAFLKTYNYTLG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaese; Kluyveromycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=2360/7;
San Vicente A., Ferminan E., Dominguez A.;
San Vicente A., Ferminan E., Dominguez A.;
"Isolation and characterization of KIPHO3 a gene encoding constitutive acid phosphatse from Kluyveromyces lactis.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ007502; CAB46490.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 MQCEAGGGGGGGEKEPLVRVLVNDRVVPLHGCGVDKLGRCKLDDFVE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 LNC-----SDTSFVRTILNDKVYPVPGCSSGPGYSCPLEDYLD 407
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5C7ABF622CEA891C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACID PHOSPHATASE
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ολ
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298 DHTST-----NHTLDS--NPATFPLNATLYADFSHDNTMVSIFFALGLY---NGTKPLS 346

272 DH-----SDFCSIFTPSBFLNFEXDSDLD-QAYGGG-------PVS 304

347 ITSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVL,VNDRVVPLHGC 406

365 TD--KNIYTYSQKTSSFVPFAGNLITELFFC-----SDSKYYVRHLVNQQVYPLIDC 414

qq οy g

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123 RNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINV---IIPEG--SGYNNT 177
                                                                          161 SDSNP-VFTSSSGRV-----HQTAKYVVSSLEEELDIQLDLQIIQENETSGANSL 209
                                                                                                          178 LDHGLCTAFEDSTLGDDAEANFTAVFAPPIRAR-LEALPGVNLT--DEDVVNLMDMCPFD 234
                                                                                                                                         210 TPADSCMTY-NGDLGDEYFENATLPYLTDIKNRWMKKNSNLNLTLEHDDIELLVDWCAFE 268
                                                                                                                                                                         235 TVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPL-GPAQGVGFNELIARL 291
                                                                                                                                                                                                                                                                                                                           366 DFQNIQ----QLSWVTPMGGRIFTEKLKC-----GNASYVRYIINDVIIPVPGCTS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTON DONOR (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                      324 TQADELDN------KVWLSFSHDTDIQQFISALGLIDNGVTEYSLDQV
                                                                                                                                                                                                      269 TNVKGSSAV-----CDLFERNDLVAYSYYANVNNFYRRGAGNPMSNPIGSYLVNASYNLL
                                                                                                                                                                                                                                      THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY-NGTKPLSTTSV
                                                                                                                                                                                                                                                                                                     351 --ESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGGEKEPLVRVLVNDRVVPLHGCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN ALCOHOL + ORTHOPHOSPHARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY. EMBL; AL023286; CAA18863.1; -. HSSP; P34755; 1QFX. InterPro; IPR000560; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (P. 6C41AF422C6D624A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
PROBABLE ACID PHOSPHATASE (EC 3.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00328; acid phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                     409 DKLGRCKLDDF-----VEGLSFARS 428
                                                                                                                                                                                                                                                                                                                                                                                                    413 GPGFSCPIEDFDDYITNRLNGIDYVSS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340
98
104
221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439
458
463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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And Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addans M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA Dodson K., Cabrelian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Weil M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Krait, K. Kall, K., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                          Ul-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) MIPPI PROTEIN.
                                               460 AA.
                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                        STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                              MIPP1 OR CG4123.
                                                                Q9VV72;
                                        Q9VV72
RESULT 12
                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 YSPFFSLADESALSPDVPKGCRVTFVQVLSRHGARYPTS--SKSKKYSA-----L 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%; Score 285; DB 3; Length 463; 24.9%; Pred. No. 4.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 24.99
hes 113; Conservative
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Query Match

Matches

δy

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.S., Pann S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Siden Kriamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q. A.,
RA Ve J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.,
R. Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.,
R. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
R. The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 HSPVQD---HISTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 VESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 SGSD----RVIASAEKFIEG-FQSAKLADPAH-------QASPVINV-IIPEGSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 YNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 YYK------FHQSKLYNDTLAD-----ISTRLGFL--YTLEEADIKLMYDMCRY 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 DTVARTSDATQLSPFCDLFTADE-WQYDYLQSLKYYGYGAGNPLGPAQGYGFNELIARLT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 E---QAWNVDRNSVWCGAFLPEQITVFEYLEDLKYY-YGS------GYGFPE-NAHLN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 CRLVQDLLTHLSN-----PVSPHVVAHFGHSTGLLTLTALGIQKDDIKLRADN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 LCQTDLIAIKLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTV----LTA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 NYNDTYYQRTTESFKAFAEGLFGSQNAAHPVEIPKQDLLLRPYDYCSSFKNVNYKDEGSE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 DIDKQYLVPGCQPQKMWIFHRHGTRLPKKSMINKASRVAELRDLIINNYQVARTKPETDA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSG-----IKFYRRYKALARNIVPFVRA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%; Score 207.5; DB 5; Length 460;
44.2%; Pred. No. 9e-09;
ve 59; Mismatches 164; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 DVPK-----GCRVTFVQVLSRHGARYPTSSKSKKYSALIE------RIQKNA 78
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00328; acid_phosphat; 1.
SEQUENCE 460 AA; 52685 MW; F00B25718E40807D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MULITEL INOSITOL POLYPHOSPHATE PHOSPHATASE 1.
MIPPI OR CG4123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 KLGRCKLDDFVE-----GLSFARSGG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 -- GLCKWSDVLEKYKTIADADCGEYYCRTGG 435
                                                                                                                                                                                                                                                                                                                                   EMBL; AE003527; AAF49450.1;
Flybase; FBgn0026061; Mippl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 24.29
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000560;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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096421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 GYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 EYYK-----FHQSKLYNDTLAD-----ISTRLGFL--YTLEEADIKLMYDMCR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 FDTVARTSDATQLSPFCDLFTADE-WQYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 YE---QAWNVDRNSVWCGAFLPEQITVFEYLEDLKYY-YGS------GYGFPE-NAHL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 THSPVQD---HTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 NCRLWODLLTHLSN------PVSPHVVXHFGHSTGLLTLLTALGIXKDDIKLRAD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 SVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 TFKGKYAFLKTYNYTLGADDLTPFGENOMVNSGIKFYRRYKALARNIVPFV----- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 ICQTDLIAIKLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTVLTANYNDTY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 ---RASGSDRVIASAEKFIEG-FQSAKLADPAH-----QASPVINV-IIPEGS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 YQFRHTDIQRITESFKAFAEGLFGSQNAAHPVELPKQDLLLRPYDYCSSFKNVNYKDEGS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 DIDKQYLVPGCQPQKMWIFHRHGTRLPKKSMINKASRVAELRDLIINNYQVARTKPETDA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEÖUENCE FROM N.A.
Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N.,
Reynolds P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                          8.4%; Score 196; DB 5; Length 467;
23.5%; Pred. No. 8e-08;
tive 59; Mismatches 173; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 DVPK-----GCRVTFVQVLSRHGARYPTSSKSKKYSALIE------RIQKNA 78
                                          Chī H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N., Reynolds P.R.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted '...', Submitted '...', And Submitted '..
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                                                                                                                                                                                                                                     Entrapro; IPR000560; -.
pfam; PF00328; acid_phosphat; 1.
SEQUENCE 467 AA; 53602 MW; 1A0571B9958B2632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE 2.
MIPP2 OR CG4317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
SEQUENCE 453 AA; 52799 MW; 9DCD3CCD0CEB8B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 DKLGRCKLDDFVE-----GLSFARSGG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 --- GLCKWSDVLEKYKTIADADCGEYYCRTGG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                       FlyBase; FBgn0026061; Mippl.
                                                                                                                                                                    EMBL; AF046913; AAD02436.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.59
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000179; -
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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RN RA RA DR DR DR DR DR SO
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A Adams M.D., Celniker S.E., Holf R.A.,
A George R.A., Lewis S.E., Kichards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Xichards S., Ashburner M., Henderson S.N.,
A Brandon R.C., Rogers Y.-H.C., Bazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Besson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Burtis K.C., Busam D.A., Bulch H., Cadleu E., Center P.,
A George R.A., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
A Burtin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
A Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                   Gaps
                                                                                                                                                                82 GKYAF-----LKTYNYT-LGADD----LIPFGENQMVNSGIKFYRRKALARNIVP-- 127
                                                                                                                                                                                                        100 TKPPICTAELEKLROWHWHLNATEDEKLLVAEGEDELIELAERMQRRFPDLLPELYNPE 159
                                                                                                                                                                                                                                                   128 --FVRASGSDRVIASAEKFIEG-----FQSAKLADPAHQASPVINVIIPEGSGYNNTLD 179
                                                                                                                                                                                                                                                                                         160 WYYFKYTATQRTLKSAESFATGLFGRHRIHTVRYPPPLHE-DPVLRFY--KGCGKWKT-- 214
                                                                                                                                                                                                                                                                                                                                     180 HGLCTAFEDSTLGDDAEANFTAVFA-PPIRARLE----ALPGVNLTDEDVVNLMDMCP 232
                                                                                                                                                                                                                                                                                                                                                                215 ------DVDKNPETLVNARRFLABFQMQSAVEQVRSSTRLP--DLQPEDVQLMYTVCA 264
                                                                                                                                                                                                                                                                                                                                                                                                                        233 FDTVART-----SDATQLSPFCDLFTADEWQ-YDYLQSLKYY---GYGAGNPLGPAQGV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 GFNELIARLTHSPVQDH----TSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 --YELTHRIACPAIADMFAAISSSEETRORR----ANATLY--FTHSGTLLKLLAHLGL 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 ARDNKPLTHKHFASERL--WRTSQIDAFATNLAFLRYDCDKG------NPQVLVLHQE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogašter (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda, Insecta,
Petrygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                24 SPFFSLA--DESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQKNATFK 81
                                                                                                                      43 TPYRAIANYDE---TPPRKYAGCHPTRIWTITRHGTRNPSESVILQAQNRLSEIKKRILDQ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                          64; Mismatches 174;
8.3%; Score 192.5; DB 5
23.4%; Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                     Matches 101; Conservative
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                    Similarity
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Murphy D.M., Nelson D.L.,
RA Relnert K., Remighton K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.-S., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Sylirskas K., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng G.D. Shorosophila melanogaster.";
R. Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 TKPPICTAELEKLRQWHWMHLNATEDEKLLVAEGEDELIELAERMQRRFPDLLPELYNPE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --FVRASGSDRVIASAEKFIEG-----FQSAKLADPAHQASPVINVIIPEGSGYNNTLD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 HGLCTAFEDSTLGDDAEANFTAVFA-PPIRARLE-----ALPGVNLTDEDVVNLMDMCP 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DVDKNPETLVNARRFLAEPQMQSAVEQVRSSTRLP--DLQPEDVQLMYTVCA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 FDTVART-----SDATQLSPFCDLFTADEWQ-YDYLQSLKYY---GYGAGNPLGPAQGV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 YNGTKPLSTTSVESIETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVND 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 SPFFSLA--DESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERIQKNATFK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 --YELTHRIACPAIADMFAAISSSEETRORR----ANATLY--FTHSGTLLKLLAHLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%; Score 191.5; DB 5; Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 1.8e-07;
64; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000179; -. **
PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
SEQUENCE 453 AA; 52781 MW; 93C3267D0D409160 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003436; AAF46121.1;
FlyBase; FBgn0026060; Mipp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 23.48
Matches 101; Conservative
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Search completed: October 26, 2001, 15:17:25

Job time: 3976 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 26, 2001, 16:40:03; Search time 57.24 Seconds Run on:

(without alignments)
462.835 Million cell updates/sec

US-09-488-265-27 Title:

Perfect score:

1 NSHSCDTVDGYQCPEISHLW......DFVEGLSFARSGGNWAEGFA 437 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

412676 seqs, 60623988 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

| SIDSI/gcgdata/geneseqy/Anisys.nasty.nast /SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:\*/SIDS1/gcgdata/geneseqf/geneseqp/AA1995.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT:\*/SIDS1/gcgdata/geneseqf/geneseqp/AA1998.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA1996.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA2001.DAT:\* /SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:\*/SIDSi/gcgdata/geneseqp/AA1981.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:\*/SIDS1/gcgdata/geneseqp/AA1984.DAT:\* A\_Geneseq\_0601:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMADIE

| Result Query Ouery Ouer, Ouery Ouer, |           |        | Description |             |          | Consensus phytase | Phytase-11, a cons | Consensus phytase | Consensus phytase | Phytase-10, a cons | Consensus phytase | Consensus phytase- | Consensus phytase | Consensus phytase | Mutant phytase-10, | Consensus phytase |
|--|-----------|--------|-------------|-------------|----------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|
| Score<br>2321<br>2321<br>2315<br>2115<br>2115<br>2019<br>2009<br>2003<br>2003<br>2003<br>2003  | SUMMARIES |        | ID          |             | AABOUSOS | 79760567          | AABOORDS           | MAD 20023         | AAV60566          | 00000144           | AAV42170          | AABOOESS           | AAB20524          | AAV60560          | AAR20531           | 1000              |
| Score<br>2321<br>2321<br>2315<br>2115<br>2115<br>2019<br>2009<br>2003<br>2003<br>2003<br>2003  |           |        | DB          | i           | 21       | 10                | 15                 | 1.0               | 2.5               | 27                 | 200               | 2 5                | 1,0               | 1 5               | 21                 |                   |
| Score<br>2321<br>2321<br>2315<br>2115<br>2115<br>2019<br>2009<br>2003<br>2003<br>2003<br>2003  | •         |        | Length      |             | 437      | 437               | 441                | 467               | 467               | 467                | 467               | 467                | 467               | 467               | 467                |                   |
| 1  | dР        | Query  | Match       | 1 1 1 1 1 1 | 100.0    | 100.0             | 91.1               | 91.1              | 91.1              | 90.4               | 90.2              | 90.2               | 90.2              | 90.2              | 89.1               |                   |
| Result NO  |           |        | Score       |             | 2321     | 2321              | 2115               | 2115              | 2115              | 2099               | 2093              | 2093               | 2093              | 2093              | 2067               |                   |
|  |           | Result | No.         |             |          | 7                 | m                  | *                 | 5                 | 9                  | 7                 | 8                  | თ                 | 10                | 11                 |                   |

|          | us phytas | •        |          | Consensus phytase | ns       | ~        | Q,       | Ascomycete consens | ਵ        | Consensus phytase | HÌ.      |          | onsensus | al consensus | consensus  | 드    | phytase | Initial consensus |       | Consphy12, a deriv | phytase  | Phytase-7, a deriv | phytas   | Mutant Aspergillus | A. fumigatus phyta | Aspergillus fumiga | Mutant Aspergillus | Aspergillus fumiga | ergillus f | A. fumigatus phyta | 4        | Aspergillus fumiga | Aspergillus fumiga | Asperdillus fumica |
|----------|-----------|----------|----------|-------------------|----------|----------|----------|--------------------|----------|-------------------|----------|----------|----------|--------------|------------|------|---------|-------------------|-------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|----------|--------------------|--------------------|--------------------|
| AAROO536 | 9         | AAR20532 | AAV43169 | AAR20526          | 07509044 | AA109068 | AAV30006 | DOCCOUNT V         | AAM95380 | AAVEOSEO          | AAMOSSOS | AAM93391 | AAMOSSOS | COCCODA A    | POCCOUNT & | ורי  | ๆ<br>กเ | ς,                | )53   | AAY69572           | AAY43172 | AAY69571           | AAB20529 | AAI 093/4          | 7                  | 200                | ) I                | 7 0                | AAW04330   | AAD20507           | 100000VV | AA109000           | AABA0300           | TCCCOTWW           |
| 21       | 21        | 21       | 10       | 2 5               | 10       | 21       | 200      | 200                | 2 5      | 7 1               | 200      | 200      | 000      | 0            | 9 0        | 2 6  | 4 6     | 7 0               | 7 5   | 77                 | 0.20     | 7 7                | 7 7      | 1 0                | 2 6                | 21                 | 1.5                | 10                 |            |                    |          |                    |                    |                    |
| 424      | 424       | 467      | 467      | 467               | 467      | 441      | 467      | 467                | 467      | 467               | 467      | 467      | 467      | 467          | 101        | 7 7  | 101     | 407               | 404   | 10.4               | 404      | 40,                | 407      | 104                | 104                | 467                | 440                | 465                | 465        | 440                | 440      | 440                | 440                |                    |
| 98.9     |           |          |          | 88.1              |          | 87.0     | 87.0     | 87.0               | 87.0     | 87.0              | 86.8     | 86.7     | 86.7     | 86.4         |            | 0.00 | 0 0     |                   | 7. 70 | 7 0<br>7 C         | 9 0      | 0 0 0              | 77. 4    | 76.6               | 76.6               | 76.6               | 75.9               | 75.9               | 75.9       | 75.8               | 75.8     | 75.6               | 75.6               |                    |
| 2064.5   | 2064.5    | 2061     | 2044     | 2044              | 2044     | 2020     | 2020     | 2020               | 2020     | 2020              | 2014     | 2013     | 2013     | 2005         | 2004       | 1997 | 1997    | 1001              | 1954  | 1922               | 1001     | 1919               | 1797.5   | 1777.5             | 1777.5             | 1777.5             | 1762.5             | ~                  | $\sim$     | 759.               | 759.     | 1754.5             | 754.               |                    |
| 12       | . 13      | 14       | 15       | 16                | 17       | 18       | 19       | 20                 | 21       | 22                | 23       | 24       | 25       | 26           | 27         | 28   | 29      | 30                | 3 6   | 3.5                |          | 3.0                | 35       | 36                 | 37                 | 38                 | 39                 | 40                 | 41         | 42                 | 43       | 44                 | 45                 |                    |
|          |           |          |          |                   |          |          |          |                    |          |                   |          |          |          |              |            |      |         |                   |       |                    |          |                    |          |                    |                    |                    |                    |                    |            |                    |          |                    |                    |                    |

## ALIGNMENTS

AAB20525 RESULT

AAB20525 standard; Protein; 437 AA.

AAB20525;

(first entry) 05-DEC-2000

Consensus phytase 11 SEQ ID NO:27.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

Synthetic.

WO200043509 A 27-JUL-2000. 21-JAN-2000; 2000WO-DK00025.

22-JAN-1999; .99DK-000092. 21-SEP-1999; 99DK-0001340. 

(NOVO ) NOVO NORDISK AS.

Lehmann M;

WPI; 2000-491161/43.

Novel phytases with improved properties such as temperature stability,

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thermostable; animal feed; morogastric animal; phytate phosphorus;
phosphate availibility; consensus; phytase-11.
                                                                                                                 can be used for producing phytasses with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 SWTYPFAARAYVEMMQCEAGGGGGGGGGFKEPLVRVLVNDRVVPLHGCGVDKLGRCKLDDFV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GLCTAFEDSTLGDDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPFDTVARTS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATQLSPFCDLFTADEWQYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQDHT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 STNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIETDGYAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLDH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stability and substrate specificity, for use in pharmaceuticals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRYKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NSHSCDTVDGYQCPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARXPT 60
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2321; DB 21; Length 437; 100.0%; Pred. No. 2.2e-218; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phytase-11, a consensus mature phytase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69567 standard; protein; 437 AA.
                                                          Claim 6; Fig 6a-e; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 EGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 eglsfarsggnwaecfa 437
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                         compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 437; Conservative
                                                                                                                                                                                                                                                                                                                                               437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY69567;
                                                                                                                                                                                                                                                                                                                nvention.
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formulation, comprising phytase (myo-inositol hexalisphosphate formulation, comprising phytase (myo-inositol hexalisphosphate formulation, comprising phytase (myo-inositol hexalisphosphate phosphohydrolase) and one or more stabilishing agents including composition for ribitol; polyethylene glycols with a molecular weight of 600 xylitol or ribitol; polyethylene glycols with a molecular weight of formolation acid; carboxymethylcellulose; and sodium alginate. Cylustric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a prosphorus. Although a large amount of phosphate is present in animal ceed in the form of phytate phosphorus, monogastric animals are unabble to the feed of such animals. Phytase enhances the nutritional phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inclusion in the animal can make use of the inclusion in the control of the feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the inorganic phosphate liberated from phytate phosphorus using the conganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents a consensus sequence, designated phytase-11, which was derived from the mature phytase sequences from a variety of fungi (AAY69544-Y69556, AAX69559-Y69562,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel stabilised dry or liquid enzyme.
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                                                                                                                                                                                                         Talaromyces thermophilus ATCC20186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 18; 101pp; English
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                                                                  Aspergillus niger str. NRRL3135.
Aspergillus fumigatus ATCC13073.
Aspergillus fumigatus ATCC3722.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC59108.
                                                                                                                                                                   Aspergillus fumigatus ATCC32239
                                    Aspergillus niger var. awamori.
                  terreus cbs16.46.
                                                                                                                                                                                                                                                Paxillus involutus NN005693.
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                                                                                                                                                                                                                                                                  Trametes pubescens NN9343. Agrocybe pediades NN009289.
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                                                                                                                                                                                                                                  Myceliophthora thermophila.
                                                                                                                                                                                                                                                                                                          Peniophora lycii NN006113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brugger R, Lehmann M,
                                                                                                                                                                                                                                                                                                                                Thermomyces lanuginosa.
                                                Aspergillus niger T213.
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                                                                                                                                                                                         Emericella nidulans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-099429/09
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Aspergillus
Aspergillus
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1 NSHSCDTVDGYQCPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPT 60

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61 SSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENOMVNSGIKFYRRYKA 120
                                LARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLDH 180
                                                                          GLCTAFEDSTLGDDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPFDTVARTS 240
                                                                                                                    DATQLSPFCDLFTADEWQYDYLQSLKYYGYGAGNPLGPAQGYGFNELIARLTHSPVQDHT 300
                                                                                                                                                            STNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIETDGYAA 360
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Consensus phytase 10 (Fcp10) SEQ ID NO:24. AAB20523 standard; Protein; 441 AA. 05-DEC-2000 (first entry) AAB20523: AAB20523 RESULT XX

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

Synthetic.

WO200043503-A1 21-JAN-2000; 27-JUL-2000

2000WO-DK00025.

99DK-0001340. 99DK-0000092 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS.

Lehmann M;

WPI; 2000-491161/43.

for use in pharmaceuticals and Novel phytases with improved properties such as temperature stability pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds

Example 2; Fig 4a-d; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g.

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temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 350
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                                                                                                                                                                                                                                  91.1%; Score 2115; DB 21; Length 441; 93.5%; Pred. No. 3.1e-198; Live 2; Mismatches 9; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                 Sequence 441 AA;
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AAB20524 standard; Protein; 467 AA. 05-DEC-2000 (first entry) AAB20524; AAB20524

Consensus phytase 10 SEQ ID NO:26.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

Synthetic.

WO200043503-A1 27-JUL-2000 

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                                                                                                                                                                                                                                                                                                                                                     The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods tem be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate profile, release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
                                                                                                                                                                                                                              Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.1%; Score 2115; DB 21; Length 467; 93.5%; Pred. No. 3.4e-198; tive 2; Mismatches 9; Indels 18;
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                                                                                                                                                                                                                                                                                                                         claim 1; Fig 5a-c; 240pp; English.
                                          99DK-0000092.
99DK-0001340.
21-JAN-2000; 2000WO-DK00025
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                                                                                                   (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                      2000-491161/43.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 AA;
                                                                                                                                                                                                         N-PSDB; AAA73232.
                                            22-JAN-1999;
                                                                 21-SEP-1999;
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                                                                                                                                              Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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RESULT

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The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including phosphohydrolase) and one or more stabilising agents including to the stabilistic polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a provides a monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional phosphate value of plant material without the need for adding additional phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Phytase signal peptide from Aspergillus terreus cbs16.46"
                                                                                                                                       Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; phytase-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mature phytase-10 consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                    Talaromyces thermophilus ATCC20186.
Myceliophthora thermophila.
Paxillus involutus NN005693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 17; 101pp; English.
             AAY69566 standard; protein; 467 AA
                                                                                                                                                                                                                                                                                          Aspergillus funigatus Arcc32722.
Aspergillus funigatus ArcC58128.
Aspergillus funigatus ArcC26906.
Aspergillus funigatus ArcC26906.
Emericella nidulans.
                                                                                                                Phytase-10, a consensus phytase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehmann M, Wyss M;
                                                                                                                                                                                                                                           Aspergillus niger var. awamori.
Aspergillus niger str. NRRL3135
                                                                                                                                                                                                                                                                              Aspergillus fumigatus ATCC13073
                                                                                                                                                                                                                             Aspergillus terreus cbs16.46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-0111949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98EP-0111960.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrocybe pediades NN009289.
Peniophora lycii NN006113.
                                                                                                                                                                                                                                                                                                                                                                                                                           Trametes pubescens NN9343.
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27..467
                                                                                                                                                                                                             Aspergillus terreus 9Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermomyces lanuginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-099429/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monogastric animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ59642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP969089-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brugger R,
                                                                                 19-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                              AAY69566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
AAY69566
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to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion designated phytase-10, which was derived from the mature phytase, sequences from a variety of fungi (AAY66944-Y66946, AAY69548-Y69556, additionally contains the Aspergillus terreus cbs116.46 signal peptide at
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467 AA; Sequence

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PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                        118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                      DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                   LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                                                                                                                               ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                   esieetdgyaaswtvpfaarayvemmqcea-----ekeplvrvlvndrvvplhgcgvd 439
                           18; Gaps
                                            1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                           175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF
                                                                                                                                                                                                    91.1%; Score 2115; DB 21; Length 467; 93.5%; Pred. No. 3.4e-198;
                             Indels
                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                               Matches 419; Conservative
           Similarity
Query Match
           Best Local
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RESULT

AAB20533 standard; Protein; 467 AA.

AAB20533;

(first entry) 05-DEC-2000

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; Consensus phytase 10 thermo 5 Q50T protein SEQ ID NO:95.

Synthetic

food; feed; phytate; manure.

WO200043503-A1 

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Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
                                                                                                                                            Disclosure; Fig 24a-c; 240pp; English.
               21-JAN-2000; 2000WO-DK00025.
                                99DK-0000092.
                                       99DK-0001340.
                                                                                                                              compound foods and feeds -
                                                      (NOVO ) NOVO NORDISK AS
                                                                                     WPI; 2000-491161/43.
                                                                                              N-PSDB; AAA73292
                              22-JAN-1999;
                                     21-SEP-1999;
-2:7-JUL-2:000
                                                                     Lehmann M;
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties engine temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it. The present sequence represents a phytase sequence from the present sequence represents a phytase sequence from the present

467 AA; Sequence

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59 PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                   118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPBGSGY 174
                                                                                                                                                                                                                                                175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                             234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                    Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NSHSCDIVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                             90.4%; Score 2099; DB 21; Length 467; 92.6%; Pred. No. 1.2e-196; tive 4; Mismatches 11; Indels 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                Best Local Similarity
Matches 415; Conserv
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the consensus phytase-10-thermo(3)-050T-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgent plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytase) simultaneously.
                                                                                                                                                                                                     Phytase; animal feed preparation; thermostable phytase; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2093; DB 20; Length 467; Pred. No. 4.8e-196;
                                                                                                                                                             Consensus phytase-10-thermo(3)-Q50T-K91A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparing animal feed using a thermostable phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                AAY43170 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 10; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98DK-0000806.
98DK-0001176.
                                                                                                                                                                                                                                                                                                                                                                                                               99WO-DK00154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99DK-0000093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98DK-0000407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 92.4*
Matches 414; Conservative
                                                                                                                             06-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-591030/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 AA;
                                                                                                                                                                                                                                          consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ31521
                                                                                                                                                                                                                                                                                                                           WO9948380-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petersen S;
                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                   AAY43170;
                  AAY43170
RESULT
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q δλ

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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inosital phosphates and/or inosital and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.
                                                                                                                   351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                  291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                       Consensus phytase 10 thermo 3 q50t, k91a protein SEQ ID NO:31.
                                                                                                                                                                                             410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                Claim 4; Fig 8a-c; 240pp; English.
                                                                                                                                                                                                                                                                                                                 AAB20527 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000; 2000WO-DK00025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99DK-0000092.
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                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                       AAB20527;
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                                                                                                                                                                                                                                                                                                     AAB20527
                                                                                                                                                                                                                                                                                      RESULT
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10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.
                                                                                                   PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                   YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                                                                                               NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF, 233
                                                                                                                                                                                           DIVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                        LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                                                                                                                     Indels 18; Caps
                                                                                                                                                                                                                                                                                                                      351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
                                         1 NSHSCDIVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                      Score 2093; DB 21; Length 467; Pred. No. 4.8e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus phytase 10 thermo 5 Q50T K91A protein SEQ ID NO:97.
                          12;
                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                 AAB20534 standard; Protein; 467 AA.
 90.28;
          92.48;
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         Best Local Similaricy Matches 414; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-2000 (first entry)
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB20534;
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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate cleavage partern, substrate binding, position specificity, substrate cleavage partern, release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes improved phytases, preferably with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2093; DB 21; Length 467;
Pred. No. 4.8e-196;
4; Mismatches 12; Indels 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant phytase-10, phytase-10-thermo[3]-Q50T-K91A.
                                                                                                            Disclosure; Fig 25a-c; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY69569 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.28;
      compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 414; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 467 AA;
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\mathbb{F}_{\mathbf{X}} \times 
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Aspergillus terreus 9A1.

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The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilishing agents including phosphohydrolase) and one or more stabilishing agents including to the phosphohydrolase; and one or more stabilishing a molecular weight of 600 xylitch or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3550 Da; the disodium salts of malonic, to 4000 Da, preferably 1000 to 3550 Da; the disodium salts of malonic, or stabilised phytase formulation is used in a method for proparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of proyides a monogastric animal with its dietary requirements of phosphate along phosphate is present in animal feed in the form of physphate, resulting in the addition of extra to the feed of such animals. Phytase enhances the nutritional phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved enzyme the phytase formulation of the invention has an improved enzyme interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents a mutant phytase-10 consensus sequence, phytase-10-thermo[3]-050T-K91A, which has a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAX69566). Its specific activity with phytate as a
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Phytase signal peptide from Aspergillus terreus cbs16.46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Mature phytase-10-thermo[3]-Q50T-K91A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substrate is also strongly increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                              Talaromyces thermophilus ATCC20186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Fig 19; 101pp; English
                                                                         Aspergillus fumigatus ATCC32722.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC5696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brugger R, Lehmann M, Wyss M;
                   Aspergillus niger var. awamori.
Aspergillus niger str. NRRL3135.
                                                                                                                                       Aspergillus fumigatus ATCC32239.
                                                            Aspergillus fumigatus ATCC13073
Aspergillus terreus cbs16.46.
                                                                                                                                                                                                      Myceliophthora thermophila.
Paxillus involutus NN005693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99EP-0111949.
                                                                                                                                                                                                                                          Trametes pubescens NN9343.
Agrocybe pediades NN009289.
Peniophora lycii NN006113.
Thermomyces lanuginosa.
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                                                                                                                                                             Emericella nidulans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1-999;
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                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                                                                                                         DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                             351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                          387 esieetdgysaswtvpfaarayvemmqcea-----ekeplvrvlvndrvvplhgcgvd 439
                                                                                                                                                                      350
                                                                                                                   118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                       PISSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                             Gaps
                                                   1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                    27 nshscdtvdggygcfpeishlwgtyspffsladesalspdvpkgcrvtfýqvlsrhgary 86
                                                                                                                                                                                                                                                                                                               LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV
                                                                                                                                                                                                                                                                                                                                                                                 Score 2093; DB 21; Length 467; Pred. No. 4.8e-196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus phytase 3 thermo 11 Q50T protein SEQ ID NO:91.
                             12; Indels
                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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99DK-0001340.
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        90.2%;
92.4%;
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         Ouery Match 90.2's
Best Local Similarity 92.4's
Matches 414; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                        291
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Synthetic.

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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved proparties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
                                                                                            Disclosure; Fig 22a-c; 240pp; English.
compound foods and feeds
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18; Gaps 1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58 89.1%; Score 2067; DB 21; Length 467; 91.3%; Pred. No. 1.7e-193; Indels 7; Mismatches Conservative Best Local Similarity Matches 409; Query Match

467 AA;

Seguence

10;

59 PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLFPFGENQMVNSGIKFYRR 117 118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174 g D δλ q ŏλ ŏ g

175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233 234 DIVARISDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290 ă q δ

424 AA;

Sequence

291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350 ò

ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409 351

g

Dp

ŏ

410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437 à q

AAB20536 standard; Protein; 424 AA.

AAB20536; 

05-DEC-2000 (first entry)

Consensus phytase protein from Fig 4.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and Disclosure; Fig 4a-d; 240pp; English. 21-JAN-2000; 2000WO-DK00025. 99DK-0001340. 99DK-0000092 compound foods and feeds -(NOVO ) NOVO NORDISK AS WPI; 2000-491161/43. WO200043503-A1 22-JAN-1999; 21-SEP-1999; 27-JUL-2000. Lehmann M; 

60 TSSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRYK 119 120 ALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLD 179 180 HGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPFDTVART 239 240 SDATQLSPFCDLFTADEWQYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQDH 299 300 ISTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE-SIETDGY 358 AASWTVPFAARAYVEMMQCEAGGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVDKLGRCKLDD 418 17; Gaps 1 NSHSCDTVD-GYQCPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 88.9%; Score 2064.5; DB 21; Length 424; 94.3%; Pred. No. 2.5e-193; 8; Indels 0; Mismatches 94.3%; Best Local Similarity 94.3 Matches 414; Conservative Query Match 294 ŏ Dp ò αG δ qq ŏ qq qq Qγ qq

12;

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value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including explited or ribitel; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alphate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of freed in the form of phytate phosphotrus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional contraction of the feed of such animals.
                                                                                                                                                                                                                                                            Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
thermostable; animal feed; monogastric animal; phytate phosphorus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                               Initial consensus mature phytase #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emericella nidulans.
Talaromyces thermophilus ATCC20186.
                                                                                                                        AAY69565 standard; protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 16; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Aspergillus niger var. awamori.
Aspergillus niger str. NRRL3135.
Aspergillus fumigatus ArCC13073.
Aspergillus fumigatus ArCC37722.
Aspergillus fumigatus ArCC58128.
Aspergillus fumigatus ArCC58128.
                                                                                                                                                                                                                                                                                                   phosphate availibility; consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus fumigatus ATCC32239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brugger R, Lehmann M, Wyss M;
                                                                                                                                                                                                                                                                                                                                                        Aspergillus terreus cbs16.46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myceliophthora thermophila.
Paxillus involutus NN005693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99EP-0111949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98EP-0111960.
419 FVEGLSFARSGGNWAECFA 437
                  406 fveq1sfarsggnweecfa 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trametes pubescens NN9343.
Agrocybe pediades NN009289.
Peniophora lycii NN006113.
                                                                                                                                                                                               19-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                         Aspergillus terreus 9A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermomyces lanuginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monogastric animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-099429/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP969089-A1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-2000
                                                                                                                                                              AAY69565;
                                                                                          RESULT 13
                                                                                                           AAY69565
                                                                                                                                             δλ
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12;
enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents an initial consensus phytase sequence determined using the program PRETY from mature phytase sequences from a variety of fungi (AAY69544, Y60546, AAX69548 Y6955, AAX69564) and the Basidiomycetes phytase consensus AAY69563. This was used as the basis for the consensus phytase designated phytase-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 AASWTVPFAARAYVEMMQCEAGGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKLGRCKLDD 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 HGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEALPGVNLTDEDVVNLMDMCPFDTVART 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 SDATQLSPFCDLFTADEWQYDYLQSLKYYGYGAGNPLGPAQGVGFNELIARLTHSPVQDH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 TSINHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE-SIETDGY 358
                                                                                                                                                                                                                                                                                                                                                              60 TSSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRYK 119
                                                                                                                                                                                                                                                                                                                                                                                   120 ALARNIYVFYVRASGSDRVIASAEKFIEGFQSAKLADPAHQASPVINVIIPEGSGYNNTLD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NSHSCDTVD-GYQCPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
                                                                                                                                                                                                                                                              8; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                             1 nshscdtvdggyqcpeishlwgqyspffsladesaispdvp-gcrvtfvqvlsrhgaryp 59
                                                                                                                                                                                                                              DB 21; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus phytase 3 thermo 11 Q50T K91A protein SEQ ID NO:93.
                                                                                                                                                                                                                        Score 2064.5; DB 21
Pred. No. 2.5e-193;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB20532 standard; Protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000; 2000WO-DK00025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food; feed; phytate; manure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 FVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 fveglsfarsggnweecfa 424
                                                                                                                                                                                                                                   88.9%;
                                                                                                                                                                                                                                                 94.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                  Matches 414; Conservative
                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                  Sequence 424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WOZ00043503-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                  (AAY69566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB20532;
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
                                                                                                                                                                 Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESALSPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2061; DB 21; Length 467;
Pred. No. 6.5e-193;
7; Mismatches 15; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                              Disclosure; Fig 23a-c; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.8%;
91.1%;
                   99DK-0000092
                                99DK-0001340
                                                                                                                                                                                                compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408; Conservative
                                                           (NOVO ) NOVO NORDISK AS
                                                                                                                      2000-491161/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 AA;
                                                                                                                                      N-PSDB; AAA73291
                 22-JAN-1999;
                              21-SEP-1999;
                                                                                         Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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animal feed preparation; thermostable phytase; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the consensus phytase-1-thermo(8)-Q5OT-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytase) simultaneously.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NSHSCDIVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.1%; Score 2044; DB 20; Length 467; 90.4%; Pred. No. 3e-191; Indels 18;
                                                                         Consensus phytase-1-thermo(8)-Q50T-K91A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           Preparing animal feed using a thermostable phytase
AAY43169 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 9; 71pp; English.
                                                                                                                                                                                                                     99WO-DK00154
                                                                                                                                                                                                                                                          98DК-0000806
                                                                                                                                                                                                                                                                     98DK-0001176.
                                                                                                                                                                                                                                             98DK-0000407
                                                                                                                                                                                                                                                                                               99DK-0000093
                                                 06-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-591030/50.
                                                                                                                  consensus seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 405; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 AA:
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ31520
                                                                                                                                                                                                                  22-MAR-1999;
                                                                                                                                                                 W09948380-A1
                                                                                                                                                                                                                                          23-MAR-1998;
                                                                                                                                                                                                                                                      19-JUN-1998;
18-SEP-1998;
                                                                                                                                                                                                                                                                                           22-JAN-1999
                                                                                                                                                                                          30-SEP-1999
                                                                                                                                                                                                                                                                                 22-JAN-1999
                                                                                                                                                                                                                                                                                                                                              Petersen S;
                                                                                                                                       Synthetic.
                                                                                                  Phytase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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X,GXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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Indels 18; Gaps

387

g ò

AAY43169

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Dp
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Oy Db

Οy

Search completed: October 26, 2001, 16:40:04 Job time: 4955 sec

Compugen Ltd GenCore version 4.5 Copyright (c) 1993 - 2000 Com

OM protein - protein search, using sw model

October 26, 2001, 16:40:45 Run on:

; Search time 32.57 Seconds
(without alignments)
276.266 Million cell updates/sec

US-09-488-265-27 Perfect score:

1 NSHSCDIVDGYQCPEISHLW......DFVEGLSFARSGGNWAECFA 437 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

197339 Total number of hits satisfying chosen parameters:

197339 seqs, 20590346 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries Maximum

Database :

Issued\_Patents\_AA:\*

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PcTu5\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PcTu5\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   |        | Description  | 1               | , c         | 7              | Sequence 8, Appli | ednence 8,                 | Sequence 2, Appli | 32.  | Sequence 20. Appl | ,               | Sociion 22 April | ,               | ò          | Sequence 3, Appli | Ļ           | ۳,           | Ċ        | ì     | 4 0          | 7 17           | 30,             | 22,          | 24,                          | 2, 4            | 2            | Segmence 28 Appl | 2 0          | ,<br>o<br>v    | `,              | 'n         | Sequence 2, Appli | 7                |
|---|--------|--------------|-----------------|-------------|----------------|-------------------|----------------------------|-------------------|------|-------------------|-----------------|------------------|-----------------|------------|-------------------|-------------|--------------|----------|-------|--------------|----------------|-----------------|--------------|------------------------------|-----------------|--------------|------------------|--------------|----------------|-----------------|------------|-------------------|------------------|
|   |        | 3 ID.        | US-09-121-425-1 | -09-121-425 | 107 - CCO- LO- | * #7/-876-70 SO   | 4264<br>110 00 014 010 011 | -08-3/4-652C      | -08  | -08-146-424-      | US-08-693-709-2 | US-08-419-448-   | US-08-819-825-3 | 010-17-00- | 09-103-042-       | -03-CCT-60- | -09-155-855- | -09 - 15 | -825- | -09-163-642- | HS-08-003-250- | C 04C C00+80-51 | 05-08-359-27 | -65E-863-356<br>-05E-863-356 | US-09-221-654-2 | US-08-989-35 | 0S-08-99         | US-08-993-35 | -705-77-K230C- | 112-07-627-5200 | 03.07.0396 | US-07-923-72      | US-08-609-426A-2 |
|   |        | Length DB    | 441 4           | 467 4       | 467            |                   | 101                        | 7 10 4            | 46/  | 467 1             | 467 1           |                  | 467 2           | 467        |                   | * (         | ٥            | 443 4    | 475 2 | 475 4        | 43             | , ~             | ה<br>ה       | # 0.4<br>7 0.4               | א<br>מ<br>מ     | J.           | 42               | 7            | و              | α               | 0 0        | ח מ               | תכ               |
| æ | Query  | Match Length | 87.0            | Η.          | 72.7           | 72.7              | 7 27                       |                   |      | 0.27              |                 |                  |                 |            |                   |             |              |          |       | ζ.           |                | 35.0            |              | 7 7 7 7                      | •               | 7. 40        | 34.2             | ٠            | 14.8           |                 | •          | ٠                 | 13.2             |
|   |        | Score        | 2020            | 1902        | 1688           | 1688              | 1688                       | 2001              | 1001 | 1064              | 1084            | 1684             | 1684            | 1684       | 1672              | 1673        | 1 1 1        | 1997     | 1322  | 1322         | 837.5          | 812.5           | 204          | . FOR                        | ) C             | •            | 56/              | 791.5        | 343.5          | 343.5           | 307 5      | 0.000             | :                |
|   | Result | No.          | H               | 7           | m              | 4                 | n                          | . 4               | 1 C  | ~ 0               | o o             | ָּע              | 10              | 11         | 12                | 13          | ,            | 7 T      | 12    | 16           | 17             | 18              | 0            | 200                          | 2 5             | 4 (          | 77               | 23           | 24             | 25              | 26         | 9 6               | 17               |

| Sequence 4, Appli<br>Sequence 3, Appli<br>Sequence 7, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 8, Appli<br>Sequence 8, Appli<br>Sequence 43, Appli<br>Sequence 43, Appli<br>Sequence 43, Appli<br>Sequence 10, Appli | ,<br>,                              |
|--|-------------------------------------|
| US-08-374-652C-4 US-08-993-359-32 US-08-680-506-7 US-08-680-506-3 US-08-08-206-3 US-08-374-652C-32 US-08-374-652C-32 US-08-241-853-8 US-08-241-853-8 US-08-850-917-8 US-08-850-917-8 US-08-850-917-8 US-08-850-917-8 US-08-850-917-8 US-08-850-917-8 US-08-850-917-8 US-08-850-917-10 US-08-849-751-4  | US-09-032-315-3<br>US-08-993-318A-3 |
|  | 2 2                                 |
| 20<br>92<br>92<br>94<br>92<br>94<br>92<br>97<br>113<br>113<br>113<br>113<br>113<br>113   | 4<br>4<br>9<br>9<br>9               |
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| 307.<br>1699<br>11001<br>1101.<br>1001.<br>1001.<br>1001.<br>100.<br>100   | 87.5                                |
| 22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2   | 4 4<br>4 5                          |

## ALIGNMENTS

; OTHER INFORMATION: Description of Artificial Sequence:consensus; OTHER INFORMATION: sequence US-09-121-425-1 Sequence 1, Application US/09121425
Patent No. 6153418
GENERAL INFORMATION:
TITLE OF INVENTION: Consensus Phytases
FILE REPERENCE: Consensus Phytases 13239
CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1988-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0 ORGANISM: Artificial Sequence US-09-121-425-1 LENGTH: 441 SEQ ID NO 1 TYPE: PRT FEATURE:

59 PTSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117 175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPF 233 DIVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290 Ouery Match 87.0%; Score 2020; DB 4; Length 441; Best Local Similarity 89.3%; Pred. No. 6e-208; Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVINVIIPEGSGY 174 1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 234 δ q QQ δ δ Óγ g

LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVIN------ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------VIIPEGSGYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-L 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTSSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8%; Pred. No. 2.9e-195;
Matches 382; Conservative 10; Mismatches 19; Indels 56; Gaps
 301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360
                                   351 ESI-ETDGYAASWIVPFAARAYVEMMQCEAGGGGGGGGGGEGKEPLVRVLVNDRVVPLHGCGVD 409
                                                     27 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:consensus; OTHER INFORMATION: sequence US-09-121-425-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 LVRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: consensus physics 13239 CURRENT APPLICATION NUMBER: US/09/121,425 CURRENT FILING DATE: 1998-07-23 EARLIER APPLICATION NUMBER: EPO 97112688.3 EARLIER FILING DATE: 1997-07-24 NUMBER: POSEQ ID NOS: 20 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                          410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
                                                                                                                                                                                                                            ; Sequence 2, Application US/09121425
; Patent No. 6153418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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-09-121-425-2
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Best Local Similarity 73.9%; Pred. No. 2.6e-172;
Matches 331; Conservative 40; Mismatches 59; Indels 18
                                                                                                                                                                                               APPLICANT: Fagerstr m. Tichard B. TITLE OF INVENTION: production of Phytase Degrading Enzymes TITLE OF INVENTION: in Trichoderma
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                                                                                                                                                                                                                                                                                            3: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue, Suite 600
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                                                        Nevalainen, Helena K.M.
Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
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FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
                                                                                                                                                     Piddington, Christopher
Rambosek, John A.
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Sequence 8, Application US/07923724
Patent No. 5780292
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REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                 Torkkeli, Tuula K.
Cantrell, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                         Turunen, Marja K
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                           GENERAL INFORMATION:
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APPLICANT:
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175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                         351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                          APPLICANT: Palohelino, Marja T.
APPLICANT: Mictinen-Oinonen, Arja S.K.
APPLICANT: Mictinen-Oinonen, Arja S.K.
APPLICANT: Cantrell, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Paldington, Christopher S.
APPLICANT: Fambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m. Richard B.
APPLICANT: Fagerstr m. Richard B.
APPLICANT: Production of Phytase Degrading Enzymes TITLE OF INVENTION: In Trichoderma
CORRESPONDENCE ADDRESS:
ANDMABR OF SEQUENCES:
ANDMABRO OF SEQUENCES:
ANDMABRO OF ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE: Sterne, Kessler, Goldstein & Fox
1100 New York Avenue, Suite 600
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ER: 1050.008000I
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PELICATION NUMBER: US,08/609,426A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION NUMBER: US 07/496,155
FILING DATE: 29-APR-1987
PRIOR APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION NUMBER: US 07/044,077
                                                                                                                                                                                                                                                                                                                              410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nevalainen, Helena K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08609426A Patent No. 5830733
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FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (202) 371-2600
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STATE:
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APPLICANT: PODGYON, CHRISTOPHER S.
APPLICANT: HOUSTON, CHRISTOPHER S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
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                                                                                                                                                                                                                                                                                                                                                                              118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASFVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Gaps
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                                                                                                                                                                                                                                                            Length 467;
                                                                                                                                                                                                                59; Indels
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                                                                                                                                                                    Query Match 72.7%; Score 1688; DB 2; Best Local Similarity 73.9%; Pred. No. 2.6e-172; Matches 331; Conservative 40; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: NEVALALINEN, HELENA K.M.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: FAGENSTROM, RICHARD B.
APPLICANT: MIETITINEN OINONEN, ARJA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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            INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TURNEN, MARJA K.
APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: PIDDINGTON, CHRIS
APPLICANT: HOUSTON, CHRISTIN
(202) 371-2540
                                                                                                   ; MOLECULE TYPE: protein US-08-609-426A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WASHINGTON
                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20005
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 TELEFAX:
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Patent No. 5436156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.7%; Score 1688; DB 2; Length 467;
73.9%; Pred. No. 2.6e-172;
tive 40; Mismatches 59; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 PISSKSKKYSALIERIQKN-ATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 NSHSCDIVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVIFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                   FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT: E.
REGISTRATION NUMBER: 41,264
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFRONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
FILASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 32, Application US/08151574
                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 467 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               ss: single
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 73.99
Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: not relevan
MOLECULE TYPE: protein
                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.6%; Score 1684; DB 1; Length 467; 73.9%; Pred. No. 6.9e-172; tive 40; Mismatches 59; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NSHSCDTVD-GYQC-PEISHIMGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Cloning and Expression of Microbial TITLE OF INVENTION: Phytase
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Murashige, Kate H. RestStrarton NUMBER: 29,959 RESTSTRATION NUMBER: 24615-20026.00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         E: Morrison & Foerster
545 Middlefield Road, Suite 200
                APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/151,574
                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 32:
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Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; ; MOLECULE TYPE: protein US-08-151-574-32
                                                                                                                                                                                                                                                                                                     ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                               CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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GENERAL INFORMATION:
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LOCATION: 1...23
OTHER INFORMATION:
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CITY: Palo Alto
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TELEFAX: 706141
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351 ESI-ETDGYAASWIVPFAARAYVEMMQCEAGGGGGGGGEKEPLVRVLVNDRVVPLHGCGVD 409
                   59 PISSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.6%; Score 1684; DB 1; Length 467; 73.9%; Pred. No. 6.9e-172; tive 40; Mismatches 59; Indels 18;
                                                                                                                                                                              Sequence 20, Application US/08146424
Patent No. 5593963
GENERAL INFORMATION:
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: BEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: SIJMONS, PETER C.
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,424
FILING DATE: 02-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44615-20011.24
                                                                410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                 ADDRESSE: MORRISON & FOERSTER STREET: 755 Page Mill Road CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: KENNEDY, BILL
REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: 4461:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
MERCEN (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 706141
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.9%
Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-146-424-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
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234 DIVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
                                                                                                                                         291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: NAN OOLJEN, ALBERT J.J.
APPLICANT: RIFFUNELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: HOEKEMA, JAN
APPLICANT: BEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
INVENTION: INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
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FILING DATE: 07-AUG-1996
CLASSIFICATION: 800
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STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146,424
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08693709
; Patent No. 5770413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Signal Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 467 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                    59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
                                                                                                                                                                                              118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
                                                                                                                                                                                                                                                                 175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
                                                                         59; Indels 18; Gaps
                                                                                                          1 NSHSCDIVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
                                                                                                                            Length 467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2000 Pennsylvania Ave. N.W., Suite 5500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 SOFTWARE:
                                           72.6%; Score 1684; DB 1;
73.9%; Pred. No. 6.9e-172;
tive 40; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/419,448
FILING DATE: 10-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08419448
Patent No. 5863533
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Golcom
APPLICANT: Willem Van Hartingsveldt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                Matches 331; Conservative
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TITLE OF INVENTION:
                                                Query Match
Best Local Similarity
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US-08-693-709-2
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APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klohael W.
APPLICANT: Alan V.
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                        59; Indels
                                                                                                                                                                                                                                               Query Match
Post Local Similarity 73.9%; Pred. No. 6.9e-172;
Matches 331; Conservative 40; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 2.0
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                24615-20026.10
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; Sequence 3, Application US/08819825
; Patent No. 5866118
              REFERENCE/DOCKET NUMBER: 24(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
REGISTRATION NUMBER: 29,959
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COMPUTER READABLE FORM:
MEDIUM TYPE: Distriction
                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                       , MOLECULE TYPE: protein US-08-419-448-32
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                                                                                                                                                                                                                                                                                                                                                                                            27 NQSSCDTVDQGYQCFSFTSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86
                                                                                                                                                                                                                                                                                                                    Length 467;
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APPLICANT: Berka, Randy M.
APPLICANT: Berka, Michael W.
APPLICANT: Klotz, Alan V.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity TITLE OF INVENTION: And Nucleic Acids Encoding Same NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                            72.6%; Score 1684; DB 2;
73.9%; Pred. No. 6.9e-172;
tive 40; Mismatches 59;
                                                                         NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFENCE/DOCKET NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
                MBER: US/08/819,825
18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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Patent No. 6221644
                                                                                                                                                     TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 73.9% Matches 331; Conservative
CURRENT APPLICATION DATA:
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSE: No. 62216
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                                             CLASSIFICATION:
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                                FILING DATE:
                                                                                                                                                                                                                                                             US-08-819-825-3
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59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
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                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 4758.200-US TELECOMUNICATION INFORMATION: TELEPHONE: 212 867 0123 TELEFAX: 212 867 0298
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387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA---
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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: Patent No. 6139902
                                                                                                                                                                                                                                                                                                        33,728
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3;
                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                    NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                       : 467 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                        Diskette
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-163-642-3
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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    APPLICANT: ANAZAWA, Hideharu
    APPLICANT: ANAZAWA, Hideharu
    APPLICANT: NAGASHIMA, Tadashi
    APPLICANT: TANGE, TALESUA
    TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
    FILE REFERENCE: 81356/124
    CURRENT APPLICATION NUMBER: US/09/155,855
    CURRENT FILING DATE: 1998-10-05
    CURRENT APPLICATION NUMBER: WO PCT/JP97/01175
              APPLICANT: KNEEKO, Syunichi
APPLICANT: RAGASHIMA, Tadashi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
FILE REFERENCE: 81356/124
FILE REFERENCE: 81356/124
CURRENT APPLICATION NUMBER: US/09/155,855
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1997-04-05
NUMBER OF SEO ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                72.0%; Score 1672; DB 4; Length 443; 72.8%; Pred. No. 1.2e-170; Live 46; Mismatches 58; Indels 18
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; ORGANISM: Aspergillus niger
US-09-155-855-1
APPLICANT: ANAZAWA, Hideharu APPLICANT: KANEKO, Syunichi
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 326; Conservative
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                          LENGTH: 443
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                                                                                                                                                                                                                                                                                                                                                         27 NGSTCDTVDQGYQCFSETSHLMGQYAPFFSLANKSAISPDVPAGCHVTFAQVLSRHGARX 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KONDO, Hidemasa
APPLICANT: KONDO, Hidemasa
APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Hideharu
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124
CURRENT APPLICATION: NUMBER: 08/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER FILING DATE: 1998-10-05
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                  Ouery Match 72.0%; Score 1672; DB 4; Length 467; Best Local Similarity 72.8%; Pred. No. 1.3e-170; Matches 326; Conservative 46; Mismatches 58; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
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EARLIER APPLICATION NUMBER: JP 084314
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/09155855
; Patent No. 6139902
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                                                                                                                                                     TYPE: PRT; ORGANISM: Aspergillus niger
US-09-155-855-3
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LENGTH: 443
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                                                                                                                                    LENGTH: 467
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               ; OTHER INFORMATION: Xaa at positions 2 & 3 may be any amino acid or unknown US-09-155-855-2
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                                                                                                                                                                                                                                                                                                                                    62 SKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRYKA 120
                                                                                                                                                                                                                                                          121 LARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGYNNT 177
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                                                                                                                                                                                                                                                                                                                                                                                                              237 ARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLTH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 -ETDGYAASWTVPFAARAYVEMMQCEAGGGGGGCGEKEPLVRVLVNDRVVPLHGCGVDKLG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Gaps
                                                                                                                                                               4 SCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVFKGCRVTFVQVLSRHGARYPTS 61
                                                                                                                                                                                  Query Match
71.8%; Score 1667; DB 4; Length 443;
Best Local Similarity 73.0%; Pred. No. 4.2e-170;
Matches 325; Conservative 46; Mismatches 56; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: R1otz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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SDRVIASAEKFIEGFQSAKLADP -- - AHQASPVINVIIPEGSGYNNTLDHGLCTAFEDST 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 IGDDAE-ANFTAVFAPPIRARL-EALPGVNLTDEDVVNLMDMCPFDTVARTSDAT---Q 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRYKALARNIVPFVRASG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSPFCDLFTADEWQ-YDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT-HSPVQDHT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE---SIETDG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAASWIVPFAARAYVEMMQCEAGGGG---GEGEKEPLVRVLVNDRVVPLHGCGVDKLGRC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Gaps
                                                                                                                                                                                                                                                                                                  15 EISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIERI 74
                                                                                                                                                                                                                                                                                                                       Query Match 57.0%; Score 1322; DB 2; Length 4. Best Local Similarity 61.8%; Pred. No. 4.6e-133; Matches 273; Conservative 51; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: October 26, 2001, 16:40:46 Job time: 4957 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 KLDDFVEGLSFARSGGNWAECF 436
TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
            TELEPHONE: 212 867 0123 TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |::::||:||| ||:| || || 454 RRDEWIKGLIFARQGGHWDRCF
                                                                                 475 amino acids
                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-819-825-2
                                                                                                             STRANDEDNESS: single
                                                                                                amino acid
                                                                               LENGTH:
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October 26, 2001, 18:33:00 ; Search time 2563.44 Seconds (without alignments) 5177.342 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                    10228115 seqs, 4726426750 residues
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                                     OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                           US-09-488-265-28
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gb_est40:*
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Sequence:
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                                                             Run on:
                                                                                                        Title:
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em_esthum16:*
em_esthum17:*
em_esthum18:*
em_esthum19:*
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em_esthum15:*
em_esthum10:*
                                   em_esthum13:*
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em\_esthum24:\* em\_esthum25:\* em\_esthum26:\* em\_esthum22:\* em\_esthum23:\* em\_esthum27:\* em\_esthum28:\* em\_estin1:\*

em\_estin2:\*
em\_estin3:\*
em\_estin4:\* em\_estom1:\* em\_estom2:\* em\_estov2:\* em\_estin5;\* em\_estov1:\*

em\_estpl2:\* em\_estpl3:\* em\_estpl4:\*

em\_estpl5:\*
em\_estpl6:\*
em\_estpl7:\*
em\_estpl8:\*
em\_estpl9:\*
em\_estpl10:\*

em\_estro2:\*
em\_estro3:\*
em\_estro5:\*
em\_estro6:\*
em\_estro6:\*
em\_estro6:\*
em\_estro9:\*
em\_estro1:\*

em\_estro19:\* em\_estro20:\*

gb\_est25:\*
gb\_est26:\*
gb\_est27:\*
gb\_est28:\* gb\_est29:\*
gb\_est30:\*
gb\_est31:\*

gb\_est41:\*
gb\_est42:\*
gb\_est43:\*
gb\_est44:\*
gb\_est46:\*
gb\_est46:\* gb\_est32;

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117: 99 cet48:*
119: 90 cet50:*
110: 90 cet50:*
110: 90 cet51:*
110: 90 cet51:
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| 10:*  fun: hum2 hum3 hum4 hum4 hum6 hum6 hum6 hum6 hum6                      | em_gss_linv3:* em_gss_linv3:* em_gss_pln1:* em_gss_pln1:* em_gss_pln1:* em_gss_rod2:* em_gss_rod3:* em_gss_rod4:* em_gss_rod3:* em_gs_rod3:* em_gs_ro |   |
|--|--|---|
| 1900<br>1923:<br>1944:<br>1955:<br>1966:<br>1977:<br>1989:<br>2000:<br>2001: | 2005<br>2006<br>2007<br>2010<br>2011<br>2011<br>2010<br>2010<br>2010<br>2010   | 2334:<br>2334:<br>2338:<br>2338:<br>2440:<br>2444:<br>2444:<br>255:<br>255:<br>255:<br>255: |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4 1 2.86 : 1

SUMMARIES

| Description         | AQ25459 mgxb0019C<br>AQ25459 mgxb0019A<br>AQ274007 AJ274007<br>AQ162040 mgxb0010E<br>AQ162040 mgxb0010E<br>AQ162040 mgxb0004E<br>AQ162040 mgxb0004E<br>AQ162195 mgxb0004E<br>AQ2020E RPCIII-48<br>AV23643 AV29432<br>AV023643 AV023643<br>AV023643 AV023643<br>AV07122 AV017122<br>AV014552 AV014552<br>AV014552 AV014552<br>AV014552 AV014552<br>AV014552 AV014552<br>AV014552 AV014566<br>AV050181 AV05384<br>AV118366 AV118366<br>AV018366 AV18366<br>AV05187 AV161297<br>AV05199 AV05403<br>AV05409 AV056003<br>AV056003 AV056003<br>AV05603 AV056003<br>AV06603 AV056003<br>AV06603 AV056003<br>AV06603 AV056003<br>AV06603 AV056003<br>AV06603 AV056003<br>AV06603 AV056003<br>AV06603 AV056003<br>AV06603 AV056003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV066003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV06003<br>AV060   | Magnaporthe grisea genomic Magnaporthe grisea genomic ina; Sordariomycetes; haceae; Magnaporthe. yle, A., Kingsbury, R.,             |
|---------------------|--|--|
| SUMMARIES           | AQ324539 AQ255459 AQ255459 AQ263004 AQ162040 AQ161256 AQ161956 AQ161956 AQ161956 AV29427 AV081956 AV081963 AV081963 AV081963 AV051896 AV051896 AV051896 AV051896 AV051896 AV051896 AV051896 AV051896 AV051898   | GSS nce.  Pezizomycotina; s; Magnaporthacea dette, B., Gayle, A  |
| DB 1                | 1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009<br>1009   | 802.bp<br>UGI Rice I<br>COlr, DNA<br>:4116391<br>Isea.<br>Isea.<br>Ji, Ascomy<br>Ji, Ascomy<br>Ji, Ascomy<br>S incertae<br>BOZO,C.A. |
| Length              | 8802<br>98137<br>98137<br>98137<br>98137<br>98139<br>98139<br>98139<br>98139<br>98139<br>98139<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>9813<br>98   | 802 bp DN CUGI Rice Bla D0019C01r, DNA se CI GI:4116391 e grisea. Fungi, Ascomyco Cetes incertae syluth Boyd, C.A., (Sasinowski, M,  |
| %<br>Query<br>Match | 0 m r m n n n n u a a a a a a a a a a a a a a a  | 39<br>19C(<br>19C(<br>39.1<br>39.1<br>orth<br>orth<br>orth<br>iomy<br>iomy<br>ses<br>ses<br>Ses                                      |
| Score               | 1020.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.8<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>1022.6<br>10 |  |
| Result<br>No.       | 0 000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  | RESULT 1 AQ324539/C LOCUS DEFINITION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS                                      |

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/note="Vector: pBACKUTCH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentcus ascomycete with a haploid genome (n=") of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request." I others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      953 gtttcgctaacgaattgattgctagattgactcactctccagttcaagaccacacttcta 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1187 ctgcttcttggactgttccattcgctgctagagcttacgttgaaatgatgcaatgtcaag 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.7%; Score 150.6; DB 227; Length 802; Best Local Similarity 56.7%; Pred. No. 1.1e-33; Matches 301; Conservative 0; Mismatches 224; Indels 6;
                                                                    Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CUGI Rice Blast BAC Library"
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                                                                                                                                                                                                                                                                                               /organism="Magnaporthe grisea"
/strain="70-15"
/db_xref="taxon:148305"
                                         Clemson University Genomics Institute
                                                                                                                                                    Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 408.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          /clone="mgxb0019C01r"
    Unpublished (1998)
                             Dean RA
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Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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55.7%; Pred. No. 2.9e-25;
tive 0; Mismatches 186; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
TT: 864 655 5737
Fax: 864 656 4293
51 GCGATGCCGACAGTATGGGTCGTTGCACGCTGAGCAAGTTCGTTGAGAGCT 1
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/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
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                                                                                                                                                              clone mgxb0014M15r, DNA sequence.
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High quality sequence stop: 277.
Location/Qualifiers
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Magnaporthe grisea
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Screen, S.E., Mathur, P. and St. Leger, R.J.
EST analysis of the insect pathogenic fungus Metarhizium anisopliae Unpublished (1999)
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/note="Vector: Unizap; Metarhizium anisopliae was grown on insect cuticle for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector, Unizap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ274007 S81 bp mRNA EST 29-DEC-1999
AJ274007 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae
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                                                                                     220 ccgrcgggargcgargcraccrirgcrrcaarcrrgrcaargaggrccgcaaccc 279
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                                                                                                                                                                                                                                                                                                                                              293 CCAGCGTGCAAAATGGTACAGAACGGAAACGGTAATCCTTTGGGCCCAACTATGGGCG 352
                                                                                                                                           353 TGGGATGGGTAAACGAACTTATTGCACGATTAACCCGAAGCCCAGTCCAAGATCAAACCA 412
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4112 Plant Sciences Building, College Park, MD 20742, USA.
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/db_xref="taxon:5530"
/clone="Ma#1628"
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mgxb0021D19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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Yu, Y., Zhu, H., Boyd.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                           442 aaggetttggetagaaa~-~gattgttecatteattagagettetggttetgacagagtt 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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/clone_lib="CUGI Rice Blast BAC Library"
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                                                                                                    520 GTCATGTCAGGGGCAAGATTTGTTCATGGCTTCTACAAAGCCAAG 564
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Clemson University Genomics Institute
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/lab_host="E. coli DH10B"
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Location/Qualifiers
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Class: BAC ends
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                                                                                                                                                                                                     AQ163004
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249 GTATGCACCATTTTTCGTTGCACCGTCAGCACCATCGGATTATGATTCCTCTGCTACCTT 308

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AQ162040 699 bp DNA GSS 09-SEP-1998 mgxb0010F06r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0010F06r, DNA sequence.
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/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: PBACWCH's ite_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                              309 GCCAGGGTGTAGCATTACGTTTGCCCAAGTCCTTCAGAGGCACGGGGCTCGATACCCAAC 368
208 ---gactgtagagttactttcgttcaagttttgtctagacacggtgctagatacccaac 263
                                                                                                                                264 ttcttctgcgtctaaggcttactctgctttgattgaagctattcaaaagaacgctactgc 323
                                                                                                                                                                                       369 GGTICAAACGGGGGGAAATTCTCGAACATTCACGAATCCAAACCTCACGTACGG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          564 accacaccaagettetecagttattaaegtgateattecagaaggateeggttacaacaa 623
                                                                                                                                                                                                                                                             324 tttcaagggtaagtacgctttcttgaagacttacaactacactttgggtgctgacgactt 383
                                                                                                                                                                                                                                                                                                                           429 TAGTGGCGTATTGAATAACTACATTAAAAACTACAAATACAATCTCGGAGTCGAGGAATN 488
                                                                                                                                                                                                                                                                                                                                                                                             384 gactccattcggtgaaaaccaaatggttaactctggtattaagttctacagaagatacaa 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                           489 GAATGATTIGGGCCGTCGGCAAACAGAACTCCGGGTATTNATTTTACCAAAGATACCA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 AAATCTGGCCAGAAGGAACGAACCATTTATTGGCTATGATGACAAANAACGCGTGTTTGA 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504 ttctgctgaaaagttcattgaaggtttccaatctgctaagttggctgacccaggttctca 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609 TAGCGCAGAACTCTGGGCTAGGGGTTT-CATCGAGCTTCTATAACAGATAAAGGCCGGGC 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 ggctttggctagaaagattgttccattcattagagcttctggttctgacagagttattgc 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         668 TAGACCAGAAACCTTTCCCTACAAAGCTGTGGCGCTTCCTCACCGACATGGGTTTAATAA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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Location/Qualifiers
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Seq primer: GGAAACAGCTATGACCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              624 cactttggaccacggtacttg 644
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a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 Kbp was, constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
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mgxb0008K02r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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Y.Y., Zhu H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                 1178 acggitactctgcttcttggactgttccattcgctgctagagcttacgttgaaatgatgc 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1238 aatgicaagcigaaaaggaaccatiggitagagittiggitaacgacagagitgitccat 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 IGCAGAACTGCGATGCCGACAGTATGGGTCGTTGCACGCTGAGCAAGTTCGTTGAGAGCT 472
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
                                                                                                                                                                                                                                                                                                                                                                                                            09-SEP-1998
                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                           5.7%; Score 79.8; DB 225; Length 699; 59.5%; Pred. No. 1.4e-12; tive 0; Mismatches 92; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Magnaporthe grisea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dean RA
Clemson University Genomics Institute
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AQ161556
AQ161556.1 GI:3557957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 864 656 5737
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                Matches 135; Conservative
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VERSION KEYWORDS

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SOURCE

TITLE

FEATURES

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/note="Vector: DBACWICH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with
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a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 closes with an average insert size of 130 kbp was constructed. This library represents greater
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                than 25x genome coverage. High density colony filters are available upon request."
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     530 GCAGAACTGCGATGCCGACAGTATGGGTCGTTGCACGCTGAGAGTTCGTTGAGAGCTT 471
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                                                                                                                                                                                                                                                                                                         5.3%; Score 74; DB 225; Length 810;
58.0%; Pred. No. 7.8e-11;
tive 0; Mismatches 95; Indels (
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/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coll DH10B"
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Clemson University Genomics Institute
Clemson University
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Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Location/Qualifiers
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1 (bases 1 to 769) Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

100 Jordan Hall, Clemson Universiy, Clemson, SC 29634 Tel: 864 656 5737 Fax: 864 656 4293

Email: rdean@llemson.edu Seg primer: TAATACGACTCACTATAGGG Class: BAC ends High quality sequence start: 51 High quality sequence stop: 416. Location/Qualifiers

Contact: Dean RA Clemson University Genomics Institute

Clemson University

Unpublished (1998)

JOURNAL

TITLE

REFERENCE AUTHORS

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a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              627 TITGCCGAAAGATAATGAACTTTTATCCCTTTCTAATGGAGCCGAACGAGTTGTTAAAAG 568
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                                                                                                                                                                                                                                                                                                                                  Length 669;
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a haploid genome (n=7) of approximately 40 Mpp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kpb was constructed. This library represents greater
than 25% genome coverage. High density colony filters
are available upon request.

a 185 c 157 g 213 t 3 others

BASE COUNT

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7; Gaps

/note="Vector: pBACWICH, Site\_1: HindIII; Site\_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with

/db\_xref="taxon:148305"
/clone="mgxb004112f"
/clone=lb="CGI Rice Blast BAC Library"
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/organism="Magnaporthe grisea"

/strain="70-15"

source

FEATURES

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87 ctcttgtgacactgttgacggtggttaccaatgtttcccagaaatttctcacttgtgggg 146
                                                                                                                             273 CIGITITGATGCGCCAGCCCGCGGTTTTCAATTTAAAGCAGCAATCACTCATAATTGGGG 332
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5.0%; Score 69.8; DB 227; Length
50.3%; Pred. No. 1.4e-09;
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1 (bases 1 to 481)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other GSS: RPCIII-48014.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library availability, please contact Pieter de Jong pieter de Jong please contact Pieter de Jong please contact Pieter de Jong pacpac med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (htfo@fresgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Class: BAC ends.
                                                                                                                                         AQ202816 481 bp DNA GSS 20-APR-1999
REPLILI 48J14.TK RPCII-11 Homo sapiens genomic clone RPCI-11-48J14,
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII.Human Male BAC Library"
RPCIII. And Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AGATAAGAAGCTCCTAAGATGGTCCACCCCGGCTTTTAACACCACTATCAGAAAAGTTCG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/db_xref="GDB:7518277"
501 tgcttctgctgaaaagttcattgaaggtttc 531
                                          692 TGATAGCGCAGAACCTTGGGCTTAGGGTTTC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
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                                                                                                                                                                                                                                   AQ202816.1 GI:3613607
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trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1988))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1988))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 231) to 11 (bases I to 231) to 231 to
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Thermostabilization and thermoactivation of thermolabile enzymes by
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AV129427 Mus musculus C57BL/6J 11-day embryo Mus musculus CDNA
clone 2700068B02, mRNA sequence.
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51 c 66 q 55 t
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/db_xref="taxon:10090"
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AV129427.1 GI:5315662
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Fax: 81-298-36-9098
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Unpublished (1999)
Contact: Chie Owa
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Matches 91; Conservative
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SOURCE

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AV293643.1 GI:6307674
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DEFINITION
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JOURNAL
                                                                    ACCESSION
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                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                   KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-54 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                          AV064132 Mus musculus small intestine C57BL/6J adult Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Mus musculus small intestine C57BL/6J adult"
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                                                                                   24-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="small intestine"
                                                                                                                        cDNA clone 2010009L02, mRNA sequence.
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/db_xref="taxon:10090"
                                                                                MRNA
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45 c 72 q
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Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
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                                                                            234 bp
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                                                                                                                                                                                                                                                                                                             (bases 1 to 234)
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Fax: 81-298-36-9098
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hes 91; Conservative
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KEYWORDS
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09-NOV-1999

EST

mRNA

247 bp

AV293643

AV293643 LOCUS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 247)
S Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., C., Kawai, J., Ishi, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K. Kagawa, I., Kagusai, Y., Kayai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Salto, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shipata, Y., Shipata, Y., Suzuki, H., Takahashi, F., Tateno, M., Sato, K., Shibata, K., Suzuki, H., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yasunda, Y., Voshin, Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y. Ahibata, Y., Ozawa, Y., Muramatsu, M., Okazaki Automated filtrathon-based high-throughput plasmid preparation Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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/clone="5430440C16"
/clone_lib="RIKEN full-length enriched, 6 days neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 264)

Carninoi,P.; Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hoii,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigania,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Matanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length CDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 AAGATGACATGGGCTTCGTTCTTTTGACTAAACTGCTTTTGTTAAGTTGGCTA 229
                                                                                                                                                                                                                       Query Match 2.9%; Score 41.2; DB 28; Length 247; Best Local Similarity 52.3%; Pred. No. 0.31; Matches 91; Conservative 0; Mismatches 83; Indels 0.
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/tissue_type="kidney"
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    .264
    /organism="Mus musculus"

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/db_xref="taxon:10090"
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                                                                                                                                  67 g
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Fax: 81-298-36-9098
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
St. (bases 1 to 269)

Saroinci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigemcto, Y., Shiraki, T., Soqabe, Y., Suqahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N.,
Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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AV077122 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
clone 2210021P10, mRNA sequence.
                                                                                                                                                                     89 AGCAGCTGGAGGTGCGCTGCTCGTGGTGCTGTTCCATTCACTGCCGCCGCCCCAGCTGA 148
                                                                                                                                                                                                                                                                                            149 GGAAAAGAAAGTGGAGGCAAAGAAGGAAGATTCCGAGGAATCTGAAGATAACATGGGCTT 208
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   DB 108; Length 264;
2.9%; Score 41.2; DB 108; Length 53.8%; Pred. No. 0.32; tive 0; Mismatches 73; Indels
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/clone="2210021P10"
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/dev_stage="adult"
65 c 73 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                 85; Conservative
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A. Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Stikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shiqemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 278)
1154 ctgttgaatctattgaagaaactgacggttactctgcttcttggactgttccattcgctg 1213
                                                                                                            1214 ctagagcttacgttgaaatgatgcaatgtcaagctgaaaaggaaccattggttagagttt 1273
                               AVI14552 278 bp mRNA EST 30-JUN-1999 AVI14552 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610034L24, mRNA sequence.
                                                                                                                                                                                                                   1274 tggttaacgacagagttgttccattgcacggttgtgctgttgacaagttgggta 1327
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/clone="2610034L24"
/clone_11b="Mus musculus C57BL/6J 10-day embryo"
                                                                                                                                                                                                                                                                          198 AAGATGACATGGCTTCGTTCTTTTGACTAAACTGCTTTGTTAAGTTGGCTA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Unpublished (1999)
Contact: Chie Owa
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oy Db

2.9%; Score 41.2; DB 25; 52.3%; Pred. No. 0.32; tive 0; Mismatches 83;

Query Match Best Local Similarity 52.3% \*\*\*rhes 91; Conservative

0; Gaps

83; Indels

Length 278;

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|        | Description            | AX021809 COM | AF205325 Sin+hot: | A19452 phytash ofN | 113430 COMMON 22 | 133881 60000000 10 | 216414 A nigon phy | MOVESO ASSOCIATION | A19451 phytase gen |
|--------|------------------------|--------------|-------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|
|        | ID                     | <br>AX021809 | AF295325          | A19452             | 113430           | 133881             | ANPHYAG            | ASNPHYTASE         | A19451             |
|        | ore Match Length DB II | <br>1426 9   | 1350 56           | 1404 9             | 1404 10          | 1404 10            | 2000 13            | 2665 13            | 6 9529             |
| Query  | Match Le               | <br>6.96     | 56.9              | 45.2               | 45.2             | 45.2               | 44.9               | 44.9               | 44.9               |
|        | Score                  | <br>1360.8   | 798.8             | 635                | 635              | 635                | 631 4              | 631                | 631                |
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| Il3429 Sequence 31 | $\sim$ | Sednenc  | AR051916 Sequence | AR053934 Sequence | L02421 Aspergillus |       |     | n   | AX000634 Sequence | U59804 Aspergillus | AX000630 Sequence | U59803 Emericella | A46793 Sequence 11 | AX000632 Sequence | U59802 Talaromyces | AX000636 Sequence | U60412 Aspergillus | A46783 Sequence 1 | 35    | Н   | m     | 2        |          | ທ     |          | AX085208 Sequence | A46785 Sequence 3 | U59806 Myceliophth | AX085210 Sequence | AJ299239 Magnaport | U19789 Saccharomyc | X01079 Yeast gene | AX072908 Sequence | Z35962 S.cerevisia | X01080 Yeast genes | 993 S.cere |  |
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## ALIGNMENTS

| 07-SEP-2000   |   |   |   |                         |
|---|---|---|---|-------------------------|
| AX021809 1426 bp DNA PAT Sequence 3 from Patent EP0897985, AX021809 GT.10045052 | synthetic construct. synthetic construct. synthetic desirect. | 1 (bases 1 to 1426)<br>Lehmann, M.<br>Consensus phytases<br>Patent: EP 0897985-A 3 24-FEB-1999;<br>HOFFMANN LA ROCHE (CH) | Location/Qualifiers 11426 /organism="synthetic construct" /db_xref="taxon:32630" /note="consensus sequence" | 338 a 311 c 308 g 469 t |
| RESULT 1 AX021809 LOCUS AX DEFINITION SO ACCESSION AX                           | S   | REFERENCE 1 AUTHORS L TITLE C JOURNAL P   | FEATURES<br>Source  | BASE COUNT<br>ORIGIN    |

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Query Match 96.9%; Score 1360.8; DB 9; Length 1426; Best Local Similarity 98.1%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 27; Indels 0; Gaps
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/ LTAIS LALLONG THE ALLONG SECTIVE SETS HIWGQYAPFFSLANESV ISPEVPAGCRVTFAQVLSRHGARY PPDSKGKKYSALIEELOONATTFPDGKYAFLKTYN ISPEVPAGCRVTFAQVLSRHGARY PPDSKGKKYSALIEELOONATTFPDGKYAFLKTYN STAGADDLTPFFESDELNNSGIKKFIEGFO STKLKDPPRAQPGOSSPKIDVY ISEASSINTULDGYCTVFFEDSELADTVBANFTAFFV PSIRQRENENDLSGYTLTDTFWTYLLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYD YLOSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPYHDDTSSHITLDSSPATFPLN STLYADFSHDMGIISILFALGLYNGTKPLSTTVENITQTDGFSSAWTVPFASRLYVE MMQCQABQEPLVRYLVNDRYVPLGREVDALGRETRDSFYRGLSTRYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy of Agricultural Sciences, Guangzhou, Guangdong 510640, China
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in Pichia pastoris"
1141 tigiciaciacticigitigaatotatigaagaaacigacggitactcigctictiggact 1200
                       1321 ttgggtagatgtaagagagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1380
                                                                                                                                                                                   1272 TIGGTIAGAGITITGGTIAACGACAGAGTIGTICCALIGCACGGTIGTGCTGTIGACAAG 1331
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                                                                                                                                                  ttggttagagttttggttaacgacagagttgttccattgcacggttgtgctgttgacaag
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Synthetic sequence of phytase gene for expression in Pichia
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                                                                 195 agacgttccagacgactgtagagttactttcgttcaagttttgtctagacacggtgctag 254
                                                                                                                              141 TGAGGTGCCAGCCGGATGTAGAGTCACTTTCGCTCAGGTCCTTTCCAGACATGGAGCTAG 200
                                                                                                                                                                                 201 ATATCCAACCGACTCCAAGGGTAAGAAATACTCCGCTCTTATTGAGGAGATCCAGCAGAA 260
                                                                                                                                                                                                              egetactgettteaagggtaagtacgetttettgaagaettacaactacaetttgggtge 374
                                                                                                                                                                                                                            375 tgacgaettgaetecatteggtgaaaaecaaatggttaaetetggtattaagttetaeag 434
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                        21 TAGAAATCAATCCTCTTGTGATACTGTCGATCAGGTTATCAATGTTTCTCCGAGACTTC 80
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332;

Pred. No. 4.4e-206; 0; Mismatches 332;

56.9%; 75.0%;

Matches 998; Conservative

Best Local Similarity

Query Match

Score 798.8; DB 56; Length 1350;

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SGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSSNNTLDPFFING
EDSELADTVEANFTATFVPGTRQRLENDLSGVTLTDVFEYTZLANDMCSFDTISTSTVDT
KLSPFCDLFTHIDEMINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHD
DTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTYSNTTQT
DGSSAWHYLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTYSNITQT
DGSSAWHYLDSSPATFPLNSTLYVEMMQCQAEQEPLVRVLNDFRVLYVENIGCPVDALGRCTRDSFV
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SHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEI
QQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRS
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                                                                                           1221 GGTTAATGATAGATGTTGTCCCACTGCATGTTGTCCTGTTGATGCTTTGGGTAGATGTAC 1280
1155 tgttgaatetattgaagaaactgaeggttaetetgettettggaetgtteeattegetge 1214
                                                                      1215 tagagettacgitgaaatgatgeaatgicaagetgaaaaggaaeceattggitagagitit 1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           artificial sequence.

1 (bases 1 to 1404)
van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A., Veenstra,A.E., Luiten,R.G.M. and Selten,G.C.M.
Cloning and expression of microbial phytase
patent: EP 0420358-A 41 03-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Local Similarity 65.8%; Pred. No. 1.3e-161;
Les 923; Conservative 0; Mismatches 480:
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/db_xref="taxon:32630"
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/protein_id="CAA01464.1"
/db_xref="GI:583196"
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121 ttoccagaaatttotcacttgtggggtacctactctccatacttctctttggcagacgaa 180
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|  | 201 gttccattcgctgctagagcttacgttgaaatgatgcaagctgaaaggaacca 126, [111   1   1   1   1   1   1   1   1 | 113430 | Ouery Match Best Local Similarity 65.8%; Score 635; DB 10; Length 1404;  Bast Local Similarity 65.8%; Pred. No. 1.3e-161;  I appgrograticy of the control of |

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961 aacgaattgattgctagattgactcactctccagttcaagaccacactctactaaccac 1020
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421 ATCAAGTTCTACCAGCGGTACGAATCGCTCACAAGGAACATCGTTCCATTCATCCGATCC 480
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PAT

Sequence 19 from patent US 5593963. I33881

I33881.1 GI:1824672

1404 bp

I33881

RESULT 133881

DEFINITION ACCESSION VERSION

| KEYWORDS                         |  |  |
|----------------------------------|--|--|
| ORGANISM<br>REFERENCE<br>AUTHORS | <pre>Unknown. Unclassified.</pre>  |  |
|                                  | and Verwoe<br>Expression<br>Patent: US   |  |
| source<br>BASE COUNT<br>ORIGIN   | ce 1. 1404<br>/organism="unknown"<br>T 293 a 436 c 344 g 331 t   |  |
| Query Ma<br>Best Loc<br>Matches  | / Match<br>Local Similarity 65.8%; Pred. No. 1.3e-161;<br>hes 923; Conservative 0; Mismatches 480; Indels 0; Gaps 0; |  |
| Qy 1<br>Db 1                     | atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60  |  |
| Qy 61<br>Db 61                   | gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt 120<br>   |  |
| Oy 121<br>Db 121                 | ttcccagaaatttctcacttgtgggtacctactctccatacttctttggcagacgaa 180<br>  |  |
| Qy 181<br>Db 181                 | tctgctatttctccagacgttccagacgactgtagagttactttcgttcaagttttgtct 240<br>   |  |
| Qy 241<br>Db 241                 | agacacggtgctagatacccaacttcttctgcgtctaaggcttactctgctttgattga  |  |
| Qy 301<br>Db 301                 | gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360<br>   |  |
| Oy 361<br>Db 361                 | tacactttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggt 420<br>   |  |
| Qy 421<br>Db 421                 |  |  |
| Oy 481                           |  |  |
| Qy 541<br>Db 541                 |  |  |
| Qy 601<br>Db 601                 | ccagaaggatccggttacaacaacactttggaccacggtacttgtactgctttcgaagac 660   |  |
| Qy 661<br>Db 661                 | 1 tctgaattaggtgacgacgttgaacttcactgctttgttcgctccagctattaga 720<br>  |  |
| Oy 721                           |  |  |
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eukaryota; Fungi; Ascomycota; Aspergillus.

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

I (bases 1 to 2000)

van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J., Suykerbuyk, M.E.G., Luiten, R.G.M., Van Paridon, P.A., Selten, G.C.M., Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.

Cloning, molecular characterization and overexpression of the phytase gene (phyA) of Aspergillus niger

Gene (1992) In press

2 (bases 1 to 2000)

van Hartingsveldt, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical
Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                1261 ttggttagagttttggttaacgacagagttgttccattgcacggttgtgctgttgacaag 1320
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                                                                                                                                                                                                                                                                                                                          06-0CT-1992:
                                                                                                                                                      961 aacgaattgattgetagattgactcactctccagttcaagaccacacttctactaaccac 1020
                                                                                                                                                                    841 ttctgtgctttgttcactcacgacgaatggatccaatacgactacttgcaaagcttgggt 900
                                                         PLN
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/strain="Van Tieghem strain"
/db_xref="taxon:5061"
131. .134
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A.niger phyA gene.
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SOURCE
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SGSSRVIASGKKFIEGEQSTELKDERAQPGGSSPKIDVVIEBASSSNNTLDPGTCTVF
EDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTIGTSTVDF
KLSPFCDLFFTHDEMINYDYLQSLKKYYGHGAGNPLGPTGYGYGYANELIARLTHSPVHD
DTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLNGTKFPSTTTPSPVHD
DGFSSAMTVPPRASRTVEMMQCQAEQEPLVRVLVNDFVGLYGYGYANELGERTTYVENITOT
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QONATTFDGKYAFLKTYNYSLGADDLTPFGEGELVNSGIKFYORYESLTRNIVPFIRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 cgiggiaattotcactctigigacacigitgacggiggitaccaaigittcccagaaatt 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 glcgtgctactgtccattgccaccttgttcggttccacatccggtaccgccttgggtcct 72
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                                                                                                                                                     gene"
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                                                                                                                                         /function="primary transcript of phyA
join(210. .253,356. .365)
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                                                                                                                                                                                                                                                   /protein_id="CAA78904.1"
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/codon -
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                                                   166. .1871
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166. .1871
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 166. .253
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1732. .1760
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356. 1878
/number=2
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Best Local Similarity 65.9%
Matches 916; Conservative
                                                                                     prim_transcript
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                                                                                                                                                           sig_peptide
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984 GATACCGICGAAGCCAATTICACCGCCACGITICGTCCCTCCATICGTCAACGICIGGAG 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 agagttattgettetgetgaaaagtteattgaaggtteeaatetgetaagttggetgae 552
                                                                                                                                          613 ggttacaacaacactttggaccacggtacttgtactgctttcgaagactctgaattaggt 672
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                                           673 gacgacgttgaagctaacttcactgctttgttcgctccagctattagagctagattggaa 732
                                                                                                                                                                                                                                                        733 gctgacttgccaggtgttactttgactgacgaagacgttgtttacttgatggacatgtgt 792
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                                                                                                                                                          924 TCATCCAACAACACTCTCGAACCTGGAACTGTCTTCGAAGAACAGCGAATTGGCC 983
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                                                                                  553 ccaggttctcaaccacaccaagcttctccagttattaacgtgatcattccagaaggatcc
                                                                                                                                                                                                                                                                                                                                                                       853 ttcactcacgacgaatggatccaatacgactacttgcaaagcttgggtaagtactacggt
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ASNPHYTASE 2665 bp DNA PLN 27-APR-1993 Aspergillus niger myo-inistol hexaphosphate phosphohydrolyase gene,

complete cds. M94550

ASNPHYTASE LOCUS DEFINITION

RESULT

ACCESSION

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. 1 (bases 1 to 2665)
Mullaney, E.J., Gibson, D.M and Ullah, A.H.
Positive identication of a lambda gtil clone containing a region of fungal phytase gene by immunoprobe and sequence verification Appl. Microbiol. Biotechnol. 35, 611-614 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MGYSAVLLPLYLLSGVTSGLAVPASRNGSSCDTVDGGYQCFSET
SHIMGOYAPPFSLANBSVISPEVPAGCRVTFRQVLSHGARYPDDSKGKKYSALIEEI
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SGSSRVTASGKKFIEGEQSTKIKDPRAQPGGSSPKIDVVISEASSSNNTLDFGTCTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDSELADTVEANFTATEVPSTRQRLENDLSGYTLTDFEYTYLADMCSFDTISTSTVDT
KLSPFCDLFTHDEMINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHD
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DGFSSAMTVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGCPVDALGRCTRDSFV
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/product="myo-inosito1 hexaphosphate phosphohydrolyase"
808 c 574 g 650 t
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M94550.1 GI:166520
myo-inositol hexaphosphate phosphohydrolyase; phytase.
Aspergillus niger (library: EMBL 3; NRRL 3135) DNA.
Aspergillus niger
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/db_xref="taxon:5061"
/tissue_lib="EMBL 3; NRRL 3135"
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/db_xref="GI:166521"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="phytase gene"
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                                                            1157 GCAGATGACCTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTAC 1216
                                                                                                            1217 CAGCGGTACGAATCGCTCACAAGGAACATCGTTCCATTCATCCGATCCTCTGGCTCCAGC 1276
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BDSELADVEANFTATFVPSIRQRLENDLSGYTLTDTFGYTXLMDMCSFDTISTSTVDT
KLSPFCDLFTHDEWINYDYLOSIKKYTYGHGAGNPLTDTFGYTXLMDMCSFDTISTSVDT
DTSSNHTLDSSSPATFLYADFSHDNGIISILERALGIYNGTRELSTTYVBNITQT
DGFSSAWIVPFASRLLYVEMMQCQAEQEPLVRYLVNDRYVPLHGCPVDALGRCTRDSFV
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SHIMGOYAPPFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEI
QQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRXESLTRNIYPFIRS
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                                                                                                                                                                      artificial sequence.

1 (bases 1 to 6756)

2 And Gorcom, R.F.M., van Hartingsveldt, W., van Paridon, P.A., Veenstra, A.B., Luiten, R.G.M. and Selten, G.C.M.

Cloning and expression of microbial phytase.

Patent: EP 0420338-A 40 03-APR-1991;
                                                                 PAF 2-6, pAF 2-7.
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/db_xref="taxon:32630"
join(210. .254,357. .1715)
/gene="phytase gene"
join(210. .254,357. .1715)
/gene="phytase gene"
join(210. .254,357. .1712)
/gene="phytase gene"
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phytase gene locus of plasmids pAF 2-3,
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/gene="phytase gene"
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/gene="phytase gene"
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Van Gorcom, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A., Venstra, A.E., Luitten, R.G.M. and Selten, G.C.M.
Cloning and expression of phytase from aspergillus patent: US 5436156-A 31 25-JUL-1995;
1584 TIGGITAATGATCGCGITGTCCCGCTGCATGGGTGTCCGGTTGATGCTTTGGGGAGATGT
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Pred. No. 1.8e-160;
0; Mismatches 475; Indels
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                                                                                                                                                              Sequence 31 from patent US 5436156.
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                   613 ggttacaacaacactttggaccacggtactgtactgcttcgaagactctgaattaggt 672
553 ccaggttctcaaccacaaccaagcttctccagttattaacgtgatcattccagaaggatcc 612
                                                                                                                                                                                                                                                                                                                                                                                                       853 ttcactcacgacgaatggatccaatacgactacttgcaaagcttgggtaagtactacggt
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Aspergillus niger Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

Aspergillus niger myo-inositol hexaphosphate phosphohydrolyase

DNA

1528 bp

AF218813

precursor, gene, complete cds.

AF218813.1 GI:6694940

AF218813

Aspergillus niger.

16-JAN-2000

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SGSSRVIASGKKFIEGFOSTKIKDPRAQPGGSSPKIDVVISEASSSNNTLDBGTCTUP
BDSELADAVEANETATEVPTIRQRLENDLSCVSLTOTEVTXLMDMGSFDTISTSTVDT
KLSPECDLFFIEDEMINNDTACSLKKYTYGHGAGONGFORDLARLHSBYHD
DTSSNHTLDSNNSATELYADFSHIDNGTISILFALGLYNGTKFLSTTVQNITQT
DGFSSAWIVPFASRLYVEMMQCQAEQEPLARVLAVLNUNVVPLHGCPVDALGRCTRDSFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traislation="MGVSAVLLPLYLLSGVTSGLAVPASRNGSTCDTVDGGYQCFSET
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QQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 TCGAGAAATCCATTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACT 247
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                Hongning, W., Ol.W. and Jing, X. PCR, cloning and characterization of the phytase (phyA) gene
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                                                                                                                                                Submitted (24-DEC-1999) Aniaml Sci. & Tech. College, Sichuan Agricltural University, Ya'an City, Sichuan Province 625014,
                                                                                                                                                                                                                                                                                                                                                                                                                    /function="catalyzes the hydrolysis of phytic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.8%; Score 629.4; DB 13; Length 1528; 65.8%; Pred. No. 4.5e-160; tive 0; Mismatches 476; Indels 0;
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/EC_number="3.1.3.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF25481.1"
/db_xref="G1:6694941"
                                                        Aspergillus niger (China Strain)
                                                                                                                                                                                                                                                               /db_xref="taxon:5061"
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Hongning, W., Qi, W. and Jing, X.
Direct Submission
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                                                                                                                                                                                                                                                                                   /country="China"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="phytase"
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Patent: US 5780292-A 7 14-JUL-1998;
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nilarity 65.8%; Pred. No. 4.6e-160;
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Nevalainen, H.K.M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K., Torkkeli, T.K., Cantrell, M., Piddington, C.S., Rambosek, J.A., Turunen, M.K., Fagerstrom, R.B. and Houston, C.S.
Nucleic acid molecules encoding phytase and pH2.5 acid phosphatase patent: US 5830733-A 7 03-NOV-1998;
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Nevalainen, H.K.M., Paloheimo, M.T., Fagerstrom, R.B.,
Mettinen-Oinonen, A.S.K., Turunen, M.K., Rambosek, J.A.,
Piddington, C.S., Houston, C.S. and Cantrell, M.A.
Recombinant cells that express phytate degrading enzymes in desired
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65.8%; Pred. No. 4.6e-160;
tive 0; Mismatches 476;
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1. .2379
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1674 ACCGIGGAGAATAICACCCAGACAGAIGGGIICICGICIGGCIIGGACGGIICCGIIIIGCI 1733
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              433 agaagatacaaggetttggetagaaagattgttecatteattagagettetggttetgae 492
313 aacgctactgcfttcaagggtaagtacgctttcttgaagacttacaactacactttgggt
                                                                      373 gctgacgacttgactccattcggtgaaaaccaaatggttaactctggtattaagttctac
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SHLMGOYAPPFELANEGAISPUVPAGCRYTFRQVLSRHGARYPTESKGKKYSÅLIBEI
QONVTTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRS
SCSSRYIASGEKFIEGFOSTKIKDPRAAPQGSSPKIDVVISASSSSNWTLDPGTTVY
ENDSELATVEANRTAFFAPSIRQRLENDLSGYTLTDTEVTYLMDMCSFDTISTSTVDT
KLSPFCDLFTHDEWIHTYDYLOSLKKYYGHGAGNPLGPTQGVGVYANELIARLYHSPVHD
DYSSNHTLDSNPATFPLNSTLYVBKAGNPLGPTQGVGVYANELIARLYHSPVHD
DGFSSAWTVPFASRLYVENMQCQAEQEPLVRVLVNDRKVVPLHGCPIDALGRCTRDSFV
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/function="conversion of phytate to inositol and inorganic
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/db_xref="G1:166519"
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                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                        piddington, C.S., Houston, C.S., Paloheimo, M., Cantrell, M., Miettinen-Oinonen, A., Nevolainen, H. and Rambosek, J. The Cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carter, J.R., Franden, M.A., Aebersold, R.H. and McHenry, C.S. Molecular cloning, sequencing and overexpression of the gene encoding the psi subunit of E. coli DNA polymerase III holoenzyme Unpublished (1992)
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                                                                                                                                                                                                                                                          Aspergillus niger (strain ALK0243, sub_species awamori) DNA.
                                                                                                                                                   Aspergillus niger var awamori phytase gene, complete cds.
L02421
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/db_xref="taxon:5061"
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join(420. .463,566. .1925)
/EC_number="3.1.3.8"
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94040796
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/citation=[2]
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133 totcaettgtggggtacctactccatacttctctttggcagacgaatctgctatttct 192
           193 ccagacgttccagacgactgtagagttactttcgttcaagttttgtctagacacggtgct 252
                                                            1134 TCATCCAACAACACTCTCGACCCAGGCACCTGCACTGTCTTTGAAGACAGCGAATTGGCC 1193
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                                                                                                                                                313 aacgctactgctttcaagggtaagtacgctttcttgaagacttacaactacactttgggt 372
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Submitted (21-378-1999) to the DDBJ/EMBL/GenBank databases. Tadashi Nagashima. Shin Nihon Chemical Co.,Ltd, Research and Development Div., Showa-cho 19-10, Anjo, Aichi 446-0063, Japan (E-mail:laagashma@dl.dion.ne.jp, Tel:81-566-76-5171(ex.264), Fax:81-566-75-0010)
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 1515)
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Aspergillus niger gene for phytase, complete cds.
AB022700
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Direct Submission
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/strain="SK-57"
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| ctactete 137<br>         <br>ATACGCGC 268   | tgtagag 21<br>  <br>  <br>NTGCCATG 32          | cgcgtcta 277<br>   | gggtaagt 337<br>        <br>GGGGAAAT 448                     | attcggtg 397<br>       <br>CTTCGGAG 508                                  | jetagaa 45<br>       <br>                             | ctgaaaagt 517<br>        GCAATAAAT 628          | ccaagctt 577<br>        <br> CCAATCGT 688              | ggaccacg 637<br>                         | cttcactg 697<br>        <br>TTTCACCG 808                   | tactttga 757<br>        <br>GTCTCTCA 868             | tagaactt 817<br>   | ggatccaat 877<br>         <br>GGATCAACT 988                    | cattgggtc 937<br>         <br>  GCTCGGCC 1048 | tccagttc 997<br>        <br> GCCTGTCC 1108                          | cattgaacg 1057<br>           <br>  CCTCAACT 1168    | tcgctttgg 1117<br>         <br>  TGCTTTGG 1228            | aagaaactg 1177<br>        <br> CCAGACCG 1288              |
|---|--|--|--|--|---|---|--|--|--|--|--|--|---|---|---|---|---|
| acttgtggggtac<br>         <br>ATCTTTGGGGCCA | acgttco<br>                                    | tacccaacttcttctgcgtcta<br>                               | aacgctactgctttcaa<br>                 <br> aacgcgaCaaccTTCGA | tgggtgctgacgacttgactco<br>                     <br>TGGCGCGGATGATCTGACTCO | jatacaaggc<br>         <br>                           | ttattgettetg<br>        <br>grgArrgeererg       | ggttctcaaccacac<br>                                    | tacaacaacactti<br>                       | cgacgttgaagctaac;<br>               <br>  GACATCGAAGCCAT   | gacttgccaggtgt<br>                                   | cattcgacactgtcgct<br>  | cgttcactcacgacgaatg<br>  | ggtgctggtaacc<br>  .                          | tagattgactcactctc<br>                         <br> CGTCTCACCCACTCGC | actetaacceagetaettteceattgaae<br>                   | tgatatetattttet<br>                  <br> TCATCTCTATCCTCT | gtacaacggtaccaagccattgtctactactctgttgaatctattgaagaaac<br> |
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| 98 ctgttgacggt<br>       <br>09 CGGTCGATCAG | 58 catacttctct<br>                             | 18 ttactttcgtt<br>         <br>29 TCACTITCGCC            | 278 aggettaetet<br>         <br>389 AGAAATACTCC              | 38 acgetttettg<br>             <br>49 ATGCCTTCCTG                        | 98 aaaaccaaatgg<br>           0<br>09 AGCAGGAGCTGG    | 58 agattgttccat<br>          <br>69 ACATTGTCCCG | 518 tcattgaagg1<br>           629 TCATCGAGGG           | 578 ctccagttattaa<br>                    | 638 gtacttgtac<br>          <br>749 GCACCTGCAC             | 698 ctttgttcgctcc<br>           <br>809 ccAcGTTCGTCC | 758 ctgacgaaga<br>         <br>869 CGGACACAGA                  | 818 ctgacgctactgaatt<br>                  929 CCGTCGACACCAAGCT | 878 acgactactt<br>                            | 938 cágctcaagg<br>  1      <br>049 CGACCCAGGG                       | 998 aagaccacac<br>         1<br>109 ACGATGACAC      | 1058 ctactttgtacg<br>             <br>1169 ccacrcrcrar    | 1118 gtttgtacaa<br>         <br>1229 GTCTGTACAA           |

QY

Dp

da Qy

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Db

 Db Qy

QQ

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Qγ

QY DP DD QY DD OA

Search completed: October 26, 2001, 17:47:03 Job time: 8779 sec

John John

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

October 26, 2001, 17:50:17 ; Search time 210.38 Seconds (without alignments) 4190.388 Million cell updates/sec Run on:

US-09-488-265-28

Title: Perfect score:

1 atgggcgtgttcgtcgtgct......gggctgaatgtttcgcttaa 1404 Sequence:

Scoring table:

IDENTITY\_NUC Gapor 10.0 Gapor 1.0

730101 seqs, 313950809 residues Searched:

1460202 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description              | Consensus phytase Consensus phytase DNA encoding a mut Consensus phytase Consensus phytase Ascomycete consens Fungal phytase gen Consensus phytase DNA encoding phyta Consensus phytase Consensus phytase Consensus phytase |
|--------------------------|---|
| ID                       | AAZ31520<br>AAA73233<br>AAZ59715<br>AAA73291<br>AAA73290<br>AAZ37423<br>AAX23022<br>AAAZ3022<br>AAA73231<br>AAZ59637<br>AAZ59637  |
|                          | 20<br>20<br>20<br>20<br>20<br>20<br>21  |
| Ouery<br>Match Length DB | 1404<br>1404<br>1404<br>1404<br>1404<br>1426<br>1426<br>1426<br>1404  |
| Query                    | 100.0<br>100.0<br>98.9<br>98.6<br>96.9<br>96.9<br>96.9<br>96.9<br>94.5  |
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| 1404<br>1404<br>1426<br>1426<br>1426<br>1426<br>1404<br>1404<br>1404<br>1404<br>1404<br>1404<br>11404<br>11515<br>11511  | 1931<br>1931<br>1912<br>1845<br>1845<br>1567<br>2327<br>2327<br>1922<br>11664<br>1584           |
| 4446600000000044444446611  | 44<br>11.0<br>20.0<br>20.0<br>20.0<br>44.0<br>60.0<br>60.0<br>60.0<br>60.0<br>60.0<br>60.0<br>6 |
| 1327.2<br>1324<br>1326.8<br>1317.6<br>1292<br>1292<br>1292<br>1292<br>635<br>631.8<br>635<br>631.8<br>631.8<br>639.4<br>629.4<br>629.4<br>629.4<br>629.4<br>629.4<br>629.4<br>629.4  | 78.<br>78.<br>59.<br>39.<br>39.<br>50.  |
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## ALIGNMENTS

AAZ31520 standard; DNA; 1404 BP. 06-JAN-2000 (first entry) AAZ31520; AAZ31520 RESULT

Consensus phytase-1-thermo(8)-Q50T-K91A coding sequence.

Phytase; animal feed preparation; thermostable phytase; transgenic plant; consensus sequence; ds.

Synthetic.

98DK-0000407. 98DK-0000806. 98DK-0001176. 99WO-DK00154 99DK-0000091 (NOVO ) NOVO-NORDISK AS 19-JUN-1998; 18-SEP-1998; 22-JAN-1999; 22-JAN-1999; W09948380-A 22-MAR-1999; 23-MAR-1998; 30-SEP-1999 

Petersen S;

WPI; 1999-591030/50. P-PSDB; AAY43169

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                                                                    The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal phytase-expressing transgenic plants. These plants provide a feed phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed additive (phytase) simultaneously.
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                                                       This sequence encodes the consensus phytase-1-thermo(8)-Q50T-K91A.
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Preparing animal feed using a thermostable phytase
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                               Example 3; Fig 9; 71pp; English.
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Best Local Similarity 100.
Matches 1404; Conservative
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99DK-0001340.
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(NOVO ) NOVO NORDISK AS

21-SEP-1999;

WPI; 2000-491161/43. Lehmann M;

Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -Claim 10; Fig 7a-c; 240pp; English. P-PSDB; AAB20526 

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods of an be used for producing phytases with improved properties e.g. temperature stability, plm stability, plm profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate. Trom corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it min lower inositol phosphates and/or inositol and inorganic phosphate. present sequence encodes a phytase sequence from the present invention.

Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

goottgggtcotcgtggtaattotcactcttgtgacactgttgacggtggttaccaatgt 120 300 300 360 tacactttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggt 420 361 tacaetttggggtgetgacgaettgaetceattcggtgaaaaccaaatggttaaetctggt 420 tctggttctgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct 540 aagttggctgacccaggttctcaaccacaccaagcttctccagttattaacgtgatcatt 600 1 algggegigitegiegigetactglecattgecacettgleeggtleeacateeggtaee 60 1 atgggggtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60 Gaps gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac DB 21; Length 1404; .; 0 Indels ; 0 Query Match
100.0%; Score 1404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1404; Conservative 0; Mismatches 181 181 241 301 361 421 421 481 481 541 δ qq g qq à δ ò g δŽ g Qγ g ò g ŏ g ò g

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Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; ds. DNA encoding a mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A. BP. AAZ59715 standard; DNA; 1404 19-APR-2000 (first entry) AAZ59715; RESULT AAZ59715 

Aspergillus terreus 9Al Aspergillus terreus cbs

terreus cbs16.46.

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translation, comparising phytase (myo-inosito) hexakisphosphate formulation, comparising phytase (myo-inosito) hexakisphosphate formulation, comparising phytase (myo-inosito) hexakisphosphate formulation for more stabilising agents including composition for indicate a first a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animals (e.g., pigs, poultry) and prosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional continue of plant material without the need for adding additional phosphate continued by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved and enzyme formulation of the invention has an improved and can withertand feed processing methods such as a microal a material and pelleting rithe present sequence represents DNA encoding a matent of phytase-1 consensus sequence, phytase-1-thermo[8]-0507-K91A, which has a temporal of phytase-1 thermolesius point 7 degrees Celsius higher than that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel stabilised dry or liquid enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New stabilized enzyme formulation, useful for feed compositions
                                                                                                                                                                                                                                                                           /product= "Phytase-1-thermo[8]-Q50T-K91A"
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Бц
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                            Talaromyces thermophilus ATCC20186 Mycellophthora thermophila.
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                                                  Aspergillus fumigatus ATCC32722.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC26906.
                 NRRL3135
                                 Aspergillus fumigatus ATCC13073
                                                                                                         Aspergillus fumigatus ATCC32239.
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Aspergillus niger var.
Aspergillus niger str.
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                                                                                                                                Emericella nidulans.
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Sequence 1404 BF; 329 A; 319 C; 304 G; 432 I; 0 Cinci,

Ouery Match

100.0%; Score 1404; DB 21; Length 1404;

Best Local Similarity 100.0%; Pred. No. 0; Assmatches 0; Indels 0; Gaps

Matches 1404; Conservative 0; Mismatches 0; Indels 0; Gaps

> oy Og

cacgacaacactatgatatctattttcttcgctttgggtttgtacaacggtaccaagcca 1140 1081 cacgacaacatatgatatctattttcttcgctttgggtttgtacaacggtaccaagcca 1140 1141 ttgtctactacttctgttgaatctattgaagaaactgacggttactctgcttcttggact 1200 aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020 aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgct 960 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgct 960 780 780 840 900 540 009 900 099 720 240 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 301 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 361 tacactttgggtgctgactacacttgactccattcggtgaaaaccaaatggttaactctggt 420 361 tacactttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggt 420 480 gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt 120 actitiggactetaacceagetactiteceatigaacgetactitgiacgetgaetieië atggacatgtgtccattcgacactgtcgctagaacttctgacgctactgaattgtctcca 481 totggttctgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct ccagaaggatccggttacaacaacactttggaccacggtacttgtactgctttcgaagac tctgaattaggtgacgacgttgaagctaacttcactgctttgttcgctccagctattaga atggacatgtgtccattcgacactgtcgctagaacttctgacgctactgaattgtctcca ttetgtgetttgtteacteacgaegaatggatecaatacgaetacttgeaaagettgggt tetggttetgacagagttattgettetgetgaaaagtteattgaaggttteeaatetget ccagaaggatccggttacaacaacactttggaccacggtacttgtactgctttcgaagac totgaattaggtgacgacgttgaagctaacttcactgctttgttcgctccagctattaga 61 gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt tteccagaaattteteaettgtggggtacetaetetecatacttetetttggeagaegaa tetgetatttetecagaegttecagaegaetgtagagttaetttegtteaagttttgtet 1081 1021 601 661 721 781 781 901 961 601 721 901 661 121 181 241 301 421 δŏ qq qq δ Вb οy g δy Op g δ g δ g δ QQ δy δ qq qq δy qq δy Dp δý qq δ g δy g δ ōλ q δ

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BP. AAA73291 standard; DNA; 1404

AAA73291;

05-DEC-2000 (first entry)

Consensus phytase 3 thermo 11 Q50T K91A polynucleotide SEQ ID NO:92.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds.

W0200043503-A1 27-JUL-2000 Synthetic 

2000WO-DK00025 21-JAN-2000;

99DK-0000092. 99DK-0001340. 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS.

Lehmann M;

WPI; 2000-491161/43: P-PSDB; AAB20532. Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds

Disclosure; Fig 23a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, substrate cleavage pattern, release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present

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61 gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt 120
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                                                              Pred. No. 0;
0; Mismatches 10; Indels
          Sequence 1404 BP; 328 A; 321 C; 303 G; 452 T; 0 other;
                                                    Score 1388;
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                                                                        Matches 1394; Conservative
                                                              Best Local Similarity
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Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
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Consensus phytase 3 thermo 11 Q50T polynucleotide SEQ ID NO:90.
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99.1%; Pred. No. 0;
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Ascomycete consensus phytase coding sequence.
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This sequence encodes the consensus Ascomycete phytase sequence.
The invention relates to variant phytase enzymes with specific amino acid substitutions for improved properties. The phytase variants can be used for liberating phosphorus from a phytase substrate. They can be used for reducing phytate levels in animal manure. They can be used in feed or food preparations. The phytase DNA can also be used to produce transgenic plants which can be used in feeds or foods. The phytase variants can also be used in soy processing and in the manufacture of inositol or stability, temperature stability, pH profile, temperature profile, specific activity (in particularly in relation to pH and temperature), substrate specificity, substrate cleavage pattern, substrate binding, con position specificity, the velocity and level of release of phosphate con manufacture and end level of
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                                           Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical; ds.
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This invention describes a novel process for the preparation of a consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inosttol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                             compositions. This sequence encodes the consensus phytase protein used in the method of the invention.
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/product= "phytase"
Location/Qualifiers
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inosition for phytate in animal manure, by converting it.
                                          Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt 120
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             Consensus phytase polynucleotide sequence SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;
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0; Mismatches
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Pred. No. 0;
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                                                                                                                tood; feed; phytate; manure; ds.
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98.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compound foods and feeds -
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                                                                                                                                                                          WOZU0043503-A1.
                                                                                                                                                                                                                                                                           22-JAN-1999;
                                                                                                                                                                                                                                                                                          21-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                         Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                             Synthetic
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                                     421 attaagttetacagaagatacaaggetttggetagaaagattgttecatteattagaget 480
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         792 atggacatgtgtccattcgaaactgttgctagaacttctgacgctactgaattgtctcca
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/*tag= b
/note= "Signal peptide from Aspergillus terreus cbs16.46"
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                                                                                                                                                                                                    Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
thermostable; animal feed; monogastric animal; phytate phosphorus;
phosphate availibility; consensus; phytase-1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Mature phytase-1"
                                                                                                                                                                             DNA encoding phytase-1, a consensus phytase
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/product= "Phytase-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Talaromyces thermophilus ATCC20186 Myceliophthora thermophila.
                                                                                                                                                                                                                                                                                                             Aspergillus niger str. NRRL3135.
Aspergillus fumigatus ATCC13073.
Aspergillus fumigatus ATCC3272.
Aspergillus fumigatus ATCC36128.
Aspergillus fumigatus ATCC26906.
Aspergillus fumigatus ATCC26906.
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                                                                                                                                                                                                                                                           Aspergillus terreus 9A1.
Aspergillus terreus cbs16.46.
Aspergillus niger var. awamori.
Aspergillus niger 7213.
                                                                                             AAZ59637 standard; DNA; 1426
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                                                                                    AAZ59637
                                                                    RESULT
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provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional control of plant material without the need for adding additional phosphate to the feed. The lovel of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of reduced by adding phytase liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved the invention has an improved and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents sequence represents a consensus sequence, designated phytase-1, which was derived from the mature additionally contains the Aspergillus terreus cbs116.46 signal peptide at 

Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;

ó ttcccagaaatttctcacttgtgggtacctactctccatacttctttggcagacgaa 180 tctgctatttctccagacgttccagacgactgtagagttactttcgttcaagttttgtct 240 300 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 tctggttctgacagagttattgcttctgctgaaaagttcattgaaggttccaatctgct 540 1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60 541 aagttggctgacccaggttçtcaaccacaccaagcttctccagttattaacgtgatcatt 600 0; Gaps ttoccagaaatttotcacttgtggggtcaatactctccatacttctctttggaagacgaa tctgctatttctccagacgttccagacgactgtagagttactttcgttcaagttttgtct 96.9%; Score 1360.8; DB 21; Length 1426; 27; Indels 0; Mismatches Pred. No. 0; 98.18; Conservative Similarity Best Local Simi Matches 1377; Query Match 372 61 121 132 181 192 241 312 361 301 552 601 612 481 199 672 q ŏ Db δ g g οğ δ g ò g δ qq δ g g qq ò δ ŏ q

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Phytase; animal feed preparation; thermostable phytase; transgenic plant; consensus sequence; ds.
                                                                                                                                                                                                          961 aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020
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                                      781 atggacatgtgtccattcgacactgtcgctagaacttctgacgctactgaattgtctcca
                                                     852 ttotgtgctttgttcactcacgacgaatggagacaatacgactacttgcaatctttgggt
                                                                                                                        901 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgct
 Consensus phytase-10-thermo(3)-Q50T-K91A coding seguence.
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98DK-0001176.
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18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                         ingredient and a feed additive (phytase) simultaneously.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;
                                                                                                                                                            Preparing animal feed using a thermostable phytase
                                                                                                                                                                                              Example 3; Fig 10; 71pp; English.
99DK-0000091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1356; Conservative
                                                    (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                WPI; 1999-591030/50.
                                                                                                                                 P-PSDB; AAY43170
     22-JAN-1999;
22-JAN-1999;
                                                                                    Petersen S;
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Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds. Consensus phytase 10 thermo 3 q50t, k91a polynucleotide SEQ ID NO:30. 05-DEC-2000 (first entry) 

Synthetic

BP.

AAA73234;

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21-JAN-2000; 2000WO-DK00025
                     99DK-0000092
                        99DK-0001340
                               (NOVO ) NOVO NORDISK AS
WO200043503-A1
                    22-JAN-1999;
                        21-SEP-1999;
       27-JUL-2000
                                      Lehmann M;
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WPI; 2000-491161/43. P-PSDB; AAB20527 Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -

Claim 10; Fig 8a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inosicol and inorganic phosphate.

Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;

ö goottggggtcotcgtggtaattotcactcttgtgacactgttgacggtggttaccaatgt 120 ttoccagaaatttotcacttgtggggtacctactotccatacttotctttggcagacgaa 180 240 240 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 tacactttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggt 420 9 0; Gaps 1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc tctgctatttctccagacgttccagacgactgtagagttactttcgttcaagttttgtct 94.5%; Score 1327.2; DB 21; Length 1404; 96.6%; Pred. No. 0; 48; Indels 0; Mismatches Matches 1356; Conservative Similarity Query Match Best Local ( 61 61 121 121 181 361 301 421 q ŏ δ qq QY g οy q δy g δ qq δ a

ВР

AAZ59716 standard; DNA; 1404

AAZ59716;

XXXXXX

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Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
                                        thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; ds.
              DNA encoding a mutant phytase-10, phytase-10-thermo[3]-250T-K91A.
                                                                                                                                                                                                                                                            /product= "Phytase-10-thermo[3-Q50T-K91A"
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                 Emericella nidulans.
Talaromyces thermophilus ATCC20186.
                                                                                   Aspergillus niger var. awamori. Aspergillus niger str. NRR13135. Aspergillus fumigatus ATCC13073. Aspergillus fumigatus ATCC32722. Aspergillus fumigatus ATCC59128. Aspergillus fumigatus ATCC5906. Aspergillus fumigatus ATCC
                                                                            Aspergillus terreus cbs16.46.
                                                                                                                                                                  Myceliophthora thermophila.
Paxillus involutus NN005693.
Paxillus involutus NN0343.
Agrocybe pediades NN09289.
                                                                                                                                                                                                                                                                                                                 99EP-0111949
                                                                                                                                                                                                Peniophora lycii NN006113.
Thermomyces lanuginosa.
Synthetic.
(first entry)
                                                                    Aspergillus terreus 9Al.
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                                                                                                                                                                                                                                                                                                                                                                                                             monogastric animals -
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                                                                                                                                                                                                                                                                                 EP969089-A1.
                                                                                                                                                                                                                                                                                                               23-JUN-1999;
19-APR-2000
                                                                                                                                                                                                                                                                                                 05-JAN-2000
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stabilized enzyme formulation, useful for feed compositions for Ξ., (HOFF ) HOFFMANN LA ROCHE & CO AG Example 5; Fig 19; 101pp; English Brugger R, Lehmann M, Wyss M; 98EP-0111960

The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including to phosphohydrolase) and one or more stabilising agents including to the phosphohydrolase) and one or more stabilising agents including to to 4000 ba, preferably loud to 3350 ba; the disodium salts of malonic, to 4000 ba, preferably loud to 3350 ba; the disodium salts of malonic, and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of physphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for additing additional phosphate consents adding phytase formulation of the invention has an improved the inorganic phosphate liberated from phytate phosphorus using the caryme. The phytase formulation of the invention has an improved and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents DNA encoding a mutant phytase-10 consensus sequence, phytase-10-thermo(3)-050T-K91A, which has

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a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAX69566). Its specific activity with phytate as a substrate is also strongly increased.
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                                                    Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;
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RESULT 13

AAA73293 standard; DNA; 1404 AAA73293

BP

AAA73293;

05-DEC-2000 (first entry)

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure, ds. Consensus phytase 10 thermo 5 Q50T K91A polynucleotide SEQ ID NO:96.

Synthetic.

WO200043503-A1

27-JUL-2000

22-JAN-1999;

21-JAN-2000; 2000WO-DK00025

99DK-0000092. 21-SEP-1999;

(NOVO ) NOVO NORDISK AS.

Cehmann M;

WPI; 2000-491161/43.

P-PSDB; AAB20534 

rel phytases with improved properties such as temperature stability, stability and substrate specificity, for use in pharmaceuticals and moound foods and feeds compound foods and feeds Novel

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                          The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
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Pred. No. 0;
 Disclosure; Fig 25a-c; 240pp; English.
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temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate specificity, substrate profile, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present
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                                                                                                                  Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
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0; Mismatches
                                                                                                                                                                                 Disclosure; Fig 24a-c; 240pp; English.
                                                                                                                                                   compound foods and feeds -
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Best Local Similarity
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Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                              Consensus phytase 10 polynucleotide sequence SEQ ID NO:25.
                       BP.
                 AAA73232 standard; DNA; 1426
                                                                                             (first entry)
                                                                                             05-DEC-2000
                                                       AAA73232;
AAA73232
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temperature stability, in pharmaceuticals and
                                                                                                                                                            such as for use
                                                                                                                                                          Novel phytases with improved properties PH stability and substrate specificity,
                                                                                                                                                                                          Claim 8; Fig 5a-c; 240pp; English.
ds.
food; feed; phytate; manure;
                                                                                     99DK-0001340.
                                                            21-JAN-2000; 2000WO-DK00025
                                                                             99DK-0000092
                                                                                                                                                                          compound foods and feeds -
                                                                                                    (NOVO ) NOVO NORDISK AS.
                                                                                                                                   WPI; 2000-491161/43.
                                                                                                                                           P-PSDB; AAB20524
                              WO200049509-A1
                                                                            22-JAN-1999;
                                                                                     21-SEP-1999;
                                              27-JUL-2000
                                                                                                                    Lehmann M;
               Synthetic
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods and be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate specificity, the profile, temperature profile, substrate binding, position specificity, the velocity and level of relasse of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds the feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present

Sequence 1426 BP; 340 A; 308 C; 310 G; 468 T; 0 other;

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61 gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt 120
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                                                                                             0; Gaps
                                                                           1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60
    DB 21; Length 1426;
                                        54; Indels
                                          0; Mismatches
  Score 1317.6;
Pred. No. 0;
  93.8%;
96.2%;
                                  Matches 1350; Conservative
                    Best Local Similarity
Query Match
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372 tacactttgggtgctgacgacttgactccattcggtgaacaacaaatggttaactctggt
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|         | Ltd.      |
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| GenCore | (c) 1993  |
|         | Copyright |

OM nucleic - nucleic search, using sw model

October 26, 2001, 15:19:58 ; Search time 87.5 Seconds (without alignments) 3037.632 Million cell updates/sec Run on:

US-09-488-265-28

Title: Perfect score:

l atgggcgtgttcgtcgtgct.......gggctgaatgtttcgcttaa 1404 Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

649198 Total number of hits satisfying chosen parameters:

324599 seqs, 94655562 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*
l: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
l: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
l: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
l: /cgn2\_6/ptodata/2/ina/RE\_COMB.seq:\*
l: /cgn2\_6/ptodata/2/ina/RE\_COMB.seq:\*
l: /cgn2\_6/ptodata/2/ina/RE\_COMB.seq:\*
l: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| ,                   | NOTI AT TORRA | Sequence 3, Appli | 33,          | 10               |                 | 7 6              | 2 5    | Sequence 31, Appl | , ,   | , ,              | -                | Segment 5 Appli | ` ~             | · .             | ì -             | · -             | - F              | Segience 23 Appli | 5 5  | 10   | 27,              | 000              | 177    | , ,   | 1 -        | 7 4           | Sequence 3, Appli | 'n           |  |
|---------------------|---------------|-------------------|--------------|------------------|-----------------|------------------|--------|-------------------|-------|------------------|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|------------------|-------------------|------|------|------------------|------------------|--------|-------|------------|---------------|-------------------|--------------|--|
| SOMMENTES           |               | 09-121-425-       | -08-151-574- | US-08-146-424-19 | US-08-693-709-1 | US-08-419-448-33 | 1-574- | -08-419-448-      | -724- | US-08-609-426A-7 | US-08-374-652C-1 | US-09-155-855-5 | US-09-155-855-4 | US-08-819-825-1 | US-09-163-642-1 | US-09-221-654-1 | US-08-989-358A-1 | 08-993-3          |      | ٠.,  | US-08-993-359-27 | US-08-993-359-29 | 2-463- | -574- | -08-419-44 | -08-498-263-5 | -08-977-06        | -09-014-583- |  |
| DB                  |               |                   |              |                  |                 |                  |        |                   |       |                  |                  |                 |                 |                 |                 |                 |                  |                   |      |      |                  |                  |        |       |            |               | 7                 |              |  |
| Length              | 100           | 14.20             | 1404         | 1404             | 1404            | 1404             | 6756   | 6756              | 2363  | 2363             | 2379             | 1515            | 1332            | 2200            | 2200            | 1320            | 1320             | 1593              | 1501 | 1522 | 1642             | 1536             | 7218   | 66    | 66         | 1631          | 1631              | 1631         |  |
| %<br>Query<br>Match | 0 90          |                   | ٠            |                  | 45.2            |                  | ٠      | •                 | 44.8  | •                | 44.8             | 43.6.           | 43.5            | 3               | 23.7            | 8.7             | 8.7              |                   | •    | •    | •                | •                |        |       |            |               | 3.0               |              |  |
| Score               | 1360 0        | 1200.0            | 030          | 635              | 632             | 635              | 631    | 631               | 629.4 | 629.4            | 629.4            | 612.4           | Ċ               | 333.2           | 333.2           | 122.8           | $^{\circ}$       | 122.8             | a    | 92.6 | œ                | m<br>m           |        | 45.2  |            | 42.4          | 42.4              | 42.4         |  |
| Result<br>No.       |               | ۱ (               | 7 (          | η.               | 4               | ഹ                | 9      | 7                 | Φ,    | 6                | 10               | 11              | 12              | 13              | 14              | 15              | 16               | 17                | 18   | 19   | 20               | 21               | 22     | 23    | 24         | 25            | 26                | 27           |  |

| Patent No. 5221624            | Segmence 3. Appli | , ,              | Segmence 11 Appl | Segmence 11. Appl | Sequence 75. April | ` .             | , ,              |                  | ,               | · -             | 10               | Sequence 2, Appli | ٠<br>-<br>-      | Sognordo 74 Appt  | Sequence /4, Appl | Seguence /4, Appl | : |
|-------------------------------|-------------------|------------------|------------------|-------------------|--------------------|-----------------|------------------|------------------|-----------------|-----------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|---|
|                               |                   |                  |                  |                   |                    |                 |                  |                  |                 |                 |                  |                   |                  |                   |                   |                   |   |
| 5221624-4<br>US-08-882-501-28 | US-08-261-110A-3  | US-08-261-110A-1 | US-08-151-574-11 | US-08-419-448-11  | US-08-235-836C-75  | US-08-747-788-1 | US-09-121-425-13 | US-09-121-425-14 | US-07-689-008-4 | US-07-689-008-1 | US-08-657-868B-2 | US-08-657-868B-1  | US-08-084-718-74 | 115-08-443-976-74 | US-08-443-977-74  | US-09-479-309-4   |   |
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| 1309                          | 1167              | 1404             | 99               | 99                | 2126               | 1193            | 32               | 32               | 2406            | 9540            | 1803             | 1829              | 412              | 412               | 412               | 720               |   |
| 2.4                           | 2.3               | 2.3              | 2.3              | 2.3               | 2.3                | 2.3             | 2.3              | 2.3              | 2.3             | 2.3             | 2.3              | 2.3               | 2.5              | 2.2               | 2.2               | 2.5               |   |
| 33.2<br>32.6                  | 32.6              | 32.6             | 32.4             | 32.4              | 32.4               | 32.2            | 32               | 32               | 31.8            | 31.8            | 31.6             | 31.6              | 31.2             | 31.2              | 31.2              | 31.2              |   |
| 28                            | 30                | 31               | 32               | 33                | 34                 | 32              | 36               | 37               | 38              | 39              | 40               | 41                | 42               | 43                | 44                | 45                |   |
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RESULT

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|-----------------|-------------------------------------|--------------------|----------------------|----------------------------|--|--|---|---------------------------------|--|---------------------------------|--------------------------|-----------------------------|-------------|--------------|-----------|-------------------------------|----------|--|--------------------|-----------------|
|                 | 25                                  |                    |                      |                            | vtases                                 | es 13239                                 | 9/121.425                                 |                                 | 97112688.3                                 |                                 |                          |                             |             |              |           |                               |          | of Artific   |                    |                 |
|                 | Sequence 3, Application US/09121425 |                    |                      | Martin                     | TITLE OF INVENTION: Consensus Phytases | FILE REFERENCE: consensus phytases 13239 | CURRENT APPLICATION NUMBER: US/09/121.425 | : 1998-07-23                    | EARLIER APPLICATION NUMBER: EPO 97112688.3 | : 1997-07-24                    | S: 20                    | Ver. 2.0                    |             |              |           | al Sequence                   | •        | Description  | sednence           |                 |
| -425-3          | e 3, Applicat                       | Patent No. 6153418 | GENERAL INFORMATION: | APPLICANT: Lehmann, Martin | OF INVENTION:                          | EFERENCE: con                            | T APPLICATION                             | CURRENT FILING DATE: 1998-07-23 | R APPLICATION                              | EARLIER FILING DATE: 1997-07-24 | NUMBER OF SEQ ID NOS: 20 | SOFTWARE: Patentin Ver. 2.0 | NO 3        | LENGTH: 1426 | DNA       | ORGANISM: Artificial Sequence | RE:      | INFORMATION:   | OTHER INFORMATION: | -425-3          |
| US-09-121-425-3 | Sednenc                             | Patent             | GENERAL              | APPLIC                     | TITLE                                  | FILE R                                   | CURREN                                    | CURREN                          | EARLIE                                     | EARLIE                          | NUMBER                   | SOFTWA                      | SEQ ID NO 3 | LENGT        | TYPE: DNA | ORGAN                         | FEATURE: | OTHER  | OTHER              | US-09-121-425-3 |
| _               | •                                   | •                  | •                    |                            |  |  | •   |                                 | ••   | ••                              |                          | •••                         | •••         | ••           | •-        | ••                            | ••       | ••   | ••                 | ⊃               |

ttcccagaaatttctcacttgtggggtacctactctccatacttctctttggcagacgaa 180 1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60 0; Gaps DB 3; Length 1426; 27; Indels Score 1360.8; Pred. No. 0; 0; Mismatches Ouery Match Best Local Similarity 98.1%; Matches 1377; Conservative 121 ŏ g ŏ g δy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.2%; Score 635; DB 1; Length 14 Best Local Similarity 65.8%; Pred. No. 5.8e-190; Matches 923; Conservative 0; Mismatches 480; Indels
                                                                                                                                                                                                          TITLE OF INVENTION: Cloning and Expression of Microbial TITLE OF INVENTION: Phytase NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NRRL 3135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24615-20026.00
                                                                                                                                                                                                                                                                                          : Morrison & Foerster
545 Middlefield Road, Suite 200
                                                                                          APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/151,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                Sequence 33, Application US/08151574 Patent No. 5436156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 24,959
REFERENCE/DOCKET NUMBER: 246
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA
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STRANDEDNESS: double
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                                                                            GENERAL INFORMATION:
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RESULT 2
US-08-151-574-33
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                   Sequence 19, Application US/08146424
Patent NO. 5583963
GENERAL INFORMATION:
APPLICANT: NEWPELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: BEN'JSM
APPLICANT: PEN'JSM
APPLICANT: PEN'JSM
APPLICANT: FEN'JSM
APPLICANT: FEN'JSM
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
NUMBER OF SEQUENCES: 31
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REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: 44615-20011.24
TELECOMMUNICATION INFORMATION:
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FILING DATE: 02-NOV-1993
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755 Page Mill Road
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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(415) 494-0792
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 923; Conservative
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STATE: California
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LOCATION:
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                                      gttccattcgctgctagagcttacgttgaaatgatgcaatgtcaagctgaaaaggaacca 1260
                                                                                                                                  1321 ttgggtagatgtaagagagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1380
                                                                                                                                                                                                               APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOEND, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
NUMBER OF SEQUENCES: 28
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FastSEQ for Windows Version 2.0
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07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VAN OOIJEN, ALBERT J.J. APPLICANT: RIETVELD, KRIJN
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOEKEMA, ANDREAS
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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FILING DATE: 07-AUG
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OTHER INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                 US-08-693-709-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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; NAME/KEY: Signal Sequence LOCATION: 1...72 ; OTHER INFORMATION: US-08-693-709-1

Gaps ; 0 45.2%; Score 635; DB 1; Length 1404; 65.8%; Pred. No. 5.8e-190; vative 0; Mismatches 480; Indels ( Matches 923; Conservative Query Match Best Local Similarity

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 $1 \ {\tt atgggcgtgttcgtcgttgctactgtccattgccaccttgttcggttccacatccggttacc} \ 60$ 1 AIGGCGICTCTGCTGTTCTACTTCCTTTGTATCTCCTGTTGGAGTCACCTCCGGACTG 60 q

61 gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt 120 Ω

61 GCAGTCCCCGCCTCGAGAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAATGC 120 ttcccagaaatttctcacttgtggggtacctactctccatacttctttggcagacgaa 180 121 q ŏ

181 tctgctatttctccagacgttccagacgactgtagagttactttcgttcaagttttgtct 240 Op ŏ g

181 regerearcrecereagerecegecegeargeagareacatricecreagerecrete 240 δy

gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 241 CGICATGGAGGGGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCATTGAG 300 301 g

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841 ttctgtgctttgttcactcacgacgaatggatccaatacgactacttgcaaagcttgggt 900 qq ò

901 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgct 960 901 δ

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Cloning and Expression of Microbial Phytase E: Morrison & Foerster 2000 Pennsylvania Ave. N.W., Suite 5500 APPLICANT: Robert F.M. Van Gorcom APPLICANT: Willem Van Hartingsveldt APPLICANT: Petrus A. Van Paridon APPLICANT: Annemarie E. Veenstra APPLICANT: Rudolf G.M. Luttin APPLICANT: Gerardus Sellen TITLE OF INVENTION: Cloning and Expres Sequence 33, Application US/08419448 Patent No. 5863533 CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy NUMBER OF SEQUENCES: STREET: 2000 Peni CITY: Washington GENERAL INFORMATION: 20006-1888 ADDRESSEE: COMPUTER: US-08-419-448-33 COUNTRY: STATE:

PatentIn Release #1.0, Version #1.25 PC-DOS/MS-DOS 3: Floppy disk IBM PC compatible CURRENT APPLICATION DATA:
APPLICATION NUMBER: US, OPERATING SYSTEM: SOFTWARE: SOFTWARE:

REFERENCE/DOCKET NUMBER: 24615-20026.10 UMBER: US/08/419,448 10-APR-1995 ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959 CLASSIFICATION: FILING DATE:

TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500 INFORMATION FOR SEQ ID NO: 33; SEQUENCE CHARACTERISTICS: ø

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65.8%; Pred. No. 5.8e-190;
tive 0; Mismatches 480; Indels
                                                                                          : Aspergillus ficuum (Aspergillus niger)
NRRL 3135
                                                    CDNA to mRNA
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                     Conservative
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                                                     MOLECULE TYPE:
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US-08-419-448-33
                                                                                ANTI-SENSE:
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APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Baridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Carardus Selten
ITTLE OF INVENTION: Cloning and Expression of Microbial
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STREET: 545 Middlefield Road, Suite 200
CITY: Menlo_Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
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Best Local Similarity 65.9%; Pred. No. 2.5e-188;
Matches 916; Conservative 0; Mismatches 475; Indels
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                                                                                                                                                                                                                                                                                                                      ORGANISM: Asperqillus ficuum (Aspergillus niger)
STRAIN: NRRL 3135
                                                  NAME: MUZASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEHONE: 415-37-7250
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
LOCATION: 381..1712
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="inositol phc
OTHER INFORMATION: phosphatase"
OTHER INFORMATION: /product="phytase"
OTHER INFORMATION: /evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: join(210..253, 356..1715)
OTHER INFORMATION: /codon_start= 210
OTHER INFORMATION: /product= "Phytase"
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: lambda Ar
CLONE: pAF2-3, pAF2-6, pAF2-7
                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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LOCATION:
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1164 TTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCTTGAAAAAGTATTACGGC 1223
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                       313 aacgctactgctttcaagggtaagtacgctttcttgaagacttacaactacactttgggt 372
                                                                       373 gotgacgacttgactccattcggtgaaaaccaaatggttaactctggtattaagttctac 432
                                                                                      433 agaagatacaaggetttggetagaaagattgtteeatteattagagettetggttetgae 492
                                                                                                                                                                                                                         aacccagctactttcccattgaacgctactttgtacgctgacttctctcacgacaacat 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 CGGTATCCGACCGACTCCAAGGGCAAGAATACTCCGCTCTCATTGAGGAGATCCAGCAG 623
                                                                                                                                        804 CGCGTCATCGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCACCACGAGGAT 863
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                                       793 ccattcgacactgtcgctagaacttctgacgctactgaattgtctccattctgtgctttg
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APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OKGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NRL 3135
                                                                                                                                                                                                                                                                                                                                                                                                        2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
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FR: 24615-20026.10
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OTHER INFORMATION: /codon_start= 210
OTHER INFORMATION: /product= "Phytase"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/419,448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            Sequence 31, Application US/08419448
Patent No. 5863533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: pAF2-3, pAF2-6, pAF2-7
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CLONING
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08 FILING DATE: 10-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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254..355
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                                      1704 TGTTTTGCTTA 1714
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20006-1888
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LOCATION:
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                                                                                                              US-08-419-448-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                            Length 6756;
                                                                                                                                                                              44.9%; Score 631; DB 2; Length 67 65.9%; Pred. No. 2.5e-188; ive 0; Mismatches 475; Indels
                                                                              /function= "inositol phosphate
phosphatase"
                                                                                                            /product= "Phytase"
/evidence= EXPERIMENTAL
                                                                      experimental
sig_peptide
210..380
                                                                                                                                                                                 Query Match 44.9
Best Local Similarity 65.9
Matches 916; Conservative
                                                               IDENTIFICATION METHOD:
                                         mat_peptide 381..1712
                                                                                                            ) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-419-448-31
                                                                                  OTHER INFORMATION: OTHER INFORMATION:
               LOCATION:
  NAME/KEY:
                                           NAME/KEY:
                                                      LOCATION:
                              FEATURE:
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                                                                 913 tacggtggtggtgaacccattgggtccagctcaaggtgttggtttcgctaacgaattgatt 972
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APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, Sulte 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miettinen-Oinonen, Arja S.K.
Torkkeli, Tuula K.
Cantrell, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: in Trichoderma NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nevalainen, Helena K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/07923724 Patent No. 5780292 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paloheimo, Marja T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT:
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COUNTRY:
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1058 CCTCGTGCCCAGCCGGGCCAATCGTCGCCCAAGATCGACGTGGTCGTTTCCGAGGCCAGC 1117
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0
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                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFRA: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      join(404..447, 550..1906)
                                                                                                                              APPLICATION NUMBER: UK 8610600 FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             NAME: Cimbala, Michele A. REGISTRATION NUMBER: 33,851
                                                                                                                                                                                                                                                                                                                   2363 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 65.8
Matches 915; Conservative
                                                                                                                                                                                                                                                                                                                               nucleic acid
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                1298 TCCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCCCTTCTGTGACCTG 1357
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613 ggttacaacaacactttggaccacggtacttgtactgctttcgaagactctgaattaggt 672
                                                              673 gacgacgttgaagctaacttcactgctttgttcgctccagctattagagctagattggaa 732
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APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m. Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08609426A Patent No. 5830733 GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
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US-08-609-426A-7
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44.8%; Score 629.4; DB 2; Length 2363;
Best Local Similarity 65.8%; Pred. No. 4.4e-188;
Matches 915; Conservative 0; Mismatches 476; Indels 0;
                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                    E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TORNEY/Aben.
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
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                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/496,155 FILING DATE: 19-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-WAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-ARR-1987
PRIOR APPLICATION DATA:
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UK 861.0600
                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                         Washington
                                                                                                                          U.S.A.
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                                                                                                                                      20005
                                                                                                           STATE: D.C.
                                                        ADDRESSEE:
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US-08-609-426A-7
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1178 GATACCGTCGAAGCCAATTTCACCGCCACGTTCGCCCCCTCCATTCGTCAACGTCTGGAG 1237
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                                                              553 ccaggttctcaaccacaccaagcttctccagttattaacgtgatcattccagaaggatcc
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APPLICANT: TURUNEN, MARJA K.
APPLICANT: RAMBOSEK, JOHN A.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: HOUSTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL, TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
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Pred. No. 4.5e-188;
0; Mismatches 476;
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APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 41,264
REPERENCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2609
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31-JUL-1992
7N: 435
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APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
                                                             GENERAL INFORMATION:
APPLICANT: NEVALAINEN, HELENA K.M.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: FAGERSTROM, RICHARD B.
APPLICANT: MIETIINEN-OINONEN, ARJA
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                      Sequence 1, Application US/08374652C Patent No. 5834286
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COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-
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Matches 915; Conservative
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LENGTH: 2379 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
US-08-374-652C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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US-08-374-652C-1
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1093 atgatatetattttettegetttgggtttgtacaaeggtaecaageeattgtetaetaet 1152
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654 TCGCATCTTTGGGGTCAATACGCGCCGTTCTTCTCTCTGGCAAACGAATCGGCCATCTCC 713
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APPLICANT: ANAZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
APPLICANT: MAGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
ITILE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
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65.5%; Pred. No. 7.8e-183;
Live 0; Mismatches 471;
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CURRENT PILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09155855 Patent No. 6139902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 5
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; LOCATION: (157)...(1512)
US-09-155-855-5
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LOCATION: (184)..(1512)
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LOCATION: (157)..(183)
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LOCATION: (1)..(45)
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Best Local Similarity
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ö 1298 tgcacggttgttgtctgttgacaagttgggtagatgtaagagagacgacttcgttgaaggtt 1357 77 gtaattotoactottgtgacactgttgacggtggttaccaatgtttcccagaaatttotc 136 137 acttgtggggtacctactctccatacttctctttggcagacgaatctgctatttctccag 196 acgttccagacgactgtagagttactttcgttcaagttttgtctagacacggtgctagat 256 317 ctactgctttcaagggtaagtacgctttcttgaagacttacaactacactttgggtgctg 376 377 acgacttgactccattcggtgaaaaccaaatggttaactctggtattaagttctacagaa 436 0; Gaps 5 gaaatcaatccacttgcgatacggtcgatcaggggtatcaatgcttctcggagacttcgc 64 APPLICANT: KONDO, Hidemasa
APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Hideharu
APPLICANT: ANAZAWA, Hideharu
APPLICANT: NAGASHIWA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REPERENCE: 81356/124
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1997-04-04
EARLIER PILING DATE: 1997-04-04
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEC:ID NOS: 7
SOFTWARE: Patentin Ver: 2.0 185 atccgaccgactccaagggcaagaaatactccgctctcatcgaggagatccagcagaacg Length 1332; 1358 tgtctttcgctagatctggtggtaactgggctgaatgtttcgctta 1403 Indels 43.5%; Score 610.2; DB 3; 66.2%; Pred. No. 3.6e-182; tive 0; Mismatches 448; Sequence 4, Application US/09155855 Patent No. 6139902 ORGANISM: Aspergillus niger Best Local Similarity 66.2 Matches 879; Conservative ; NAME/KEY: CDS ; LOCATION: (1)..(1332) US-09-155-855-4 GENERAL INFORMATION: LENGTH: 1332 US-09-155-855-4 SEQ ID NO 4 Query Match 197 δy qq g οy g Dp òγ ò QC a δ οy g

437 gatacaaggctttggctagaaagattgttccattcattagagcttctggttctgacagag 496

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; Sequence 1, Application US/08819825 ; Patent No. 5866118 ; GENERAL INFORMATION:

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                                                                                                                   No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 333.2; DB 2; Length Pred. No. 6.6e-95; o; Mismatches 523; Indels
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
ATILE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                       405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/819,825 FILING DATE: 18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                   33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.7%;
Best Local Similarity 56.6%;
Matches 745; Conservative (
                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                        CORRESPONDENCE ADDRESS
                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                          New York
                                                                                                                                                                                            RY: U.S.A.
10174-6401
                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                            COUNTRY:
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                                                                                                                                          STREET:
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1147 GACCCAACCCAGCCCGCAGAGTTCCTGCAAGTTTTCGGCCCGCGTGTCTTGAAAAGATC 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacactttggactctaacccagctactttcccattgaacgctactttgtacgctgacttc 1077
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607 ggatccggttacaacaacactttggaccacggtacttgtactgcttcgaagactctgaa 666
                                                                     667 ttaggtgacgacgttgaagctaacttcactgctttgttcgctccagctattagagctaga 726
                                                                                                                                            727 ttggaagctgacttgccaggtgttactttgactgacgaagacgttgtttacttgatggac 786
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NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
                                                                          GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Alana V.
APPLICANT: Klotz, Alana V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
                            Sequence 1, Application US/09163642 Patent No. 6221644
US-09-163-642-1
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1087 GAAACTGGGAGTAACAATAGGGTGACGTGCCCGGGGGCCGAGGCACCC 1146

667 ttaggtgacgattgaagctaacttcactgctttgttcgctccagctattagagctaga 726

607 ggatccggttacaacaacactttggaccacggtacttgtactgctttcgaagactctgaa 666

547 getgacccaggttctcaaccacaccaagcttctccagttattaacgtgatcattccagaa 606

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967 TCCGCGCGAGTCATTGCGTCGGCAGAGTTCTTCAACCGCGGATTCCAGGATGCCAAAGAC 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 ttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggtattaag 426
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                                                                                                                                  SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                        RECISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
TELECOMMINICATION INFORMATION:
TELEPHONE: 212 867 0123
                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILING DATE:
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                   NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 56.69
Matches 745; Conservative
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
                                                                                                         COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-09-163-642-1
  New York
                  COUNTRY: .U.S.A.
ZIP: 10174-6401
                                                                                                                                                                                                                                       CLASSIFICATION:
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STATE:
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COMPUTER:

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3: No. 60543060 No. 6054306disk of No. 6054306th America, Inc.
405 Lexington Avenue
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1147 GACCCAACCCAGCCCGCAGAGTTCCTGCAAGTTTTCGGCCCCGCGTGTCTTGAAAAAAAC 1206
                                                                        1207 ACTAAA---CACATGCCGGGTGTGAACCTCACCTTGGAGGATGTCCCGTTGTTCATGGAT 1263
                                                                                                                                             1264 CTTGICCGTTTGACACGGIGGGCTCCGACCCAGTTCTTTCCCACGCAGCTCTCTCCG 1323
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                                                                                                             787 atgtgtccattcgacactgt-----cgctagaacttctgacgctactgaattgtctcca 840
                                                                                                                                                                                      841 ttctgtgctttgttcactcacgacgaatggatccaatacgactacttgcaaagcttgggt 900
                                   727 ttggaagctgacttgccaggtgttactttgactgacgaagacgttgtttacttgatggac 786
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APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglasng, Claus
APPLICANT: Onmann, Anders
APPLICANT: Ostergaard, Jens
APPLICANT: Ostergaard, Peter
APPLICANT: Ostergaard, Peter
NUMBER OF ESDUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-221-654-1; Sequence 1, Application US/09221654; Patent No. 6054306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10174
COMPUTER READABLE FORM:
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963 cgaattgattgctagattgactcactctccagttcaagaccacacttctactaacacac 1022
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8.7%; Score 122.8; DB 3; Length 1320;
Best Local Similarity 55.7%; Pred. No. 7.8e-29;
Matches 263; Conservative 0; Mismatches 197; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1083 cgacaacactatgatatctattttcttcgctttgggtttgtacaacggtacc 1134
                SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                            35,127
FP. 5101.200-US
                                                                    US/09/221,654
                                                                                                                                                                                                          APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                           08/989,358
                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/989,356
FILING DATE: 12-DEC-1997
FILING DATE: 07-MAX-1997
FILING DATE: 07-MAX-1997
APPLICATION NUMBER: 60/046,083
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
IBM Compatible
                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
                                   SOFTWARE: FASTSEQ for CURRENT APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                   NAME: Gregg, Valeta A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA US-09-221-654-1
                  OPERATING SYSTEM:
                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             843
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Search completed: October 26, 2001, 15:20:18 Job time: 574 sec

ä



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2001, 15:17:25; Search time 75.85 Seconds (without alignments) 814.587 Million cell updates/sec

US-09-488-265-29 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62. Gapop 10.0 , Gapext 0.5

.425026 seqs, 132305027 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_16:\* Database :

sp\_arche:\*
sp\_bacteria:\*
sp\_bacteria:\*
sp\_lungi:\*
sp\_human:\*
sp\_mammal:\*
sp\_mcganelle:\*
sp\_phage:\*
sp\_phage:\*
sp\_phage:\*
sp\_phage:\*
sp\_phage:\*
sp\_phage:\* sp\_unclassified:\*
sp\_vertebrate:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|               |   | æ              |                          |        |                |                       |
|---------------|---|----------------|--------------------------|--------|----------------|-----------------------|
| Result<br>No. | Score                                   | Query<br>Match | Query<br>Match Length DB | DB     |                | Description           |
|               | 1 |                |                          | 1      |                |                       |
|               | 1868                                    | 75.9           | 467                      | m      | 090027         | Odinie 7 agreentiling |
| 7             | 1867                                    | 75.8           | 465                      | m      | 00000          |                       |
| 3             | 1860                                    | 75.5           | 467                      | m      | 093838         |                       |
| 4             | 1850                                    | 75.1           | 467                      | m      | 09HEO          |                       |
| S             | 1839                                    | 74.7           | 466                      | ~      | 000100         |                       |
| 9             | 1761                                    | 71.5           | 466                      | . ~    | 00000          |                       |
| 7             | 1719                                    | 0              | 7.0                      | י ר    | 50000          | -                     |
| - 0           | 10101                                   |                | 7                        | n (    | 960000         |                       |
| ю (           | 1313.5                                  | 53.4           | 487                      | m      | 000107         | 000107 thielavia h    |
| 9             | 344.5                                   | 14.0           | 469                      | m      | Q9Y846         |                       |
| 10            | 328.5                                   | 13.3           | 442                      | m      | 074677         | Older and the and     |
| 11            | 297.5                                   | 12.1           | 463                      | ~      | 060172         |                       |
| 12            | 000                                     |                |                          | ۱ ۱    | 7/1000         | Up01/2 Schizosacch    |
| 77            | 502                                     | 7.5            | 460                      | ς.     | Q9VV72         | Q9vv72 drosophila     |
| 13            | 192.5                                   | 7.8            | 467                      | Ŋ      | 096421         | 096421 drosophila     |
| 14            | 189                                     | 7.7            | 451                      | 11     | 035217         | 035217 rattus porm    |
| 15            | 186                                     | 7.6            | 481                      | -      | 9.12260        | 000016 200 20011      |
| 16            | 175 5                                   | 7              | 452                      | ן<br>ע | 0000           | ntnoshin shin atzaca  |
| 7 -           | 100                                     |                | 7 .                      | ٠ ،    | 020470         | O96420 drosophila     |
| / [           | C'C/T                                   | 7 · T          | 48/                      | 4      | OBUMI<br>OBUMI | Q9unw1 homo sapien    |
| 87            | 174.5                                   | 7.1            | 453                      | S      | Q9W438         | -                     |
| 19            | 174.5                                   | 7.1            | 487                      | 4      | 095172         |                       |

| Oguqa3 homo sapien | 092170 qallus qall | 004509 arabidonsis | Ogutx1 schizosacch | ulusum spii0 | OBject Start Control | ulusum sim Spx90 | O19076 caenorhabdi | 000838 leishmania |        |        | 047871 eubacterium | Oguide homo santen | Ognoho homosanien | 09ilx9 retroperito | 022525 caenorhahdi | 093123 human calic | 019709 caenorhabdi | 020330 caenorhabdi | 019175 caenorhabdi | ulusum sum Zdaxh7 | 025327 leishmania | P72194 porphyromon |        | _      |        |
|--------------------|--------------------|--------------------|--------------------|--------------|----------------------|------------------|--------------------|-------------------|--------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------|--------|--------|
| Q9UGA3             | 092170             | 004509             | Q9UTX1             | Q9JJD5       | Q9JMG5               | 090xG5           | 019076             | 000838            | 000839 | 046334 | 047871             | 09UIG6             | 0HdN60            | 6XII60             | 022525             | 093123             | 019709             | 020330             | 019175             | O90XH7            | 025327            | P72194             | 024719 | 920826 | Q9P2C1 |
| 4                  | 13                 | 10                 | ٣                  | 11           | 11                   | Π                | 2                  | 5                 | Ŋ      | 7      | ~                  | 4                  |                   |                    |                    |                    |                    |                    | 'n                 | 11                | 2                 | 7                  | 7      | Ŋ      | 4      |
| 487                | 449                | 468                | 198                | 274          | 374                  | 381              | 449                | 683               | 707    | 513    | 827                | 421                | 428               | 1013               | 380                | 853                | 354                | 1225               | 452                | 381               | 516               | 1723               | 513    | 730    | 758    |
| 7.0                | 6.9                | 5.9                | 5.5                | 5.5          | 5.3                  | 5.3              | 4.8                | 4.8               | 4.8    | 4.7    | 4.6                | 4.5                | 4.5               | 4.4                | 4.3                | 4.3                | 4.2                | 4.2                | 4.1                | 4.1               | 4.1               | 4.1                | 4.1    | 4.1    | 4.0    |
| 173.5              | 170.5              | 145.5              | 136.5              | 136          | 131.5                | 129.5            | 119                | 117               | 117    | 114.5  | 113                | 110.5              | 110.5             | 107.5              | 106.5              | 106                | 104                | 103                | 102                | 101.5             | 101.5             | 101.5              | 100.5  | 100.5  | 99.5   |
| 20                 | 21                 | 22                 | 23                 | 24           | 25                   | 56               | 27                 | 28                | 29     | 30     | 31                 | 32                 | 33                | 34                 | 32                 | 36                 | 37                 | 38                 | 33                 | 40                | 41                | 42                 | 43     | 44     | 4 5    |
|                    |                    |                    |                    |              |                      |                  |                    |                   |        |        |                    |                    |                   |                    |                    |                    |                    |                    |                    |                   |                   |                    |        |        |        |

## ALIGNMENTS

| RESULT 1 Q9UUZ7 D Q9UUZ7 PRELIMINARY; PRT; 467 AA. | 01-MAY-2000 (TrEMBLrel. 13, Creat 01-MAY-2000 (TrEMBLrel. 13, Last 01-CCC-2000 (TrEMBLrel. 13, Last 01-CCC-2000 (TrEMBLrel. 13, Last 01-CCC-2000 (TrEMBLrel. 13, Last 01-CCC) | OI OCI ZOOO (IIEMBLIEL.<br>MYO-INOSITOL HEXAPHOSPHA<br>Aspergillus niger |  | OX NCBI_TAXID=5061; RN [1] RP SECITENCE FROM N A |  | Aspergillus niger (China Strain)."; Submitted (DEC-1999) to the EMBL/GenBank/DDRJ databases | DR EMBL; AF218813; AAF25481.1; , DR HSSP; P34752: 11HP. |  | DR Ptam; PF00328; acid_phosphat; 1.<br>DR PROSTMF, DSANG16, HTS ACTD DEOSEBARM 1. 1 |  | KW Signal; Lyase; Hydrolase.<br>FT Signal | SEQUENCE 467 AA; 51029 MW; | Ouery Match 75.9%; Score 1868; DB 3; Length 467; Best Local Similarity 75.2%; Pred. No. 1.3e-141; Matches 351; Conservative, 43; Mismatches 73; Indels 0; Gaps | OY 1 MGVHVVLLSTATLFGSTSGTALGRAGOTODGGYQCFPEISHLMGTYSPYFSLADE 60 | Db 1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLMGQYAPFFSLANE 60 | QY 61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 | Db 61 SAISPDVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAPLKTYN 120 |
|--|---|--|--|--|--|---|---|--|---|--|---|----------------------------|--|---|--|--|--|
|--|---|--|--|--|--|---|---|--|---|--|---|----------------------------|--|---|--|--|--|

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121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Qγ

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-!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-
241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                             241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
                                                                                                                                                                                                                                                                                                            301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                          361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE PHOSPHOHYDROLASE A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL; U59804; AAB96872.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 LVRVLVNDRVVVPLHGCPVDALGRCTRDSFVKGLSFARSGGDWAECFA 467
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Prémi PF00328; acid_phosphat; 1.
PROSTE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 27-37. STRAIN=ATCC 34625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-PHYTASE A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5061;
                                                                                                                                  (POTENTIAL).
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                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                             75.8%; Score 1867; DB 3; Length 465; 76.0%; Pred. No. 1.6e-141;
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Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
"Phytase having high-affinity for phytic acid.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO22700; CAB19824.1; -.
HSSP; P34752; 11HP.
                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
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                                                                                                                                                                                                                                      LINKED (GLCNAC. . .) (POSFECID9058C9B2C9 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                     50836
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 76.0%
Matches 355; Conservative
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                                                                                      CARBOHYD
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InterPro; IPR000560; -. Pfam; PF00328; acid\_phosphat; 1.

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                                                                                                                             121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                 241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                       HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                                                             1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANK 60
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5058;
                                                                                                                                                                                         KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR
                                                                                                                                                                                                                                                                KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
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                                               Length 467;
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                                                                                                                                                                                                                                                                                                                                                  Indels
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY013315; AAG40885.1; -.
         HIS_ACID_PHOSPHAT_2; 1.
51028 MW; 7A38AD543EDC265C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51012 MW; 3F69AD543C0B565B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                             Score 1860; DB 3;
Pred. No. 5.8e-141;
3; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.1%; Score 1850; DB 3; 74.1%; Pred. No. 3.7e-140;
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HIS_ACID_PHOSPHAT_1; 1. HIS_ACID_PHOSPHAT_2; 1.
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                                                               48;
                                             74.18;
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                                                              Matches 346; Conservative
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                 467 AA;
PS00616; H
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                                                      Similarity
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Matches 346;
PROSITE; PROSITE;
                  SEQUENCE
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SEQUENCE FROM N.A.

STRAIN-CBS.116.46;

PASAMONITES L., Haiker M., Henriquez Huecas M., Hug D., Mitchell D.B.,

Broger C., van Loon A.P.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
FROM PHYTATE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- SUMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                               241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHEEWINYDYLQSLN 300
  YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                           241 ARLEADLPGVILIDEDVVYLMDMCPFDIVARTSDATELSPFCALFIHDEWIQYDYLQSLG 300
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NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=33178;
                      181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR
                                                                                                   301 KYYGYGAGNPLGPAQGYGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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01-JUL-1997 (TTEMBLrel. 04, Last sequence update)
01-JUL-1997 (TTEMBLrel. 13, Last annotation update)
01-MAY-2000 (TTEMBLrel. 13, Last annotation update)
3-PHYTASE PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE PHOSPHOHYDROLASE) (3 PHYTASE) (MYO-INOSITOL HEXAKISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3-PHYTASE.
REQUIRED FOR BINDING SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                 421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan: PF00328; acid_phosphat; 1. PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1. PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1. Hydrolase; Glycoprotein; Signal.
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                                                                                                                                                                                                                                              YTLGADDLIPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                             241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATËLSPFCALFTHDEWIQYDYLQSLG 300
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                                                                                                                                                 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE
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01-JUL-1997 (TremBlrel. 04, Last sequence update)
01-MAY-2000 (TremBlrel. 13, Last annotation update)
3-PHYTAES A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE PHOSPHOHYDROLASE A).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                 Length 466;
                                                                                                 74.7%; Score 1839; DB 3; Length 4 73.0%; Pred. No. 2.8e-139; Live 49; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECF 466
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                                                              F2AECEC1AF7C22C4 CRC64;
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                                                              51055 MW;
                                                                                                              Best_Local Similarity 73.0
Matches 340; Conservative
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                                                              466 AA;
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 QRLEADLPGVQLSTDDVVNLMAMCPFETVSLTDDAHTLSPFCDLFTATEWTQYNYLLSLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 HDSNLVSIFWALGLYNGTAPLSQTSVESVSQTDGYAAAWTVPFAARAYVEMMQCRAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
        -i- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO 7.5, WITH MAXIMAL ACTIVITY AT PH 5.5. ALSO ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO
                                                                                                                                                                                                           REQUIRED FOR BINDING SUBSTRATE (BY SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ARLEADIPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGFLAIVLSVALLFRSTSGTPLGPRGKHSDCNSVDHGYQCFPELSHKWGLYAPYFSLODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYYGYGAGNPLGPAQGYGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
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                                               MORE ACIDIC PH VALUES.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL. 949805; AAB$2507.1; -.
InterPro; IPRO00560; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVRVLVNDRVMPLHGCPTDKLGRCKRDAFVAGLSFAQAGGNWADCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                                                                                                                         Pfan; PF00328; acid phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.5%; Score 1761; DB 3; 69.5%; Pred. No. 5.1e-133;
                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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58; Mismatches
                                                                                                                                                                                  POTENTIAL.
3-PHYTASE A.
-! - SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                      Hydrolase; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                    230 N-
339 N-
352 N-
376 N-
51093 MW;
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                                                                                                                                                                                     19
466
82
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361
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339
352
376
466 AA;
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ACT_SITE
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DISULFID
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Cloning of the phytases from Emericella nidulans and the thermophilic
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-!- MISCELLANEOUS: HAS POTENTIAL AS FOOD AND FEED ADDITIVE. IT CAN FACILITATE THE DECRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS USED AS FOOD FOR MONOGASTRIC ANIMALS.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL: U59802; AAB96873.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                         fungus Talaromyces thermophilus.";
Biochim. Biophys. Acta 1353:217-223(1997).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                              01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
3-HYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE
                                                                                                                                            Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; Talaromyces.
                                                                                                                                                                                                                            STRAIN=ATCC 20186;
MEDLINE-98007872; PubMed=9349716;
Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
Van Loon A.P.G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (PC
FC4575B521A5C929 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
3-PHYTASE A.
               01-JUL-1997 (TrEMBLrel: 04, Created)
01-JUL-1997 (TrEMBLrel: 04, Last segments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Glycoprotein; Signal SIGNAL 1 14 PO
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                                                                                                                                 ralaromyces thermophilus.
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                                                                                               PHOSPHOHYDROLASE A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 AA;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=28565;
                                                                                                                                                                                                                                                                                                                                                            FROM PHYTATE,
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212
261
432
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                                                                                                           59 DESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKT 118
                                                                                                                                             YNYTLGADDLTPFGENQMVNSGIKFYRFYRALARKIVPFIRASGSDRVIASAEKFIEGFQ 178
                                                                                                                                                                                               SAKLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPA 238
                          8; Gaps
                                              1 MGVFVVLLS--LATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLA 58
                                                            69.8%; Score 1719; DB 3; Length 466; 69.3%; Pred. No. 1.2e-129;
                            Indels
                            94;
                         42; Mismatches
                     Matches 325; Conservative
            Similarity
Query Match
              Local
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-!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-
              LGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYAD 358
                                                              359 FSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEK 418
                                                                                                               ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes for two novel phytases from the fungi Aspergillus terreus and
Myceliophthora thermophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microbiology 143:245-252(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INOSITOL 1.2,4,5,6-PENTAKISPHOSPHATE TRIBLIANDE H(2)0 - D.M. SUBCELLULAR LOCATION: SECRETED.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF 3.5 TO 8.5, WITH MAXIMAL ACTIVITY BETWEEN PH 5.5 AND 6.0. ALSO ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO MORE ACIDIC PH VALUES.
-!- SIMILARITY: BELLONG TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
--- SIMILARITY: BELLONG TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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PROTON DONOR (BY SIMILARITY).
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BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
239 IRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQS
                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHATBORDASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The phytase subfamily of histidine acid phosphatases: isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQUIRED FOR BINDING SUBSTRATE (BY
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Chaetomiaceae; Thielavia.
NCBI_TaxID=78579;
                                                                                                                                               419 EPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                               Mitchell D.B., Vogel K., Weimann B.J., Pasamontes L., van Loon A.P.G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 AA.
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3-PHYTASE A.
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-97177792; PubMed-9025298;
                                                                                                                                                                                                                                                                                                                                                   Thielavia heterothallica.
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                                                                                                                                                                     FAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTS-------DATELSPFCA 283
                                                                                                                                                                                                                                                                                                                                                284 LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLD 343
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                                                                                                                                                      58 ADESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK 117
                                                                                                                                                                                                      118 TYNYTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGF 177
                                                                                                                                                                                                                                                    QSAKLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFED---SELGDDVEANFTAL 234
                                                                                   Gaps
                                                                                                        1 MGVFVVL---LSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSL 57
                                                                                                                               4 LGVMVVMVGFLAIASL-------OSESRPCDTPDLGFQCGTAISHFWGQYSPYFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
97D10EDC83D051DB CRC64;
                                                                                  43;
                                                           Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Vicente A., Ferminan E., Dominguez A.;
"Isolation and characterization of KIPHO3 a gene encoding a constitutive acid phosphatse from Kluyveromyces lactis.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJO07502: CA846490.1; -...
HSSP; P34755: 10FX.
                                                        53.4%; Score 1313.5; DB 3; Length 52.7%; Pred. No. 4.1e-97; ive 58; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACID PHOSPHATASE (EC 3.1.3.2).
 247 247 N
346 346 N
487 AA; 52537 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 ESMAFARGNGKWDLCFA 487
                                                                                   Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000560; -.
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-2360/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase.
             CARBOHYD
SEQUENCE
    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9Y846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09Y846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 RVHQTAKYVVSSLEEELDIQLDLQIIQEN------ETSGANSLIPADSCMTY-NGDLG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDVEANFTALFAPAIRAR---LEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 CALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 LDSNPATFPLNATLYADFSHDNTMISIFFALGLY-NGTKPLSTTSVESIEETDGYSASWT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 VPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDF-----VEGL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 DESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKT 118
                                                                                                                                                                                                                                                                                                                                                                                                                               54 QSFGIPVEVPDQCTVEHVQMLARHGERYPTASKGKLWIALWDKLKEFQGQYNGPMEVFND 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 YEFFVSNTKYFDQLTNSTDVDPSNPYAGAKTAQHLGKYIAYNYGDLFSDSNP-VFTSSSG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 RVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 YNY----TLGADDLT-----PF-GENQMVNSGIKFYRRYKALARKIVPFIRASGSD 164
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                            7 LLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCF-----PEISHLWGTYSPYFSLA 58
                                                                                                                                                                                                                                                                                   224 DEYFENATLPYLTDIKNRWMKKNSNL-NLTLEHDDIELLVDWCAFETNVKGSSAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 CDLFERNDLVAYSYYANVNNFYRRGAGNPMSNPIGSVLVNASYNLLTQADELDN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomyeetales; Saccharomycetaceae; Pichia.
NCBI_TaxID=4905;
                                                                                                                                                                                  79;
                                                                                                                        DB 3; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphatase (PHO1) from the methylotrophic yeast Hansenula polymorpha.";
                                                                                                                        14.0%; Score 344.5; DB 3; Length 424.9%; Pred. No. 2e-19; ive 70; Mismatches 215; Indels
                             52560 MW; 5C7ABF622CEA891C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
REPRESIBLE ACID PHOSPHATASE (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000560; ... Pfam: PF00328; acid_phosphat; 1. PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1. Hydrolase.
ACID PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appl. Microbiol. Biotechnol. 50:77-84(1998).
EMBL, AF051161; AAC62537.1; -.
HSSP, P34755; 1QFX.
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MEDLINE=98386672; Pubmed-9720203;
                                                                                                                                                                                     Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                        Similarity
                             469 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 SFARS 458
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SEQUENCE

So

6C41AF422C6D624A CRC64;

52758 MW;

463 AA;

SEQUENCE

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15;
                                                                                                   66 DVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQK-NATAFKGKYAFLKTYNYTLG 124
                                                                                                                     125 ADDLTPFGENOMVNSGI----KF----YRRYKAL--ARKIVPFIRASGSDRVIASAEKFI 174
                                                                                                                                                                                 115 DSDNYELETTRGLYSGLINAFKFGTYLRERYDSLVDTSSVLPIFAAS-EDRVVDTARSFG 173
                                                                                                                                                                                                                                                     174 RGFFG------PDYATSCSIQVVNETDTSKGANALTTKDNCPTYNSSFYDYSFGDEI 224
                                                                                                                                                                                                                         175 EGFQSAKLADPGSQPHQASPVINVIIPE---GSGYNNTLDHGTC----TAFEDSELGDDV 227
                                                                                                                                                                                                                                                                                                                                            285 FTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDS 344
                                                                                                                                                                                                                                                                                                                                                                                                         345 NPATFPL---NATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTV 401
                                                                                                                                                                                                                                                                                     ---EANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCAL 284
                                                                                                                                                                                                                                                                                                                                                                                                                             81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                   -----RLNELSPGFNITADDIITMGTYCAYETNVKGH-----SSFCDA
                                                                                                                                                                                                                                                                                                                                                                 Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN ALCOHOL + ORTHOPHOSPHATE.
-! SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL; AL022286; CAA18863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTON DONOR (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                               Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 PFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVE 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
7087D91A85B05C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
                                          13.3%; Score 328.5; DB 3; 25.1%; Pred. No. 3.4e-18; Live 63; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 AA
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InterPro; IPR000560; --
Pfam; PF000328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Last annotate PROBABLE ACID PHOSPHATASE (EC 3.1.3.2).
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N-LINKED
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49370 MW;
                                                                       Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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104
221
324
439
458
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442 AA;
                                                          Local Similarity
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                                            Query Match
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CARBOHYD
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Addams M.D., Celniker S.E., Ili P.W., Hoskins R.A., Galle R.F.,
Gocrge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Tandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Basley E.M.,
Ballew R.M., Basu A., Baxman B.P., Bhandari D., Bolshakov S.,
A. Ballew R.M., Bacos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,
                                                                                                                                                                                                         89 LNNFQEKLLNÖSIPVNESYPENPLCFIKQWTPVIDAENADQLSSRGRLELFDLGRQLYQR 148
                                                                                                                                                                                                                                                                                                                149 YYKLFDSYVYDINTAEQERVYESAKWFTYGLFGDKMYEKTN------FILISEGKAA 199
                                                                                                                                                                                                                                                                                                                                                               205 GYNNTLDHGTCTAFEDSEL----GDDVEANFTALFAPAIRARLEADL-PGVTLTDEDVVY 259
                                                                                                                                                                                                                                                                                                                                                                                            260 LMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 ANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 PLSTISVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVD 439
                                                                                                                                                                               -----LIEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGENQMVNSGIKFYRR 146
                                                                                                                                                                                                                                                                       147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEG--S 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 LFYICEYEIAIK-----DHSDFCSIFTPSEFLNFEYDSDLDQAYGGGPVSEWASTLGGAY 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 INNLADSL-----RNVINPDFDRK-----VFLAFIHDSNIIPVEAALGFFPDIT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 PONPLPIDKNIYTYSOKTSSFVPFAGNLITELFFC-SDSKYYVRHLVNQOVYPLIDCGYG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota; Medazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pherygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                    Gaps
                                                                                                                             35 HL-GILSPYHEPYFDGLDSA----FPETCEIQQVHLLQRHGSRNPTGDVTATDVYSSQY 88
                                                                                       46 HLWGTYS----PYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPTS--SASKAYSA-- 97
                                               , 29
       Length 463;
                                             67; Mismatches 203; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
12.1%; Score 297.5; DB 3; 25.3%; Pred. No. 1.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 KLGR----CKRDDFVEGLSFARSGGNWAECF 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418 PSGTSDGLCELQAYLNSPIRANSTSNGISIF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                          Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR CG4123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIPP1 PROTEIN.
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VV72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09VV72
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223 SKLYNDTLAD-----ISTRL-----GFLYTLEEADIKLMYDMCRYE---QAMNVDRN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 NHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSAS 398
                                                                                                                                                                                                                                                                                                                                                                                                      115 KLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTVLTANYNDTYYQRTTESFK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 KFIEG-FQSAKLADPGSQPHQ-----ASPVINV-IIPEGSGYNNTLDHGTCTAFED 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTST 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 KTYNYTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVP-FIRASGSD----RVIASAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 WIVPFAARAYVEMMQCQA--EKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVE---- 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 --------VVAHFGHSTGLLTLTALGIQKDDIKLRADNYDSL-TSRRWKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SELGDDVEANFTALFAPAIRARLEADLPG - - VTLTDEDVVYLMDMCPFDTVARTSDATEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVWCGAFLPEQITVFEYLEDLKYYYGSGYGFPENAHLNCRLVQDLLTHLS-NPVSPH---
                                                                                                                                                                                                                                                                                                                                                                     98;
                                                                                                                                                                                                                                                                                                                                            8.2%; Score 203; DB 5; Length 460; 24.0%; Pred. No. 4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                    60; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                          71 CRVTFVQVLSRHGARYPTSS----ASKAYSALIEAIQKNATAFKGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 AFAEGLFGSQNAAHPVEIPKQDLLLRPYDYCSSFKNVNYKDEGSEYYK---
                                                                                                                                                                                                                                                                                                              F00B25718E40807D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                   Pfam; PF00328; acid_phosphat; 1.
SEQUENCE 460 AA; 52685 MW; F
                                                                                                                                                                                                                                                                             FlyBase; FBgn0026061; Mippl.
                                                                                                                                                                                                                                                                                                                                                                    Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 ADADCGEYYCRTGG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 ----GLSFARSGG 460
                                                                                                                                                                                                                                                                                           IPR000560; -
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Best Local Similarity
                                                                                                                                                                                                                                                                                           InterPro;
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Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 RITESFKAFAEGLFGSQNAAHPVEIPKODLLLRPYDYCSSFKNVNYKDEGSEYYK---- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 TCTAFEDSELGDDVEANFTALFAPAIRARLEADLPG--VTLTDEDVVYLMDMCPFDTVAR 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 ----FHQSKLYNDTLAD-----ISTRL-----GFLYTLEEADIKLMYDMCRYE---Q 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 TSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AWNVDRNSVWCGAFLPEQITVFEYLEDLKYYYGSGYGFPENAHLNCRLVQDLLTHLS-NP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 VSPH-------VVXHFGHSTGLLTLTALGIXKDDIKLRADNYDSL-T 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 TDGYSASWTVPFAAR--AYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDF 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 SRRWKSSLIDPFAANFVAVKYDLPADLDREKVV-FFLNQQAVQLDWCSV---GLCKWSDV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 KLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTVLTANYNDTYYQFRHTDTQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 RVIASAEKFIEG-FQSAKLADPGSQPHQ-----ASPVINV-IIPEGSGYNNTLDHG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 VQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 CQPQKMWIFHRHGTRLPKKSMINKASRV-AELRDLIINNYQVARTKPETDALCQTDLIAI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 KTYNYTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFI---------RASGSD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 11-451 FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                 Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N., Reynolds P.R.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF046913; AAD02436.1; --
FlyBase; FBgn0026061; Mippl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 3.1.3.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                7.8%; Score 192.5; DB 5; Length 467;
22.9%; Pred. No. 3e-07;
ive 61; Mismatches 174; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 CRVTFVQVLSRHGARYPTSS----ASKAYSALIEAIQKNATAFKGK----
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00328; acid_phosphat; 1.
SEQUENCE 467 AA; 53602 MW; 1A0571B9958B2632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-AUG-2000 (TrEMBLrel. 13, Last annotation update)
HEPATIC MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE 1. MIPP1 OR CG4123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 VE------GLSFARSGG 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 22.9 Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                 IPR000560;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                     InterPro;
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16;
                                                                                                                                                                                               specificity.";
J. Biol. Chem. 266:16499-16506(1991).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INOSITOL 1,3,4,5-
TETRAKISPHOSPHATE TO INOSITOL 1,4,5-TRIPHOSPHATE AND INOSITOL
1,3,4,5,6-PENTAKISPHOSPHATE TO INOSITOL 1,4,5,-TRISPHOSPHATE
AND THEN TO INOSITOL 1,4,5-TRISPHOSPHATE. DEPHOSPHORYLATES
INOSITOL HEXAKISPHOSPHATE WITHOUT SPECIFICITY TOWARDS A PARTICULAR
                                                                                                                                                                  "Purification of an inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase activity from rat liver and the evaluation of its substrate
                                                                                                                                     Nogimori K., Hughes P.J., Glennon M.C., Hodgson M.E., Putney J.W. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 ALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 OLOGILOTRESVDGGSRVAAALDOWPLWYDD---WMDGOLVEKGRODMRQLALRLAALFP 130
                             Craxton A., Caffrey J.J., Burkhart W., Safrany S.T., Shears S.B.;
"Molecular cloning and expression of a rat hepatic multiple inositol
polyphosphate phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --FIR------ASGSDRVIASAEKFIEGFQSAKLADPGSQPHQAS-----PVINVI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 DLFCRENYGRLRLITSSKHRCVDSSAAFLQGLW--QHYHPGLPPPDVSDMECDPPRVN-- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALF-----APAIRARLE----ADL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPYFS------LADESAISPD---VPDDCRVTFVQVLSRHGARYPTSSASKAYS 96
                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF00328; acid_phosphat; 2. PROSITE: PS00014; ER_TARGET: UNKNOWN_1. PROSITE: PS00016; HIS_ACID_PHOSPHAT_1; FALSE_NEG. Hydrolase; Glycoprotein; Phosphorylation; Multifunctional enzyme. ACT_SITE 59 59 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREVENT SECRETION FROM ER (POTENTIAL) EB1C05512A03020B CRC64;
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-! SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-! TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY AND LIVER.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL. AF012714, AAC33453.1;
-- InterPro; IPR00056;
-- InterPro; IPR000866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 451;
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S -> P (IN AAC53453)
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20.7%; Pred. No. 5.5e-07;
.ve 66; Mismatches 193;
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              MEDLINE=98028656; PubMed=9359836;
                                                                                                                     MEDLINE=91358435; PubMed=1653239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51592 MW;
                                                          polyphosphate phosphatase.";
Biochem. J. 328:75-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                       CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448
451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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218
391
412
447
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Best Local Similar
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CARBOHYD
CARBOHYD
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308 GNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMIS 367
                                   292 GYAINSRSSCNLFQDIFLHLDKAVEQKQRSQ------PVSSSVILQFGHAETLLP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVIASAEKFIEGFQSAKLADPGSQPHQAS-----PVINVIIPEGSGYNNTLDHGTCTAF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCVDSSAAFLOGLW--OHYHPGLPPPDVSDMECGPPRIN-----DKLMRFFDH--CEKF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 DLAIKGVH----SPWCDVFDVDDARVLEYLNDLKQYWKRSYGYTINSRSSCNLFQDIFLH 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 DESAISPD---VPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 LKTYNYTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVP--FIR------ASGSD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDSELGDDVEANFTALF-----APAIRARLE-----ADLPGVTLTDEDVVYLMDMCPF 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 L----TDVERNETALYHVEAFKTGPEMQKVLKKVAATLQVPMNSLNADLIQVAFFTCSF 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 DIVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 LDKAVEQKQRSQ------PVSSPVILQFGHAETLLPLLSLMGYFKDKEPLTAYNF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chi H., Wang J., Romano P.R., O'keefe R.J., Puzas J.E., Rosier R.N., Reynolds P.R.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 ATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFS------LA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AALLSSFARCSLPGRGD-----PVASVL----SPYFGTKTRYEDANPWLLV 62
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                       368 IFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP----LVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.6%; Score 186; DB 11; Length 481; 21.0%; Pred. No. 1e-06; tive 66; Mismatches 206; Indels 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prom; PFO0018; acid_phosphat; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SEQUENCE 481 AA; 54537 MW; 7CE78356B11F4606 CRC64;
                                                                                                                                                                                                                                                                                                                              1-MAY-1999 (TEMBLrel. 10, Last sequence update)
01-CCT-2000 (TEMBLrel. 15, Last annotation update)
MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE.
                                                                                                                                                                                                                                                                            481 AA
                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF046908; AAD02434.1; MGD; MGI:1336159; Minppl.
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InterPro; IPR000886;
                                                                                                                                            424 VLVNDRVVPL 433
                                                                                                                                                                   400 MLLNEKVLPL 409
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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QQ δy

Search completed: October 26, 2001, 15:17:26 Job time: 3977 sec

Copyright (c) 1993 - 2000 Compugen Ltd. GenCore version 4.5

OM protein - protein search, using sw model

October 26, 2001, 15:10:28 ; Search time 48.78 Seconds

(without alignments)
729.264 Million cell updates/sec

US-09-488-265-29 Title: Perfect score:

1 MGVFVVLLSIATLFGSTSGT.........DFVEGLSFARSGGNWAECFA 467 Sequence:

BLOSUM62 Scoring table:

219241 seqs, 76174552 residues Gapop 10.0 , Gapext 0.5 Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description         |         | ~      | - phytaco | יי<br>ביי<br>ביי | Fig case (EC 3. | phospharas | acid phosphatase ( | d phosphatas | n phosphatas | 17     |        |        | + hismin monacett | Chiamin' Lepressiol |        |        | -      |        |          | tase   | nypothetical prote | ت      |        | ٠.                                    | hypothetical prote | hypothetical prote | +      | hypothetical prote | 2     | TOWNS TOTAL TOTAL | hypothetical prote |
|---------------------|---------|--------|-----------|------------------|-----------------|------------|--------------------|--------------|--------------|--------|--------|--------|-------------------|---------------------|--------|--------|--------|--------|----------|--------|--------------------|--------|--------|---------------------------------------|--------------------|--------------------|--------|--------------------|-------|-------------------|--------------------|
| SUMMARIES           |         | JN0889 | JN0656    | JN0482           | S53476          | 248996     | PABYC              | PABYCC       | JC4285       | S52495 | 0680NC | JN0715 | T39929            | A25326              | 814119 | 04447. | AB6233 | 110110 | . 011611 | T14/47 | 110000             | 307570 | 116883 | , , , , , , , , , , , , , , , , , , , | 147171             | Tros46             | S06167 | T20556             | (     | 95                | T16455             |
| DB                  | 1       | -      | Н         | -                | 7               | C          |                    | Н            | 7            | ~      | Н      | Н      | · C               |                     | 10     | ٠,     | ۰,     | ٥.     | 4 (      | ٦,     | ۱,                 | 4 C    | 10     | , (                                   | <b>v</b> c         | 7                  | -      | 7                  | 7     | 7                 | 7                  |
| Length              |         | 467    | 467       | 441              | 467             | 467        | 467                | 467          | 468          | 468    | 479    | 479    | 463               | 453                 | 463    | 465    | 468    | 7.00   | 421      | 440    | 700                | 7.07   | 380    | 200                                   | 100                | v                  | 423    | 2                  | œ     | 563               | 3                  |
| %<br>Query<br>Match | 1       | 76.3   | 76.2      | 73.7             | 16.0            | 16.0       |                    | 15.4         | 14.4         | 14.4   | 14.1   | 4      | 12.1              | $\sim$              | Н      | 9      |        | , r.   |          |        | 7 7                | . 4    | 4      |                                       | 9 (                | ٠                  | •      | 4.1                | 4.1   | 4.1               | 4.1                |
| Score               | •       | 1879   | 1875      | 1814             | 395             | 395        | 392                | 380          | 355          | 354    | 347.5  | 346.5  | 297.5             | 297                 | 278.5  | 149    | 145.5  | 13     | , .      | =      | 114.5              |        | 106.5  | 104                                   | 101                | 100                | 102.5  | 102                | 101.5 | 101               | 100.5              |
| Result<br>No.       | 1 1 1 1 | П      | 2         | æ                | 4               | S          | 9                  | 7            | 8            | 6      | 10     | 11     | 12                | 13                  | 14     | 15     | 16     | 17     | 8        | 19     | 20                 | 21     | 22     | 23                                    | 20                 | 7 6                | 52     | 56                 | 27    | 28                | 29                 |

| acid phosphatase ( probable formate C | transforming prote hypothetical prote | acid phosphatase (<br>probable LTR retro | NADPHferribemon  | hypothetical prote<br>lysine-specific cy | promante peptide s<br>alpha-amylase (EC<br>III.25 protein - hum | exo-poly-alpha-gal |
|---------------------------------------|---------------------------------------|--|------------------|--|---|--------------------|
| JH0152<br>E69144<br>S63895            | TVMSMY<br>S09774                      | JHU610<br>A71444<br>T18945               | G84312<br>A37890 | T17291<br>T30836<br>T50176               | JH0638<br>WMBEW5  | A36715             |
| 000                                   | 40                                    | 400                                      | 100              | 200                                      | 77  | 7                  |
| 381<br>642<br>680                     | 715                                   | 386<br>1433<br>413                       | 473              | 845<br>1732<br>4924                      | 605<br>580  | 602                |
| 4 4 4<br>0 . 0 .                      | 0.8                                   | n m m                                    | . e. e.          | თ თ თ<br>თ თ თ                           | 6 8<br>8  | 3.8                |
| 98.5<br>98.5<br>5.8                   | 97.5                                  | 96.5<br>96.5                             | 95.5             | 95.5                                     | 95<br>94.5  | 94.5               |
| 30<br>31<br>32                        | 33<br>44<br>44                        | 36<br>37                                 | 38               | 4 4 4<br>0 1 2                           | 43<br>44  | 45                 |

## ALIGNMENTS

| - |     |
|---|-----|
|   | 088 |

June 1970 and 1970 an

A. Cross-references: GB:L02421; NID:g166518; PIDN:AAA16898.1; PID:g166519
A. Experimental source: strain ALK0243
A. Note: part of the sequence, including the amino end of the mature protein, was conf C; Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic

C; Genetics:

A; Gene: phyA

A; Introns: 15/2

C. Superfamily: yeast acid phosphatase
C. Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F):1-19/Domain: signal sequence #status predicted <SIG>
F):20-467/Product: 3-phytase A #status experimental <MAT>
F:20,59,105,120,207,230,339,352,376,388/Fainding site: carbohydrate (Asn) (covalent) #
F:81,361/Active site: Arg, His #status predicted
F:82/Active site: His (phosphohistidine intermediate) #status predicted

0; Gaps 76.3%; Score 1879; DB 1; Length 467; 75.6%; Pred. No. 1.4e-143; Live 41; Mismatches 73; Indels ( Matches 353; Conservative Best Local Similarity Query Match

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1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60 δy g

δ

61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120

61 SAISPDVPAGGRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAPLKTYN 120 pp

YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 δ

qq

181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240 δλ

241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300  ~

chemic

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A Residue: 48-70 < 0.02 
A; Residue: 48-70 < 0.02 
A; Residue: 48-70 < 0.02 
C; Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phyt 
C; Superfamily: yeast acid phosphatase 
C; Keywords: extracellular protein; 91ycoprotein; phosphohistidine; phosphoprotein; ph 
E; 43, 68, 29, 97, 184, 207, 316, 329, 533, 365, fainding site: carbohydrate (Asn) (covalent) #sta 
F; 58, 318/Active site: Arg, His #status predicted 
F; 59, 74ctive site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 1-441 <ULbat
A,Note: authors state that the 9 Asn followed by Thr or Ser after an intervening resi
R;Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
Biochem Biophys. Res. Commun. 178, 45-53, 1991
A;Title: Cyclohexanedione modification of arginine at the active site of Aspergillus
A;Title: Cyclohexanedione modification of arginine at the active site of Aspergillus
A;Reference number: PN0023; MUID:91298982
                                                                                                                                                                                                                                                 N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein c;Species: Aspergillus ficuum c;Species: Aspergillus ficuum by N0023 and 19-oct-1995 #text_change 07-May-1999 (;Date: 30-Sep-1993 #sequence_revision 19-oct-1995 #text_change 07-May-1999 (;Caccession: JN0482; PM0023 Jr. H.C. Biochem. Biophys. Res. Commun. 192, 747-753, 1993 Myītile: Aspergillus ficuum phytase: Complete primary structure elucidation by ciangle A;Reference number: JN0482; MUID:93249451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 266
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                                     HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 NSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.7%; Score 1814; DB 1; Length 441; 77.2%; Pred. No. 2.3e-138;
                                                                                                                    LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Mismatches
                                                                                                                                                                                                                                            3-phytase (EC 3.1.3.8) A - Aspergillus ficuum
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les 338; Conserv
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R;van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.
A.M.J.J.
Gene 127, 87-94, 1993
                                                                                                                                                                                                                                                                                                                                                                     N; Alternate names: myo inositol hexakisphosphate phosphohydrolase; phyA protein C; Species: Aspergillus niger
C; Date: 03-Feb-1994 #sequence_revision 19-oct-1995 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                           301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ORLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR
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                                                                                                                                                                                                                               LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWABCSA 467
                                                                                                                                                                                                         LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                          3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Mismatches
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A;Cross-references: EMBL:U00029; NID:g551322; PIDN:AAB69729.1; PID:g458917; MIPS:YHR2
                                                                                                                                                                                                                                   C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 22-Jun-1999
C;Accession: $48996; $59659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-16,'L',18-81,'AR',84-149,'H',151-467 <XUL>
A;Cross-references: EMBL:U19789; NID:g847754; PIDN:AAA73479.1; PID:g847755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 NISLQ-----TISEAESAGANTLSAHHSCPAWDD-DVNDDILKKYDTKYLSGIAKRLNKE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 NKGLNLTSSDANTFFAWCAYEINAR----GYSDICNIFTKDELVRFSYGODLETYYOTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMI 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 ERYPTVSKAKSIMTTWYKLSNYTGQFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 TPF-GENQMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 NPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSNRCHDTAQYFIDG-----LGDKF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PLGKLSDIDKIGTQTEIFPFL---GGSGPYYSFPGDYGISRDLPESCEMKQVQMVGRHG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 PRGNSHSCDIVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 LPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYG
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                                                                                                                                                                               yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                   R.Macri, C.
submitted to the EMBL Data Library, February 1994
A; Description: The sequence of S. cerevisiae cosmid 9177.
A; Reference number: S46671
A; Accession: S48996
399 NDAVVPIETCSTGPGFSCEINDFYGYAEKRVAGTDFLK 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 ARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, January 1995
A;Reference number: $59658
A;Accession: $59659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Map position: 8R
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphoric monoester hydrolase
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                                                                                                                                                                         acid phosphatase (EC 3.1.3.2) PH012 N;Alternate names: protein YHR215w
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Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA A; Residues: 1-467 <MAC>
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A; Residues: 1-16, L'. 18-149, 'H', 151-353, 'Q', 355-422, 'G', 424-467 < CHE>
A; Residues: 1-16, L'. 18-149, 'H', 151-353, 'Q', 355-422, 'G', 424-467 < CHE>
A; Wote: this paper is, in Chinese, with an English abstract
C; Genetics: SDD: PHO11
A; Gene: SDD: PHO11
A; Cross-references: SGD: SO000094; MIPS: YAR071w
A; Map position: IR
C; Superfamily: yeast acid phosphatase
C; Reywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
F; 1-17/Domain: signal sequence #status predicted < SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:L28920; NID:g1616966; PIDN:AAC09508.1; PID:g456155; MIPS:YAR071 R;Chen, J.Y.; Gong, Y.; Ao, S.2.
Acta Blochim. Blophys. Sin. 21, 437-444, 1989
A;Title: The primary structure of acid phosphatase gene PH011 in S. cerevisiae and compa A;Reference number: JC1018
A;Accession: JC1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F)1-17/Domain: signal sequence #status predicted <SIG>
F:18-467/Product: acid phosphatase #status predicted <MAT>
F:74/Active site: Arg #status predicted intermediate) #status predicted F:75/Active site: His (phosphohistidine intermediate) #status predicted F:97,162,192,250,315,356,439,445,461/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                      N.; Barton, A.B.; Kabac
                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                            acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein YAR071w
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Spaces: Saccharomyces cerevisiae
C.Space: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Apr-2000
C.Accession: S53476; JC1018
R.Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Submitted to the EMBL Data Library, February 1994
A.Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of A.Reference number: S53458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 ERYPTVSKAKSIMTTWYKLSNYTGQFSCALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 TPF-GENOMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEAD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLV 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 PRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDLPESCEMKQVQMVGRHG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 PGYDVVRSVGANLFNASVKLLKESEVQDQ--------KVWLSFTHDTDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :99
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26.0%; Pred. No. 5.6e-24;
Live 66; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDRVVPLHGCAVDKLGRCKRDDF-----VEGLSFAR 457
                  DSFVRGLSFARSGGDWAE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 26.0°
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-467 <BUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S53476
                  424
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A; Cross-references: EMBL:X78993; NID:q476045; PIDN:CAA55597.1; PID:q476050
     A; Residues: 1-51, 'S', 53-60 <SIL>
                                            A;Cross-references: GB:M17306
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-467 <MAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 ADD----
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A; Accession: $45927
A; Accession: $45927
A; Accession: $45961
A; Accession: $45077
A;
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A. Reference number: S41855, MUID: 84236032

A. Reference number: S41855

A. Recession: S41855

A. Recession: S41855

A. Recession: S41855

A. Recession: S41855

A. Residues: 1-30, TT, 32-51, S., 53-75 CMEY>

A. Cross-references: EMBL: M24178; NID: 9172156; PIDN: AAA34868.1; PID: 9172157

B. Tait-Kamradt, A. G.; Turner, K. J.; Kramer, R. A.; Elliott, Q. D.; Bostian, S. J.; Thill, G. R. Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within A. Reference number: A93074; MUID: 87064474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: B25241
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-44 < TAI>
R; Bergman, L.W.
Mol. Cell. Biol. 6, 2298-2304, 1986
A; Title: A DNA fragment containing the upstream activator sequence determines nucleosome
A; Reference number: A25367; MUID:87064526
A; Accession: A25367
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A; Residues: 1-2, YY, 4-43, T', 45-51 <BER>
A; Residues: 1.2, YY and M. Hinnen, A.; Haquenauer-Tsapis, R.
Mol. Cell. Biol. 7, 3306-1314, 1987
A; Title: The yeast acid phosphatase can enter the secretory pathway without its N-termin
A; Reference number: A27774; MUID:88038886
                                                                                                   C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 19-Feb-1984 #sequence_trevision 30-Sep-1991 #text_change 12-Nov-1999
C;Accession: S05795; A38792; S48260; S45961; A00777; A38793; S41855; B25241; A25367; A27
R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
R:Laiwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeas
A;Reference number: S05794; MUID:85037940
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acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (Saccharomyces cerevisiae) N; Alternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-35, Y', 37-129, 'G', 131-293, 'Q', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467
A; Residues: 1-35, Y', 37-129, 'G', 131-293, 'Q', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467
A; Residues: BMBL:V01320; NID:94158; PIDN:CAA24630.1; PID:94159
A; Accession: A38793
A; Molecule type: protein
A; Residues: 18-26, 'X', 28 <ARI2>
EMBO J: 1, 675-680, 1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1.467 < CMAN>
A; Residues: 1.467 < CMAN>
A; Cross-references: EMBL: X78993; NID: 9476045; PIDN: CAA55598.1; PID: 9476051
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
B; Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Accession: S05795
A.Molecule type: DNA
A.Residues: 1-467 < CAAJ>
A.Kocession: S05795
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: Protein
A.Molecule type: Protein
A.Molecule type: Protein
A.Residues: 18-45 < CABJ>
A.Residues: 18-5 Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
A.Residues: 18-5 Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
A.Reference number: S48255; MulD:95208357
A.Accession: S48255; MulD:95208357
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A; Molecule type: DNA
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A.Gene: SGD:PHO5; MIPS:YBR093c
A.Cross-references: SGD:S0000297; MIPS:YBR093c
A.Map position: 2R
A.Map position: 2R
A.Map position: 2R
A.Mote: YBR003c
C; Superfamily: yeast acid phosphatase
C; Superfamily: yeast acid phosphatase
C; Superfamily: yeast acid phosphatase, repressible #status predicted <SIG>F:11-17/Domain: signal sequence #status predicted <SIG>F:18-467/Product: acid phosphatase, repressible #status experimental <MAT>F:75/Active site: His Chosphohistidine intermediate) #status predicted
F:97,103.162.192.250,315,356,390,449,445,456,461/Binding site: carbohydrate (Asn) (co
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N,Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR092c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 GDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 SNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPF 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 AARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDF-----VEGLSFA 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LTPF-GENQMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 DDDDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 SAEKFIEGFQSAKLADPGSQPHQASPVINVII-----PEGSGYNNTLDHGTCTAFEDSEL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 NDDIVNEYDTTYLDDIAKRLNKENKGLNLTSTDASTLFSWCAFEV-----NAKGYSDVCD 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 ------KVWLSFTHDTDILNFLTTAGIIDDKNNLTAEYVPFMGNT--FHRSWYVPQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 DVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK-TYNYTLG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VVYSILAASLANAGTI--PLGKLADVDKIGTQKDIFPFL----GGAGPYYSFPGDYGISR 58
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A;Status: nucleic acid sequence not shown; translation not shown
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25.6%; Pred. No. 9.8e-24;
ative 64; Mismatches 216; Indels
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Best Local Similarity 25.6°
Matches 123; Conservative
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452 GLSFARSGGNWAE 464
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A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
S: Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.

Submitted to the Protein Sequence Database, August 1994
A; Reference number: 845927
A; Residence number: 845920
A; Molecule type: DNA
A; Residence: 1-467 - KFE2.
A; Cross references: EMBL: 235961; NID:9536362; PIDN:CAA85045.1; PID:9536363; GSPDB:GNOOG
A; Molecule type: DNA
A; Residence: 1-467 - KFE2.
A; Cross references: EMBL: 235961; NID:9536362; PIDN:CAA85045.1; PID:9536363; GSPDB:GNOOG
A; Redidues: 1-218, TAZ-7732-7739; 1984
A; Reference number: 805794
A; Residues: 1-218, TMRT, 222-467 - EBAJI>
A; Residues: 1-44 - TMID: 910414
A; Residues: 91040; MID: 97064474
A; Residues: 920; PMA
A; Residues: 1-44 - TMID: 97064474
A; Residues: 1-44 - TMID: 9706296; MIRDS:YBR092C
A; Cross-references: 56D: 50060296; MIRDS:YBR092C
A; Cross-references: 56D: 50060296; MIRDS:YBR092C
A; Cross-references: 56D: 50060296; MIRDS:YBR092C
A; Cross-references: 56D: 970439, MID: 97064474
A; Residues: 1-44 - TMID: 97064474
A; Residues: 1-44 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LIPF-GENOMVNSGIKFYRRYKALAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 FNGSLSFLNDDYEFFIRDDDDLEMETTFANSDNVLNPYTGEMDAKRHAREFLAQYGYMFE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 KIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYNNTLD
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Matches 114; Conserv
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A. Molecule type: DNA
A. Residues: 1-468 <PAY>
A. Cross references: GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
A. Cross references: GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
A. Experimental source: GS115
C. Genetics:
A. Genetics:
A
                                                                                                                                                                                                                                                                                                         R;Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A;Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterizati
A;Reference number: JC4285; MUID:96001238
A;Accession: JC4285
acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichla pastoris)
N:Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum): Pho
C:Species: pichla pastoris
C:Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999
C:Accession: JC4285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 25.49
Matches 125; Conservative
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ųd

#St

16;

63;

Length 479; Indels

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3-phytase (EC 3.1.3.8) B precursor - Aspergillus ficuum
N.Alternate names: pH 2.5-optimum acid phosphatase
C; Species: Aspergillus ficuum
C; Species: Aspergillus ficuum
C; Species: 14-041-1994 #sequence_revision 19-oct-1995 #text_change 07-May-1999
C; Accession: JN0715; PN0594; PN0460
R; Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J
Biochem: Biophys. Res. Commun. 195, 53-57, 1993
A; Title: Identification and cloning of a second phytase gene (phyB) from Aspergillus A; Reference number: JN0715; MUD:93371452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: PN0594
A;Accession: PN0594
A;Molecule type: protein
A;Residues: 20-101;133-146;376-399 <EH2>
A;Residues: 20-101;133-146;376-399 <EH2>
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A;Title Identification of active-site residues in Aspergillus ficuum extracellular p
A;Reference number: PN0460; MUID:93249452
A;Accession: PN0460
                                                                    A;Residues: 1-479 <PID>
A;Cross-references: GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482
A;Cross-references: strain ALK0243
C;Comment: The highly similar enzyme from A. ficuum has been shown to have 3-phytase C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                      A introns: 261/1; 300/2; 335/2

C;Superfamily: yeast acid phosphatase

C;Superfamily: yeast acid phosphatase

C;Superfamily: yeast acid phosphatase

C;Superfamily: yeast acid protein; glycoprotein; phosphohistidine; phosphoprotein; l

E;1-19/Domain: signal sequence #status predicted <NGS

F;20-479/product: 3-phytase #status predicted <NAT>

F;81,337/Active site: Arg, His #status predicted

F;82/Active site: His (phosphohistidine intermediate) #status predicted

F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 GPYSERVSY---GIARDPPTSCEVDOVIMVKRHGERYPSPSAGKDIEEALAKVYSINTT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 IRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVII-PEGSGYNNTLDHGTCT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 TDNDQTTCDNLTYQLPQFKVAA--ARLNSQNPGMNLTASDVYNLMVMASFELNAR---- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDAT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 GTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPTSSASK-AYSALIEAIQKNAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GENOMVNSGIKFYRRYKAL--ARKIVPF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLY -- NGTKPLSTTSVESIEETDG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AGSLFFNFAHDTNITPILAALGVLIPNEDLPL----DRVAFGNP 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 F-SSGYGRVIETARKFGEGFFGYN-----YSTNAALNIISESEVMGADSLTP--TCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLTLLNQGPKE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 YSIGNIVPMGGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 347.5; DB 1
Pred. No. 3.9e-20;
!; Mismatches 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.1%; Practices 118; Conservative 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
A, Residues: 1-479 <EHR>
A, Cross-references: GB:L20567
                               A; Molecule type: DNA
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C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Species: Aspergillus awamori
C;Accession: JN0890
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optim
A;Reference number: JN0889; MUID:94040796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g1430996; PIDN:CAA98583.1; PID:g1430997; MIPS:YDL02
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                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
C;Species: Saccharomyces cerevisiae
C;Accession: S52495, $sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C;Accession: S52495, $sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C;Accession: S52495
R;Addrev, B.; Vissers, S.; Urrestarazu, L.
Submitted to the EMBL Data Library, February 1995
A;Description: The sequence of a 42 kb segment located on the left arm of chrom A;Reference number: S52492
A;Accession: S52495
A;Reference number: S488C
B;Urrestarazu, L.A.; Andre, B.; Vissers, S.
Submitted to the Protein Sequence Database, July 1996
A;Reference number: S67835
A;Reference number: S67835
A;References: EMBL:Z74072; NID:g1430996; PIDN:CAA98583.1; PID:g1430997; MA;References: EMBL:Z74072; NID:g1430996; PIDN:CAA98583.1; PID:g1430997; MA;References: EMBL:Z74072; NID:g1430996; PIDN:CAA98583.1; PID:g1430997; MA;References: EMBL:Z74072; Map position: 4L
C;Superfamily: yeast acid phosphatase
                  Species: Saccharomyces cerevisiae
Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|||| | :| | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 FEL----NAKGYSNICDIFSAAELIHYSYETDLTSFYQNGPGYKLIKSIGANLFNATVK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLS 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------LDQKVWLSFTHDTDILNYLTTAGLIDDTRNLT 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 YNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 NCTNFPIFTTNSKRIYDTAQYFAEALGDGFNISLQTLSENSS-
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Matches 114; Conservative
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Best Local Similarity 24.8
Matches 99; Conservative
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thiamin_repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T39929
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
A;Reference number: 221857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 IRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVII-PEGSGYNNTLDHGTCT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 F-SSGYGRVIETARKFGEGFFGYN-----YSTNAALNIISESEVMGADSLTP--TCD 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 AFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDAT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 ELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GENOMVNSGIKFYRRYKAL--ARKIVPF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLY -- NGTKPLSTTSVESIEETDG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAY-SALIEAIQKNAT 107
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29.3%; Pred. No. 4.7e-20;
tive 54; Mismatches 170;
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Superfamily: yeast acid phosphatase
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Matches 114; Conservative
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Best Local Si
Matches 1199
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acid phosphatase (EC 3.1.3.2) precursor [similarity] - fission yeast (Schizosaccharom C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 10-Sep-1999 #text_change 21-Jul-2000 C; Accession: A25326; T50405 R; Elliott, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J. J. Biol. Chem. 261, 2936-2941, 1986 A; Title: Isolation and characterization of the structural gene for secreted acid phos
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A;Cross-references: EMBL:AL137099; PIDN:CAB68657.1; GSPDB:GN00067; SPDB:SPBP4G3.02
A;Experimental source: strain 972h(-); clone pl p4G3
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C;Keywords: phospholistidine; phosphoprotein; phosphoric monoester hydrolase
F;68/Active site: Arg #status predicted
F;69/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                 89 LNNFQEKLLNGSIPVNFSYPENPLCFIKQWTPVIDAENADQLSSRGRLELFDLGRQLYQR 148
                                                                                                                                                                                                                                                                                                                                                                                      ----FILISEGKAA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 LMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGF 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | : |:||: |-||: | INNLADSL-----RNVTNPDFDRK------VFLAFTHDSNIIPVEAALGFFPDIT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVD 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGENQMVNSGIKFYRRYKALARKIVPF 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LIEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGENQMVNSGIKFYRR
                                                                                                                                                                                                                                                                                                              YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEG--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GANSLSMYNACPVFKDNNFHKNATDAAHAVWRNIFIEPIVNRLAKYFDSSYKLTINDVRS
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                                            HLWGTYS----PYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPTS--SASKAYSA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1%; Score 297; DB 1; I 24.8%; Pred. No. 4.3e-16; iive 60; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLGR----CKRDDFVEGLSFARSGGNWAECF 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 PSGTSDGLCELQAYLNSPIRANSTSNGISIF 448
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A; Accession: A25326
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histidine acid phosphatase (EC 3.1.3.-) - Arabidopsis thaliana histidine acid phosphatase (EC 3.1.3.-) - Arabidopsis thaliana (Grant Cress)
C.Species: Arabidopsis thaliana (Mouse-ear cress)
C.Species: Jaul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C.Species: Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C.Species: Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C.Species: Jul-1999 #sequence_revision 25-Jul-1999
Biochem: Biophys: Res. Commun. 251, 252-255, 1998
A.Reference number: JE0369; MUID:99009256
A.Reference number: JE0369; MUID:99009256
A.Retus: preliminary
A.Rocession: Jef6 Auu.>
C.Superiamily: yeast acid phosphatase
C.Superfamily: yeast acid phosphatase
C.Superfamily: yeast acid phosphatase
                                                               260 IMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGF 319
                                                                                                                                                                                                                                                                                                                                    359 PEHPLPTDKNIFTYSLKTSSEVPFAGNLITELFLC-SDNKYYVRHLVNQQVYPLTDCGYG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 LGIRVRERPPSLFEEDYHPDVYTIRATQIPRASASAVAFGMGLFSEK----GNL----- 179
      GANSLAMYYSCPVYEDNNIDENTTEAAHTSWRNVFLKPIANRLNKYFDSGYNLTVSDVRS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : :| | | | : ::| 72 LREMESLAGREKELVRDAEARKLPSDKIPGWLGGWK--SPWEGKVKGGELIRQGEDELYQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 NYKMGV----PLLEDVLHSMEEAIKAREEKLP--PGSYE-KARL--RFAHAETIVPPFSC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 -LGLYNGTKPLSTTSVESIE------ETDGYSASWTVPFAARAYVEMMQCQAEK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---- GKYAFLKTYNYTLGADDLTPFGENOMVN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGIKFYRRYKALARK----IVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 VINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTD 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 EDVVYLMDMC---PFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 EPVLNKITASVAKRYDLKFTKQDISSLWFLCKQVALLEW----TDDLEVFLLKGYGNSL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 GPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 DGGF----DVRHHLSTVTRYSTSKDVTQNLIEGSNVPSECTPIHLNLVARHGTRSPTKKR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 DGGYQCFPEISHLWGTYSPYFSLAD--ESAI-SPDVPDDCRVTFVQVLSRHGARYPTSSA 91
                                                                                                                                                                                                                    320 ANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTK
                                                                                                                                                                                                                                                                                                   PLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVD
                                                                                                    260 LYYICVYEIALRDN-----SDFCSLFTPSEFLNFEYDSDLDYAYWGGPASEWASTLGGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%; Score 149; DB 2; Length 465; 22.3%; Pred. No. 0.00037; ive 63; Mismatches 199; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 SKAYSAL---IEAIQKNATAFK---
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Matches 101;
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Schioosaccharomyces pombe
C;Species: Schioosaccharomyces pombe
C;Accession: S14119; T40455
R;Yang, J.; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990
A;Title: The structural gene coding for thlamin-repressible acid phosphatase in Schioosa
A;Accession: S14119
A;Status: preliminary
A;Reference number: S14119; MUID:91064763
A;Accession: S14119
A;Status: preliminary
A;Residues: 1-463 <ANA
A;Cross-references: GB:X56939; NID:95006; PIDN:CAA40258.1; PID:95007
A;Residues: 1-463 <ANA
A;Residues: 1-463 <ANA
A;Residues: 221931
A;Recison: T40455
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Residues: 1-463 <ANA
A;Re
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SVPIDXSVSGNPLSFVPTWTPVIEAANADALSSSGRVELFDMGRQFYERYHELFNASTYN 156
                                                                                                                                                                                                              277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDADDFTTPALEAWRNVYMPPIRQRLNPYFSNYNLTNDDILNLYGICSYEIALQ-----D 264
                                                                                                                                                                                                                                                                                                                              LSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTS 337
                                                                                                                                                                                                                                                                                                                                                                                  265 YSEFCKLFNSVDFLNFEYEGDLSFSYGMGNSVKWGSIFGGAYANSLANSL--RSVENNTQ 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 TNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LIEALQKNATAFKGKYAFLKTYNYTL---GADDLTPFGENQMVNSGIKFYRR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 IDIFQNKLLNGSIPVNFSYPENPLYFVKHWTPVIKAENADQLSSSGRIELFDLGRQVFER 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 GYNNTLDHGTCTAFEDSELGDD-VEANFTA---LFAPAIRARLEADL-PGVTLTDEDVVY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPE--GS 204
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                                                                                                                                                                                                           FEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATE
                                                                                           IRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 SWIVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGC 436
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Matches 108; Conservative
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Search completed: October 26, 2001, 15:10:29 Job time: 6335 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2001, 15:18:03; Search time 29.88 Seconds (without alignments) 535.385 Million cell updates/sec Run on:

US-09-488-265-29
2462
1 MGVEVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWAECFA 467 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 segs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | escriptio      | P34753 asperdillus | 4752 aspergillu | 93         | P35842 saccharomyc | P38693 saccharomyc |            | P24031 saccharomyc |            | sacchar    | P34754 aspergillus |            |            |            | Q01682 schizosacch | Q09549 caenorhabdi | P24638 mus musculu | P20611 rattus norv | Q9y678 homo sapien | -          |            | P50126 candida mal | P53620 bos taurus | P20646 rattus norv | P16721 human cytom | _          | Q10944 caenorhabdi | Q09451 caenorhabdi | P37201 candida tro | P29750 thermomonos | P10209 herpes simp | S        | 00   | P39679 kluyveromyc |
|-----------|----------------|--------------------|-----------------|------------|--------------------|--------------------|------------|--------------------|------------|------------|--------------------|------------|------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|------------|--------------------|-------------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|------|--------------------|
| SUMMARIES | ID             | PHYA_ASPAW         | PHYA_ASPNG      | PHYB_EMENI | PPAB_YEAST         | PPAC_YEAST         | PPA5_YEAST | PPA3_YEAST         | PPA1_PICPA | PPAD_YEAST | PHYB_ASPNG         | PHYB_ASPAW | PPA5_KLULA | PPA1_SCHPO | PPA2_SCHPO         | PPAX_CAEEL         | PPAL_MOUSE         | PPAL_RAT           | COPG_HUMAN         | NICA_CAEEL | PPAL_HUMAN | NCPR_CANMA         | COPG_BOVIN        | PPAP_RAT           | UL11_HCMVA         | PPAP_HUMAN | PPAY_CAEEL         | PPAW_CAEEL         | NCPR_CANTR         | AMY_THECU          | UL25_HSV11         | - 1      |      | MBP1_KLULA         |
|           | DB             | :                  |                 |            | <b>.</b>           |                    |            |                    |            |            | <del>.</del>       |            |            |            |                    |                    |                    |                    |                    |            |            |                    |                   |                    |                    |            |                    |                    |                    |                    |                    |          |      |                    |
|           | Length         |                    | 467             | 463        | 467                | 467                | 467        | 467                | 4.68       | 468        | 479                | 479        | 469        | 453        | 463                | 755                | 421                | 423                | . 874              | 721        | 423        | 089                | 874               | 381                | 275                | 386        | 411                | 413                | 680                | 605                | 280                | 602      | 760  | 754                |
| dР        | Query<br>Match | 9                  |                 | 4.         | 16.0               | ė.                 | Ω          | S.                 | 4.         | 4.         | 4                  | 4          | e,         | 12.1       | Η.                 | ٠                  | •                  | •                  | ٠                  | •          |            | •                  | •                 | 4.0                | •                  | ٠          | ٠                  |                    | e.<br>و.           | •                  | •                  | æ.<br>œ. | •    |                    |
|           | Score          | Н                  | 1875            | 1835.5     | 395                | 395                | 392        | 380                | 355        | 354        | 348.5              | 347.5      | 341.5      | 297        | 278.5              | 130                | 124.5              | 114.5              | 113                | 112        | 102.5      | 101.5              | 101               | 98.5               | 96.5               | 96.5       | 96                 | 96                 | 95.5               | 95                 | 94.5               | 94.5     | 94.5 | 94                 |
|           | Result<br>No.  | н                  | 7               | m          | 4                  | N.                 | 9          | 7                  | œ (        | on :       | 10                 | 11         | 12         | 13         | 14                 | 15                 | 16                 | 17                 | 18                 | 19         | 20         | 21                 | 77                | 23                 | 24                 | 25         | 26                 | 27                 | 28                 | 67                 | 30                 | 31       | 32   | 33                 |

| beta vulgar | 004931 | AGLU_BETVU | Н           | 913  | 3.6 | 88.5 | 45 |
|-------------|--------|------------|-------------|------|-----|------|----|
| saccharomyc | P38928 | AXL2_YEAST | Н           | 823  | 3.6 | 68   | 44 |
| manchester  | 069014 | POLN_MANCV | Н           | 2208 | 3.6 | 89.5 | 43 |
| schizosacch | 010061 | YAM6_SCHPO | П           | 848  | 3.6 | 89.2 | 42 |
| clostridium | P09870 | CLOS_CLOHI | <del></del> | 526  | 3.6 | 89.2 | 41 |
| saccharomyc | 008193 | YOD0_YEAST | П           | 484  | 3.7 | 90   | 40 |
| thermoanaer | P19584 | AMYB_THETU | Н           | 551  | 3.7 | 91   | 39 |
| solenostemo | 042662 | METE_SOLSC | Н           | 764  | 3.7 | 92   | 38 |
| schizosacch | 013712 | YDZ5_SCHPO |             | 844  | 3.8 | 92.2 | 37 |
| providencia | 052309 | AGP_PRORE  | 7           | 417  | 3.8 | 92.5 | 36 |
| human herpe | P52340 | TEGU_HSV6U | -           | 2077 | 3.8 | 93.5 | 35 |
| human herpe | P30002 | TEGU_HSV6G | П           | 2077 | 3.8 | 93.5 | 34 |
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                             SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                 61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
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                                                                                                                                                   Gaps
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                                                                                                                                                                                           1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Last sequence update)
1-CCT-2000 (Rel. 40, Last annotation update)
3-PHYTASE A PRECURSOR (FC 3.1.3.8) (WAYO-INOS/TOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBL_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                       1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE
                                                                                                                                                                                                                                                                                             181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR
        (POTENTIAL).
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(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIM-NRL 3135 / VAN TIEGHEM, FICUUM,
MEDLINE-9225284; PUDbed-8387447;
van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M.,
Gouka K.J., Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A.,
Selten G.C.M., Veenstra A.E., van Gorcom R.F.M.,
van den Hondel C.A.M.J.J.;
                                                                    (POTENTIAL)
                                                                             (POTENTIAL)
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0
                                                                                                                              76.3%; Score 1879; DB 1; Length 467; 75.6%; Pred. No. 6.3e-143; Live 41; Mismatches 73; Indels
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388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOHYDROLASE A).
                                                                                                 467 AA;
                                                                                                                                        Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Cloning, characterization and overexpression of the phytase-encoding gene (phya) of Aspergillus niger."; Gene 127:87-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
-!- BOTDECHNOLOGY: IS USED AS A FOOD AND FEED ADDITIVE. IT CAN FACILITATE THE DEGRAPATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS USED AS FOOD FOR MONOGASTRIC ANIMALS. SOLD BY NOVO NORDISK UNDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell D., van Loon A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-PHYTASE A. NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Aspergillus ficuum phytase: complete primary structure elucidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resolution.";
Nat. Struct. Biol. 4:185-190(1997).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Aspergillus ficuum phytase: partial primary structure, substrate selectivity, and kinetic characterization."; Prep. Biochem. 18:459-471(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.; "Cyclohexanedione modification of arginine at the active site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Crystal structure of phytase from Aspergillus ficuum at 2.5-A
                                                                                                                                                                                                                    Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 192:747-753(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus ficuum phytase.";
Biochem. Biophys. Res. Commun. 178:45-53(1991).
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-TAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE-97307250; PubMed=9164457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 71-93.
STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=91298982; PubMed=1648914;
                                                                                                                                                                                                                                                                                                                      STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE-93249451; Pubmed-8387289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION, AND PARTIAL SEQUENCE. STRAIN-NRRL 3135 / VAN TIEGHEM. / FICUUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89160685; PubMed=2852807;
                                                                                                                                                                                                                                                                                                                                                                                                         Dischinger H.C. Jr.
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EMBL; M94550; AAA32705.1; -.
PIR; JN0482; JN0482.
PIR; PN0023; PN0023.
PIR; JN0656; JN0656.
PDB; IIHP; 18 MAR-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by chemical sequencing.
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                                                                                                                                                   SEOUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXARISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                             KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
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                                                                                                                                                                                                             0;
                                                                                                                                                                                   76.2%; Score 1875; DB 1; Length 467; 75.6%; Pred. No. 1.3e-142; live 41; Mismatches 73; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBL_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98007872; PubMed-9349716;
Pasamontes L., Halker M., Henriquez-Huecas M., Mitchell D.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).

NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 YTLGADDLTIFGENQMVDSGAKFYRRYKNLARKNTPFIRASGSDRVVASAEKFINGFRKA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thermophilic fungus Talaromyces thermophilus.";
Biochim. Biophys. Acta 1353:217-223(1997).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.6%; Score 1835.5; DB 1; Length 463; 74.0%; Pred. No. 1.9e-139; Live 46; Mismatches 70; Indels 5;
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                      "Cloning of the phytases from Emericella nidulans and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (PORTION ECC5827D1E1C82A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
3-PHYTASE B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE. -!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE. -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-55249563; PubMed-7731988; Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N., Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
ACID PHOSPHATASE PHOII.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Chen J.Y., Gong Y.I., Ao S.Z.;

Chen J.Y., Gong Y.I., Ao S.Z.;

"The primary structure of acid phosphatase gene PHO11 in S.

cerevisiae and comparison with other gene families.";

Acta Biochim. Biophys. Sin. 21:437-444(1989).

-i - CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
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                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                       421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECF 466
                                           416 LURVINDRVVPLHGCAVDKFGRCTLDDWVEGLNFARSGGNWKTCF 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .)
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                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACID PHOSPHATASE PHO11 PRECURSOR (EC 3.1.3.2) (P56).
                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .)
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PROSITE; PSOU778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
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STRAIN=S288C / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 SIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 NYLTTIGIIDDKNNLTAEHVPFMENT--FHRSWYVPQGARVYTEKFQC--SNDTYVRYVI 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 NISLQ-----TISEAESAGANTLSAHHSCPAMDD-DVNDDILKKYDTKYLSGIAKRLNKE 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 ERYPTVSKAKSIMTTWYKLSNYTGQFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                21 PLGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDLPESCEMKOVQMVGRHG 76
                                                                                                                                                                                                                                                                                                            24 PRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHG 83
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                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                 Length 467;
                                                                                                                                                                                                                                                                   207; Indels
                                                                                                                                           AECDC1C046B326C3 CRC64;
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-> L (IN REF. 2).
                       A -> L (IN REF. 2).

VS -> AR (IN REF. 2).

R -> H (IN REF. 2).

C -> G (IN REF. 2).

D -> G (IN REF. 2).
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                                                                                                                                                                                                                    16.0%; Score 395; DB 1;
26.0%; Pred. No. 3.7e-24;
tive 66; Mismatches 207
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
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                                                                                                                                              52757 MW;
                                                                                                                                                                                                                                                                        Matches 119; Conservative
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83
150
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423
467 AA;
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P38693:
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
             INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE. PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE. SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYG 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACID PHOSPHATASE PHO12.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
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 + ORTHOPHOSPHATE.
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SGD; S0001258; PHO12.
InterPro; IPR000560; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C;
MEDLINE=9520837; PubMed=7900426;
Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                        Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.; "The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repressible acid phosphatase contains a signal peptide."; Nucleic Acids Res. 11:167-1672(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cluster within the acid phosphatase multigene family of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88037940; PubMed-6093051; Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.; "Structural analysis of the two tandemly repeated acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE.
-i- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONDESTER + H(2)0 = AN ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                             Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott Q.D.,
Bostian S.J., Thill G.P., Rogers D.T., Bostian K.A.;
"Reciprocal regulation of the tandemly duplicated PHO5/PHO3
                                                                                                                                                                01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (P60).
467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 18-45.
                                                                                                                                                                                                                          PHO5 OR YBR093C OR YBR0814.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 18-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 12:7721-7739(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell. Biol. 6:1855-1865(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: SECRETED
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83168913; PubMed=6300772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87064474; PubMed-3537710;
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                                                                                                                                                    (Rel. 01, Created)
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EMBL, X01079; CAA2555.1; -.
EMBL, X78993; CAA55581; -.
EMBL, Z35962; CAA85046.1; -.
EMBL, X01080; CAA25556.1; -.
PIR, S05795; PABYC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-44 FROM N.A.
                                                                                                               STANDARD;
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SGD; S0000297; PHO5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qenes in yeast,
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                                                                                                                                                  21-JUL-1986
                                                                                                           PPAS_YEAST
P00635;
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SNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPF 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 DLPEGCEMKOLOMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 DDDDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQYGYMVENOTSFAVFTSNSKRCHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 SAEKFIEGFQSAKLADPGSQPHQASPVINVII-----PEGSGYNNTLDHGTCTAFEDSEL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 TAQYFIDGL-----GDQ----FNITLQTVSEAESAGANTLSACNSCPAW-DYDA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 GDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 NDDIVNEYDTTYLDDIAKRLNKENKGLNLTSTDASTLFSWCAFEV-----NAKGYSDVCD 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 IFTKDELVHYSYYQDLHTYYHEGPGYDIIKSVGSNLFNASVKLLKOSEIQDQ----- 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 DVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK-TYNYTLG 124
                                                                                                                                                                                                                                                                                                                                                                                                           78; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VVYSILAASLANAGTI--PLGKLADVDKIGTOKDIFPFL----GGAGPYYSFPGDYGISR 58
                                                                 SIMILARITY).
                                                                                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                         (POTENTIAL)
                                                                              PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                          (POTENTIAL)
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                                                      REPRESSIBLE ACID PHOSPHATASE
                                                                  NUCLEOPHILIC ACCEPTOR (BY
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                                                                                                      N-LINKED GECONAC...)
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                          D -> Y (IN REF. 1).
A -> G (IN REF. 1).
H -> Q (IN REF. 1).
S -> V (IN REF. 1).
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Best Local Similarity 25.6%
Matches 123; Conservative
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P24031;
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                                                                                                                                                                                                                                                                                                                      Mannhaupt G., Stucka R., Ennle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
Yeast 10:1363-1381(1994).
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
ALCOHOL + ORTHOPHOSPHARE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHARASE FAMILY.
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PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                             MEDIJUE-85037940; PubMed-6093051; Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.; "Structural analysis of the two tandemly repeated acid phosphatase
                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBL_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Mismatches 196; Indels
01-MAR-1992 (Rel. 21, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CONSTITUTIVE ACID PHOSPHAFASE PRECURSOR (EC 3.1.3.2).
PHO3 OR YBR092C OR YBR0813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
HydroLase; Glycoprotein; Signal; Multigene family.
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                                                                                 Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                genes in yeast.";
Nucleic Acids Res. 12:7721-7739(1984).
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336 N-
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443 N-
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456 N-
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Best Local Similarity 26.3%
Matches 114; Conservative
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HSSP; P34752; 11HP.
SGD; S0000296; PHO3.
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467 AA;
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| 7 7 | OY 153 KIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPGSOPHOASPVINVIIPEGSGYNNTLD 211  DD 162 NQTSFPIFAASSERVHDTAQYFIDGL | QY 272 TSDATELSPECALÈTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSP 331  Db 271GYSDVCDIFTEDELVRYSYGQDLVSFYQDGPGYDMIRSVGANLFNATLKLLKQSE 325 | OY 332 VODHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEE 391 | QY 392 TDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDF 449   : | OY 450VEGLSFAR 457  Db 424 YAEKRVAGTDFLK 436 | RESULT # # PPAL_PICPA STANDARD; PRT; 468 AA.   DPAL_PICPA |
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21;
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                         SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIE-AIQKNATAFKGKYAFLKTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VLLSIATL - - - FGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPY - - FSLADE
                                                                                                                                                                                                                                                           120 NYTLG-----ARKIVPFIRASGSDR
                                                                                                                                                                                                                                                                                                           166 VIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPE---GSGYNNTLDHGTCT----A
                                                                                                                                                                                                                                                                                                                                                                                                                  394 GYSASWIVPFAARAYVEMMQC--QAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Uskraryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
                                                                                                                                          90;
                                                                                                                 Score 355; DB 1; Length 468;
Pred. No. 6e-21;
9; Mismatches 199; Indels
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15-JUL-1999 (Rel. 38, Last annotation update)
PROBABLE ACID PHOSPHATASE YDL024C PRECURSOR (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 AA
                                                                                                                  Ouery Match
14.4%; Soc
Best Local Similarity 25.4%; Pre
Matches 125; Conservative 79;
                                                                                  MM.
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163
196
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360
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52690
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468 AA;
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P52290;
  ACT_SITE
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                                                                                             entities requires.a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch). |
                                                                                                                                                                                                                                                                                                                PROBABLE ACID PHOSPHATASE YDL024C.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 GTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 GGSAPYFSFPANYGIPTDIPEGCRLTQVQMIGRHGERYPTRSEAKDIFEVWYKISNYIGK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GADDLTPF-GENQMVNSGIKFYRRYKALAR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 YEGSLSFLNNGYEFFIPDESLLEMETTLONSIDVLNPYTGEMNAKRHAREFLAKYGKLME 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 ANTLAAKSSCPNW-NSWANNDILMSYSRDYLENISDRLNDENKGLNLSRKDAAALFSWCA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFAN---E 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 FEL-----NAKGYSNICDIFSAAELIHYSYETDLTSFYQNGPGYKLIKSIGANLFNATVK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLS 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 KIVPF-IRASGSDRVIASAEKFIE----GFQSA--KLADPGSQPHQASPVINVIIPEGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 YNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4%; Score 354; DB 1; Length 468; 25.9%; Pred. No. 7.2e-21; Live 63; Mismatches 183; Indels
                                                                                                                                                                                                                    PROSTE; PF00228; acid_phosphat; 1. PRO0228; acid_phosphat; 1. PROSTE; PS00616; HIS_ACID_PHOSPHAT_1; 1. HYGNOIRE; PS00778; HIS_ACID_PHOSPHAT_2; 1. Hydrolase; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53076 MW;
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SGD; S0002182; YDL024C.
InterPro; IPR000560; -.
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                                                                             416 SCEEGTFYEYAKDRLRGVSF 435
                                                     --GLSF 455
                                                     443 RCKRDDFVE--
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RESULT 10 PHYB\_ASPNG

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Last annotation update)
(EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
(3 PHYTASE B) (MYO-INOSITOL HEXAKISPHOSPHATE Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus -! - FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE Ehrlich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr., D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE. "Identification and cloning of a second phytase gene (phyB) from (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL). SEQUENCE FROM N.A., AND SEQUENCE OF 20-101; 133-141 AND 376-399. MEDLINE=93371452; Pubmed=7916610; N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL) (POTENTIAL) 63; -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O Length 479; Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; REQUIRED FOR BINDING SUBSTRATE Indels Usage by 395D4DA2B50FDFC4 CRC64; (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) GLCNAC. . . 169; DB 1; Aspergillus niger (ficuum)."; Biochem. Biophys. Res. Commun. 195:53-57(1993) 14.2%; Score 348.5; DB 29.3%; Pred. No. 2e-20; iive 55; Mismatches 1 (GLCNAC modified and this statement is not removed. (BY SIMILARITY) 479 AA Interpro; IPR000560; -..;
Pfam: PF00328; acid\_phosphat; 1.
PROSITE; PS00016; HIS\_ACID\_PHOSPHAT\_1; 1.
PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; 1.
Hydrolase; Glycoprotein; Signal. 3-PHYTASE N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED LINKED PRT; Created) MM; EMBL; L20567; AAA02934.1; -. 82 337 106 191 227 227 250 315 425 448 458 Conservative STANDARD; 479 81 (Rel. 28, (Rel. 28, 1 3-PHOSPHOHYDROLASE B) (Rel. 29, PRECURSOR PHOSPHOHYDROLASE B) Query Match Best Local Similarity Aspergillus niger. FROM PHYTATE. 442 458 479 F NCBI\_TaxID=5061; 3-PHYTASE B 01-FEB-1994 Ullah A.H.J. 01-JUN-1994 119; PHYB\_ASPNG P34754; ACT\_SITE CARBOHYD ACT\_SITE ACT\_SITE CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD SEQUENCE SIGNAL CHAIN Matches 49 qq δy qq Qγ

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                                    218 TDNDQTTCDNLTYQLPQFKVAA--ARLNSQNPGMNLTASDVYNLIVMASFELNAR---- 270
217 AFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDAT 276
                                                                           277 ELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHT 336
                                                                                                            271 PFSNWINAFTODEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLTLLNGGP---- 325
                                                                                                                                                      STNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLY --NGTKPLSTTSVESIEETDG 394
                                                                                                                                                                                           326 ----KEAGP-----DRVAFGNP 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A., Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.; "The cloning and sequencing of the genes encoding phytase (phy) and PH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kostrewa D., Wyss M., D'Arcy A., Van Loon A.D., "Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Mol. Biol. 288:965-974(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE. + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE B) (PH 2.5 OPTIMUM ACID PHOSPHATASE).
                                                                                                                                                                                                                                  395 YSASWIVPFAARAYVEMMQCQA----EKEPLVRVLVNDRVVPLHGC 436
                                                                                                                                                                                                                                                                 368 YSIGNIVPMGGHLTIERLSCQATALSDKGTYVRLVLNEAVLPFNDC 413
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Pfam; PF00328; acid_phosphat; 1.
PR003TE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; 3D-structure.
GTGNAI.
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MEDLINE-99264417; PubMed=10329192;
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PDB; 1QFX; 19-APR-00.
InterPro; IPR000560; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus awamori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                      53 GPYSERVSY----GIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINTT 108
                                                                                                                                                                                                                                                                                                                                              158 IRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVII-PEGSGYNNTLDHGTCT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                              217 AFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDAT 276
                                                                                                                                                                                                                                                                  49 GTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPTSSASK-AYSALIEAIQKNAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 ELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHT 336
                                                                                                                                                                                                                                                                                                                           108 AFKGKYAFLKTYNYTL----GADDLT-PF-GENQMVNSGIKFYRRYKAL--ARKIVPF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLTLLNQGPKE--- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 STNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLY--NGTKPLSTTSVESIBETDG 394
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AGSLFFNFAHDTNITPILAALGVLIPNEDLPL-----DRVAFGNP 367
                                                                                                                                                                                                                                                                                                                                                                                                               169 F-SSGYGRVIETARKFGEGFFGYN-----YSTNAALNIISESEVMGADSLTP--TCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 TDNDQTTCDNLTYQLPQFKVAA--ARLNSQNPGMNLTASDVYNLMVMASFELNAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE (BY SIMILARITY).
-!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thesis (1995), University of Salamanca, Spain.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                             Length 479;
                                                                                                                                                                                                                                      54; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 YSASWIVPFAARAYVEMMQCQA----EKEPLVRVLVNDRVVPLHGC 436
                                                                                                                                               -LINKED (GLCNAC. . .).
4F8E0F3778CC3B08 CRC64;
                                                                                                                   N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update) ;
ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
3-PHYTASE B.
NUCLEOPHILIC ACCEPTOR.
PROTON DONOR.
                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                          Score 347.5; DB 1 Pred. No. 2.5e-20;
                                                                                                                                                  N-LINKED
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479 3-
82 NN
337 PF
472
441
421 N-
1191 N-
52678 MW;
                                                                                                                                                                                                          14.18;
                                                                                                                                                                                                                                      Matches 118; Conservative
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                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                            479 AA;
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                the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 TY-NGDLGDEYFENATLPYLTDIKNRWMKKNSNL-NLTLEHDDIELLVDWCAFETNVKGS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 DGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDF--- 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 -----NDPLEVENDYEFFVSNTKYFDQLTNSTDVDPSNPYAGAKTAQHLGKYIAYNYGD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 -ASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEG--SGYNNTLDHGTCT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 LFSDSNPVFTSSSGRVH--QTAKYVVSSLEBELDIQLDLQIIQENETSGANSLTPADSCM 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 DATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQ 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 DESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCF-----PEISHLWGTYSPYFSLA 58
                                                                                                                                                                                                                                                                 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC...)
                                                                                                                                                                pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00738; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
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                                                                                                                                                   InterPro; IPR000560; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGENQMVNSGIKFYRRYKALARKIVPF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 HKPYF----YGPSIDFPTTCKIKQVHTLQRHGSRNPT-GGNAAFDAVGIANFQQRLLNG 96
                                                                                                                                                                                                                                                  "Isolation and characterization of the structural gene for secreted acid phosphatase from Schizosaccharomyces pombe.";
J. Biol. Chem. 261:2936-2941(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                           Elliott S., Chang C., Schweingruber M.E., Schaller J., Rickli E.E.,
                                                                                                                                                                                                                                                                                                                                           Rieger M., McDougall R.C., Rajandream M.A., Barrell B.G.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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-!- INDUCTION: REPRESSED BY PHOSPHATE AND WEAKLY BY THIAMINE
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                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                          (Rel. 08, Last sequence update) (Rel. 40, Last annotation update)
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PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Cell wall; Signal.
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                              01-AUG-1988 (Rel. 08, Created)
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EMBL; AL137099; CAB68657.1; -
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   STANDARD;
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330
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                                                                                                                                                      Schizosaccharomyces.
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HSSP; P34752; 11HP.
                                                                                            PHO1 OR SPBP4G3.02.
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                                                            01-OCT-2000
                                            01-AUG-1988
                                                                                                                                                                                                                                                                                                                                   STRAIN=972;
PPA1_SCHPO P08091;
                                                                                                                                                                                                                                               Carbon J.;
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STATEMENT STATEM
                                                                                                                                                   158 IRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTA 217
                                                                                                                                                                                                                                                                                                                                                                                                                      157 IYTAAQQRVVDSALWYGYGMF-----GEDVHNFTNYILVSENATAGSNSLSSYNACPA 209
                                                                                                                                                                                                                                                                                                                                                       218 FEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 LSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 YSEFCKLFNSVDFLNFEYEGDLSFSYGMGNSVKWGSIFGGAYANSLANSL--RSVENNTQ 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 ------QVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMKA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 INHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 19-30.
MEDLINE-91064763; PubMed=2249257;
Yang J., Schweingruber M.E.;
"The structural gene coding for thiamin-repressible acid phosphatase in Schizosaccharomyces pombe.";
Curr. Genet. 18:269-272(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: MAY DEPHOSPHORYLATE THIAMINE PHOSPHATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: CELL WALL.
-:- INDUCTION: REPRESSED BY THIAMINE.
-:- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
THIAMINE-REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyne M., Rajandream M.A., Barrell B.G., Baker S., Mungall K., Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWIVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 SEFVPFAGNLITELFQCEDSKY-YVRHLVNEEVFPLSDC 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X56939; CAA40258.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000560; -.
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SEQUENCE FROM N.A.
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Q01682;
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PPA2_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                        89 IDIFQNKLLNGSIPVNFSYPENPLYFVKHWTPVIKAENADQLSSSGRIELFDLGRQVFER 148
                                                                                                                                                                                                                                                                                                                                                                                                                      205 GYNNTLDHGTCTAFEDSELGDD-VEANFTA---LFAPAIRARLEADL-PGVTLTDEDVVY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 PLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 PEHPLPTDKNIFTYSLKTSSEVPFAGNLITELFLC-SDNKYYVRHLVNQQVYPLTDCGYG 417
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                      46 HLWGTYS----PYFSLADESAISPDVPDDCRVTFVQVLSRHGARYPT--SSASKAYSA-- 97
                                                                                                                                                                                                                                                                                                               35 HL-GTISVYHEPYF----NGPTTSFPESCAIKQVHLLQRHGSRNPTGDDTATDVSSAQY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                               SIMILARITY).
                 THIAMINE-REPRESSIBLE ACID PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                             98 -----LIEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGENQMVNSGIKFYRR
                                                                                                                                                                                                                                                                                                                                                                                                    147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPE--GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matthews P., Lloyd C., Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 LMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 ANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTK
                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                           63;
                                                                      (POTENTIAL)
                                                                                                                                                          (POTENTIAL)
                                                                                                               (POTENTIAL)
                                                                                                   (POTENTIAL)
                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                            11.3%; Score 278.5; DB 1; Length 463; 25.5%; Pred. No. 7.8e-15; Live 65; Mismatches 187; Indels 63
                             NUCLEOPHILIC ACCEPTOR (BY SIPPROTON DONOR (BY SIMILARITY)
                                                                                                                                                                      N-LINKED (GLCNAC. ) (PC
F48EAFF8BB6B234A CRC64;
                                                                    N-LINKED GECONAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPAX_CAREL STANDARD; PRT; 755 AA. 009549; Q17843; Q17843; Q178423; Q1. 01-NOY-1995 (Rel. 32), Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).
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18
463
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463 AA;
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PPAX_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 -----TCTAFED----SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 QCAVAQLCNCRRFQELQEKWAEL-DEVKNATVAMI--ALNRRVAA---FYNVTDQP---- 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 -----EKFNRYIDAWK----CQRNWFNDTMYQQLPWYNBDLYNBAQRIYAPFKRFTEGN 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 AGNP------LGPAQGVGFANELIARLTHSPVQDHTSTNHTLD-SNPATFPLN 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 FGNPKPSIVDGIDIPQEVSTLQGGPLLNEIFERGREKIRCVADAENCSIDYLKPLKF--- 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 LADESAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 LAIEKSFMSEV-DNMKLEFVQTIWRHGDR-----SALEGLFPISEKNWTFGGG---- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 KTYNYTLGADDLTPFGENOMVNSGIKFYRRY------KALARKIVPFIRASGSDRVI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 ASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYNNTLD--HG------ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 ISAMSLLYG----MFPPGAW-----NI---QGVDYPNDVDWQQGFTFIPVHVDGID 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 MDMCPFDTVARTSDATELSPFC-----ALFTHDEWIQYDYLQSLGKYYG-----YG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.3%; Score 130; DB 1; Length 755;
Best Local Similarity 21.9%; Pred. No. 0.012;
Matches 90; Conservative 55; Mismatches 130; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
; E7F3050115A235EB CRC64;
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY
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EMBL, 24702; CAA91156.1; JOINED.
EMBL, 24702; CAA91156.1; JOINED.
WORMPEP; F26C11.1; CE05732.
InterPro; IPR000560; -.
Pfam. PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
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755 AA;
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Search completed: October 26, 2001, 15:18:04 Job time: 450 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2001, 16:40:04; Search time 57.24 Seconds Run on:

(without alignments)
494.609 Million cell updates/sec

US-09-488-265-29 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 412676 seqs, 60623988 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

ieneseq\_0601:\*
/SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:\*

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/SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1984.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:\*

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/SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT:\*

/SIDS1/gcgdata/geneseq/geneseqp/AA2001.DAT:\* 18: 19: 20: 21:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description                   | Consensus phytase- Consensus phytase-1, Consensus phytase-1, Consensus phytase Consensus phytase Fungal phytase pro Fungal phytase pro Fungal consensus phytase Consensus phytase Phytase-1, a consensus phytase | d spendence radius |
|-------------------------------|--|--------------------|
| ID                            | AAY41169<br>AAB20526<br>AAR50568<br>AAB20531<br>AAB20531<br>AAW93380<br>AAW93380<br>AAW93381<br>AAR65558   |                    |
| DB                            | 200<br>200<br>200<br>200<br>200<br>200<br>200<br>200<br>200<br>200   |                    |
| ength                         | 4 4 4 6 6 7 7 7 9 4 4 6 6 7 7 9 4 4 6 6 7 7 9 4 4 6 6 7 7 9 4 6 6 7 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9  |                    |
| %<br>Query<br>Match Length DB | 1000.0<br>1000.0<br>1000.0<br>99.2<br>99.0<br>99.1<br>97.8<br>97.8   |                    |
| Score                         | 2462<br>2462<br>2462<br>2443<br>2443<br>2414<br>2408<br>2408<br>2408<br>2408<br>2408   |                    |
| Result<br>No.                 | 1 2 2 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4  |                    |

| Fungal consensus p   | e consen | Consensus phytase-<br>Consensus phytase | phytase- | us phytas |          |          | 0        | s phyt | , a der  | us phy   | phytas   | Consensus phytase | s phytas | a der    | s phytas | nseusn   | us phytas | Phytase-11, a cons | ٦į       | A. fumigatus phyta | 44   | Mutant Aspergillus | Consensus phytase | 8          | Phytase, Asperdil | r<br>D | ombina   | spergillus | ficuum phy | ergillus | . fumigatus phyt |  |
|----------------------|----------|---|----------|-----------|----------|----------|----------|--------|----------|----------|----------|-------------------|----------|----------|----------|----------|-----------|--------------------|----------|--------------------|------|--------------------|-------------------|------------|-------------------|--------|----------|------------|------------|----------|------------------|--|
| AAW93384<br>AAW93385 | AAY39906 | AAB20527                                | AAY69569 | AAB20534  | AAB20533 | AAB20524 |          | _      | AAY69571 | AAB20529 | AAB20514 | AAB20523          | AAB20530 | AAY69572 | )53      | AAY69557 | )52       | 926                | AAY69574 | 17                 | 52   | AAY69570           | 53                | AAY69565   |                   | 23     | AAR11333 | AAW15124   |            | AAW84356 | AAY39905         |  |
| 20                   | 20       | 21                                      | 21       | 21        | 21       | 21       | 21       | 20     | 21       | 21       | 21       | 21                | 21       | 21       | 21       | 21       | 21        | 21                 | 21       | 20                 | 21   | 21                 | 21                | 21         | 15                | 15     | 12       | 18         | 20         | 19       | 20               |  |
| w w                  | 467      | J W                                     | v        | w.        | Ψ        | 9        | 9        | 9      | o        | 9        | マ        | ◂                 | o        | 9        | m        | က        | ന         | m                  | 467      | 9                  | 9    | 467                | $\sim$            | 424        | 9                 | Q      | 9        | 9          | 9          | 465      | 465              |  |
| 97.7                 | 7. 2     | OJ C                                    | ω.       | ٠.<br>س   |          |          | <u>.</u> | m.     | m        | o.       | ~;       |                   | <u>.</u> | ö        | 'n       | Ġ        | m.        | œ.                 | ς.       | _:                 | _:   | <u>.</u> .         | ά.                | <u>.</u>   |                   |        | Ġ        |            |            |          |                  |  |
| 2405<br>2399         | 2398     | 2362                                    | 2362     | 2360      | 2355     | 2342     | 2342     | 2290   | 2290     | 2287     | 2282     | 2216              | 2215     | 2215     | 2134     | 2134     | 2044      | 2044               | 2032     | 2012               | 2012 |                    | 1956.5            | $^{\circ}$ | 1879              | 1879   | 1875     | 1875       | 1875       | 1867     | 1867             |  |
| 12                   | 14       | 16                                      | 17       | 18        | 13       | 20       | 21       | 22     | 23       | 24       | 25       | 26                | 27       | 28       | 53       | 30       | 31        | 32                 | ee :     | 34                 | 35   | 36                 | 3.7               | 38         | w<br>So           | 40     | 41       | 42         | 43         | 44       | 42               |  |

## ALIGNMENTS

AAY43169 standard; Protein; 467 AA. 06-JAN-2000 (first entry) AAY43169; AAY43169 RESULT

Consensus phytase-1-thermo(8)-Q50T-K91A protein sequence.

Phytase; animal feed preparation; thermostable phytase; transgenic plant; consensus sequence.

Synthetic.

W09948380-A1

30-SEP-1999,

98DK-0000407. 98DK-0000806. 98DK-0001176. 99DK-0000091. 99WO-DK00154 18-SEP-1998; 22-JAN-1999; 22-JAN-1999; 22-MAR-1999; 23-MAR-1998; 19-JUN-1998; 

(NOVO ) NOVO-NORDISK AS

Petersen S;

WPI; 1999-591030/50. N-PSDB; AAZ31520.

N

us-09-488-265-29.rag

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                                                                                      The invention relates to a process for preparing animal feed by agglomerating feet interestable phytase, which is added before or diving agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal phytase-expressing transgenic plants. These plants provide a feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytase) simultaneously.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
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                                                                        This sequence represents the consensus phytase-1-thermo(8)-050T-K91A.
                                                                                                                                                                                                                                                                                                                                                                                     1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 2462; DB 20; Length 467; Best Local Similarity' 100.0%; Pred. No. 4e-239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus phytase 1 thermo 8 q50t, k91a protein SEQ ID NO:29
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                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20526 standard; Protein; 467 AA
                                        Example 3; Fig 9; 71pp; English.
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate specificity, substrate profile, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released prosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to creduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                         vel phytases with improved properties such as temperature stability, stability, and substrate specificity, for use in pharmaceuticals and
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100.0%; Pred. No. ~.
0; Mismatches
                                                                                                                                                                                                                                                                                           Claim 5; Fig 7a-c; 240pp; English.
                             21-JAN-2000; 2000WO-DK00025.
                                                             99DK-0000092
                                                                              99DK-0001340
                                                                                                                                                                                                                                                              compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 467; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 AA;
                                                                                                                                                                                               N-PSDB; AAA73233
                                                           22-JAN-1999;
                                                                              21-SEP-1999;
27-JUL-2000
                                                                                                                                                 Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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formulation, comprising phytase (myo-inostrol hexakisphosphate phosphoydrolase) and one or more stabilising agents including phosphoydrolase) and one or more stabilising agents including to phosphoydrolase) and one or more stabilising agents including to a value of malonic, and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a provides a monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its diactary requirements of phosphorus. Although a large amount of phosphate is present in animal to utilise this form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate.
                                                                                                                                                        Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "Phytase signal peptide from Aspergillus terreus cbs16.46"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel stabilised dry or liquid enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mature phytase-1-thermo[8]-Q50T-K91A"
                                                                                                                             Mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                              AAY69568 standard; protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         ralaromyces thermophilus ATCC20186
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                                                                                                                                                                                                                                                                                                            fumigatus ATCC13073.
fumigatus ATCC32722.
fumigatus ATCC58128.
                                                                                                                                                                                                                                                                                           Aspergillus niger str. NRRL3135.
Aspergillus fumigatus ATCC13073.
Aspergillus fumigatus ATCC32722.
                                                                                                                                                                                                                                                                                                                                                             fumigatus ATCC26906
                                                                                                                                                                                                                                                                                                                                                                          fumigatus ATCC32239
                                                                                                                                                                                                                                                          Aspergillus niger var. awamori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lehmann M, Wyss M;
                                                                                                                                                                                                                                             terreus cbs16.46
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                                                                                                (first entry)
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                                                                                                                                                                                                                            Aspergillus terreus 9A1
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Emericella nidulans.
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                                                                                              19-APR-2000
                                                                                                                                                                                                                                                                                                                                          Aspergillus
Aspergillus
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                                                                                                                                                                                                                                               Aspergillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                              AAY69568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                AAY69568
RESULT
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reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents a mutant phytase-1 consensus sequence, phytase-1-thermo[8]-Q50T-K91A, which has a temperature optimum and melting point 7 degrees Celsius higher than that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 arleadlpgvtltdedvvylmdmcpfdtvartsdatelspfcalfthdewigydylgslg 300
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDNTMISIFFALGLYNGTKPLSTISVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                100.0%; Score 2462; DB 21; Length 467; 100.0%; Pred. No. 4e-239; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus phytase 3 thermo 11 Q50T K91A protein SEQ ID NO:93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                            100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB20532 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2000; 2000WO-DK00025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2000 (first entry)
                                                                                                                                                                                                                                                   467; Conservative
                                                                                                                                    of phytase-1 (AAY69558).
                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                     467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200043503-A1.
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                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate obsciency, temperature profile, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                   Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -
                                                                                                                                                                                                                                                                                                                                                The present invention describes improved phytases, preferably with
                                                                                                                                                                                                                                                                                                           Disclosure; Fig 23a-c; 240pp; English.
                 99DK-0000092
                                  99DK-0001340
                                                                            (NOVO ) NOVO NORDISK AS
                                                                                                                                                             WPI; 2000-491161/43.
                                                                                                                                                                                     N-PSDB; AAA73291.
                 22-JAN-1999;
                                     21-SEP-1999;
                                                                                                                        Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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0; Gaps 99.2%; Score 2443; DB 21; Length 467; ilarity 99.4%; Pred. No. 3.3e-237; Conservative 0; Mismatches 3; Indels 0; Best Local Similarity Matches 464; Conserva Query Match

467 AA;

Sequence

61 SAÍS∯DVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 1 MGVEYVZLSIATLEGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60 õ g ŏ pp

121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 ò g

240 181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 181 a òγ

300 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 241 301 ò g

δ

HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420 hdntmisiffalglyngtkplsttsvesieetdgysaswtvpfaarayvemmqcqaekep 420 361 301 361 g g ò

LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467 421 ŏ

AAB20531 standard; Protein; 467 AA. 

AAB20531;

(first entry) 05-DEC-2000 Consensus phytase 3 thermo 11 Q50T protein SEQ ID NO:91.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

Synthetic.

WO200043503-A1.

27-JUL-2000. 

21-JAN-2000; 2000WO-DK00025.

99DK-0001340. 99DK-0000092 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS

Lehmann M;

WPI: 2000-491161/43. N-PSDB; AAA73290 Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -

Disclosure; Fig 22a-c; 240pp; English.

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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositiol and inorganic phosphate. The present sequence represents a phytase sequence from the present The present invention describes improved phytases, preferably with invention.

467 AA; Sequence

0; Gaps 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 99.0%; Score 2438; DB 21; Length 467; 99.1%; Pred. No. 1e-236; 4; Indels Pred. No. 1e-236; 0; Mismatches 4 Matches 463; Conservative Similarity Query Match Best Local δy

0;

61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 Op QΥ

121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 ŏ qq

qq

181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240 δλ

AAB20531

g δλ P ò g δŏ g ò

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This invention describes a novel process for the preparation of a consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or pharmaceutical compositions. This sequence is a mutant phytase protein of created from the protein represented in AAW93380.
181 kladpgsqphqaspvinviipegsgynntldhglctafedstlgddveanftalfapair 240
                                                   241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                            HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMOCQAEKEP 420
                                                                                                                                                                                                                                                                                        Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food;
feed additive; variant; mutein; feed; pharmaceutical.
                                                                                                                                                        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparation of a consensus protein, especially a phytase - using programs to compare evolutionary similarity of sequences
                                                                                                                                                                                                                                                                                                                                                                 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                               Fungal consensus phytase protein mutant Q50T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW93382 standard; Protein; 467 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page -; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW93382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytase;
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consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is
                                     61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                      121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                  181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
                                                                                                                                                         241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                          KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                                                                                                                                                              1 mgvfvvllsiatlfgstsgtalgprgnshscdtvdggyqcfpeishlwgtyspyfslede 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel process for the preparation of
421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparation of a consensus protein, especially a phytase programs to compare evolutionary similarity of sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fungal phytase protein consensus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW93380 standard; Protein; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 2; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Synthetic.
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Gaps

1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60

98.1%; Score 2414; DB 20; Length 467; 98.1%; Pred. No. 2.7e-234; Live 3; Mismatches 6; Indels 0

Conservative

458;

Matches

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Query Match Best Local Similarity

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useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or pharmaceutical compositions. This sequence represents the consensus phytase protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kyygygagnplgpaggygfaneliarltrspygdhtstnhtldsnpatfplnatlyadfs 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMOCQAEKEP 420
                                                                                                                                                                                                                           YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                        ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                            SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical.
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                                                                                                                                   Gaps
                                                                                                                                                         1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE
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                                                                                                                                                                                                                                                                                                                     KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR
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                                                                                                        Length 467;
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Pred. No. 1.1e-233;
3; Mismatches 7;
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                                                                                                          97.88;
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                                                                                                                      Best Local Similarity 97.9
Matches 457; Conservative
                                                                     467 AA;
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consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutehn. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutehn are useful in food, feed or pharmaceutical compositions. This sequence is a mutent phytase protein of the invention which does not appear in the specification but has been created from the protein represented in AAW93380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YTLGADDLTPFGENQMYNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                    1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP
                                                                                                       This invention describes a novel process for the preparation of a
                              using
                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                          Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparation of a consensus protein, especially a phytase programs to compare evolutionary similarity of sequences
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                         97.8%; Score 2408; DB 20;
97.9%; Pred. No. 1.1e-233;
                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB20515 standard; Protein; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus phytase SEQ ID NO:16.
                                                                             Claim 9; Page -; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                         Matches 457; Conservative
WPI; 1999-134647/12.
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                467 AA;
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                                                                                                                                                                                                                                                                                Sequence
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food; feed; phytate; manure.

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Synthetic.

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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
                                                                                                                                                                                                                                                                                             Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds
                                                                                                                                                                                                                                                                                                                                                                       Example 9; Fig 2a-c; 240pp; English.
                                                                  21-JAN-2000; 2000MO-DK00025.
                                                                                                                               99DK-0001340
                                                                                                               99DK-0000092
                                                                                                                                                                    (NOVO ) NOVO NORDISK AS
                                                                                                                                                                                                                                          WPI; 2000-491161/43.
                                                                                                                                                                                                                                                            N-PSDB; AAA73231;
W0200043503-A1.
                                                                                                           22-JAN-1999;
                                                                                                                               21-SEP-1999;
                                   27-JUL-2000
                                                                                                                                                                                                       Lehmann M;
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SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                    121 YTLGADDLTPFGENQWVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                 181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
                                                                                                                                                 241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                           KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                         HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                                                                                                                                                                                   Gaps
                                           1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                        ;
97.8%; Score 2408; DB 21; Length 467; 97.9%; Pred. No. 1.1e-233;
                            Indels
                         3; Mismatches
         Best Local Similarity 97.9
Matches 457; Conservative
 Query Match
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Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; phytase-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formulation, comprising phytase (myo-inositol hexalisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcollulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with list dietary requirements of phosphorus. Although a large amount of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..26
/note= "Phytase signal peptide from Aspergillus terreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel stabilised dry or liquid enzyme
421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
               /note≈ "Mature phytase-1 consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                       Talaromyces thermophilus ATCC20186. Myceliophthora thermophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 14; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cbs16.46"
                                                                                                 AAY69558 standard; protein; 467
                                                                                                                                                                                                                                                                                                        Aspergillus niger var. awamori.
Aspergillus niger T213.
Aspergillus niger str. NRRL3135.
                                                                                                                                                                                                                                                                                                                                                      fumigatus ATCC13073
                                                                                                                                                                                                                                                                                                                                                                    fumigatus ATCC32722
                                                                                                                                                                                                                                                                                                                                                                                Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC26906.
                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus fumigatus ATCC32239.
                                                                                                                                                                                        Phytase-1, a consensus phytase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wyss M;
                                                                                                                                                                                                                                                                         Aspergillus terreus 9Al.
Aspergillus terreus cbs16.46.
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                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Emericella nidulans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-099429/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monogastric animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ59637
                                                                                                                                                           19-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-1998;
                                                                                                                                                                                                                                                                                          Aspergillus
Aspergillus
                                                                                                                                                                                                                                                                                                                                                   Aspergillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brugger R,
                                                                                                                              AAY69558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                       RESULT 10
                                                                                     AAY69558
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0;

467 AA;

Sequence

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to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and pelleting. The present sequence represents a consensus sequence, designated phytase-1, which was derived from the mature phytase sequences from a variety of fungi (AAY69544-Y69556), and additionally contains the Aspergillus terreus cbs116.46 signal peptide at the
                                                                                                                                                                                                                                                                                                                                                                                  N-terminus.
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467 AA; Seguence

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                                                                                                                                                                                                      KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
                                                                                                                                                                                                                       361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                                                                                                                                                            KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                                                                                                                                                                                                                                                       361 hdnsmisiffalglyngtaplsttsvesieetdgysaswtvpfgarayvemmqcqaekep 420
                                                                                                                  ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                   SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                      YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                               Gaps
                                                                                                                                                                  ;
0
97.8%; Score 2408; DB 21; Length 467; 97.9%; Pred. No. 1.1e-233;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                        3; Mismatches
                           Matches 457; Conservative
               Similarity
  Query Match
Best Local 9
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Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical.
                                                                     Fungal consensus phytase protein mutant Q50G.
       AAW93383 standard; Protein; 467 AA.
                                                  (first entry)
                                                  11-JUN-1999
                                                                                                                                                         EP897985-A2
                                                                                                                            Fungi.
Synthetic.
AAW93383
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This invention describes a novel process for the preparation of a consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or phymaceutical compositions. This sequence is a mutant phytase protein of the invention which does not appear in the specification but has been created from the protein represented in AMM93380.
                                                                                                                                                                                                                        Preparation of a consensus protein, especially a phytase - using programs to compare evolutionary similarity of sequences
                                                                                                           (HOFF ) HOFFMANN LA ROCHE AG F.
                                                                                                                                                                                                                                                                                  Claim 9; Page -; 30pp; English
                                 98EP-0113176.
                                                                                                                                                                                       WPI; 1999-134647/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 AA;
                                     15-JUL-1998;
                                                                         24-JUL-1997;
24-FEB-1999
                                                                                                                                                       Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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ö 61 saispdypddcrvtfygvlsrhgaryptsskskaysalieaigknatafkgkyaflktyn 120 121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA,180 240 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420 61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 0; Gaps 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG Ouery Match 97.8%; Score 2407; DB 20; Length 467; Best Local Similarity 97.9%; Pred. No. 1.4e-233; Matches 457; Conservative 3; Mismatches 7; Indels 0; 421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467 361 301 g Db g g δ g ŏ g δŽ QΥ

AAW93384 standard; Protein; 467 g δŏ

AAW93384;

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consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or pharmaceutical compositions. This sequence is a mutant phytase protein of the invention which does not appear in the specification but has been created from the protein represented in AAW93380.
                                                                                   consensus; myo-inositol hexakisphosphate; hydrolysis; food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel process for the preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of a consensus protein, especially a phytase - using programs to compare evolutionary similarity of sequences
                                                                                   Phytase; consensus; myo-inositol hexakisphosphate; hy
feed additive; variant; mutein; feed; pharmaceutical.
                                                Fungal consensus phytase protein mutant Q50T-Y51N.
                                                                                                                                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page -; 30pp; English
                                                                                                                                                                                                                                                                                                      97EP-0112688.
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              11-JUN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                  24-JUL-1997;
                                                                                                                                                                                                                             24-FEB-1999.
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                                                                                                                                                                                        EP897985-42
                                                                                                                                      Fungi.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                       Lehmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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; 0 61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 121 YTLGADDLTPFGENQWVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240 241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300 KYYGYGAGNPLGPAQGYGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420 Gaps 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60 ; 0 Length 467; Indels 97.7%; Score 2405; DB 20; 97.9%; Pred. No. 2.2e-233; 3; Mismatches Best Local Similarity 97.9 Matches 457; Conservative Query Match 301 301

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consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase (myo-inositol hexakisphosphate) which acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their pharmaceutical compositions. This sequence is a mutant phytase protein of the invention which does not appear in the specification but has been created from the protein represented in AAW93380.
121 ytlgadditpfgengmvnsglkfyrrykalarkivpfirasgsdrviasaekfiegfgsa 180
                                                                                                                                                                                                                                                          Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel process for the preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparation of a consensus protein, especially a phytase - using programs to compare evolutionary similarity of sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.4%; Score 2399; DB 20; Length 467; 97.6%; Pred. No. 8.8e-233; Live 3; Mismatches 8; Indels 0
                                          421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                          Fungal consensus phytase protein mutant Q50L-Y51N.
                                                                                                                                                    ΑA
                                                                                                                                              AAW93385 standard; Protein; 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF ) HOFFMANN LA ROCHE AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page -; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              98EP-0113176.
                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-0112688
                                                                                                                                                                                                         (first entry)
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Best Local Similarity 97.65
Matches 456; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-134647/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             467 AA;
                                                                                                                                                                                                        11-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                24-FEB-1999
                                                                                                                                                                                                                                                                                                                                                   EP897985-A2
                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehmann M;
                                                                                                                                                                           AAW93385;
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                                                                                                                  RESULT 13
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301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                                                                                                                                                 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
181 KLADPGSQPHQASPYINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phytate level reduction; animal manure; food preparation; soy processing; inositol manufacture.
                                                                                                                                                                                                                                                                                        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ascomycete consensus phytase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                              AAY39906 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                AAY39906;
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98DK-0000806. 98DK-0001176. 99WO-DK00153. 98DK-0000407 99DK-0000091 (NOVO ) NOVO-NORDISK AS W09949022-A1. 19-JUN-1998; 18-SEP-1998; 23-MAR-1998; 22-MAR-1999; 22-JAN-1999; 30-SEP-1999 Svendsen A; Synthetic. 

WPI; 1999-580444/49. N-PSDB; AAZ27423

This sequence represents the ascomycets consensus phytase sequence. The invention relates to variant phytase enzymes with specific amino acid substitutions for improved properties. The phytase variants can be used for liberating phytate levels in animal manure. They can be used in feed or food preparations. The phytase bubstrate. They can be used in feed or food preparations. The phytase DNA can also be used to produce transgenic plants which can be used in feeds or foods. The phytase variants can also be used in soy processing and in the manufacture of inositol or derivatives. The phytase variants can have altered activities such as ph stability, temperature stability, pH profile, temperature profile, specific activity (in particularly in relation to pH and temperature), substrate binding, substrate cleavage pattern, substrate binding, New variant phytase enzymes, used for liberating phosphorus from a phytase substrate, for reducing phytate levels in animal manure and in feed and food preparations – Claim 26; Fig 9a-d; 141pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytase; animal feed preparation; thermostable phytase; transgenic plant;
                                                                                                                                                                                                                                                           121 YILGADDLIPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                            241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                     SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                         1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
                                                                                                     Gaps
position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytase degradation rate and end level of released phosphate reached.
                                                                                                                                                                                                                                                                                                                                                   301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
                                                                                                                                                                                                                                                                                                                                                                                                361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP
                                                                                                                                      Score 2398; DB 20; Length 467;
Pred. No. 1.1e-232;
4; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus phytase-10-thermo(3)-Q50T-K91A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA, 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY43170 standard; Protein; 467 AA
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98DK-0001176.
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                                                                                97.4%;
97.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99DK-0000091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JAN-2000 (first entry)
                                                                                            Best Local Similarity 97.4 Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus sequence
                                                  467 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1998;
18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR=1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY43170;
                                                    Sednence
                                                                                    Query Match
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Preparing animal feed using a thermostable phytase
                             Example 3; Fig 10; 71pp; English
        WPI; 1999-591030/50.
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The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytase) simultaneously. This sequence represents the consensus phytase-10-thermo(3)-Q50T-K9IA. 467 AA;

Seguence

.; 0 Gaps SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 YTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 240 ARLEADLPGVŢLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300 300 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420 1 MGVEVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPELSHLWGTYSPYFSLADE 60 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 0; Indels LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467 95.9%; Score 2362; DB 20; 95.5%; Pred. No. 4.7e-229; tive 8; Mismatches 13; Best Local Similarity 95.5 Matches 446; Conservative Query Match 61 361 61 121 181 181 301 421 g δ ò ò δ qq Qγ qq δy pp

Search completed: October 26, 2001, 16:40:04 Job time: 4955 sec

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(without alignments) 295.232 Million cell updates/sec 2462 1 MGVFVVLLSIATLFGSTSGT......DFVEGLSFARSGGNWAECFA 467 October 26, 2001, 16:40:46; Search time 32.57 Seconds GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Total number of hits satisfying chosen parameters: 197339 seqs, 20590346 residues OM protein - protein search, using sw model Gapop 10.0 , Gapext 0.5 US-09-488-265-29 Perfect score: Scoring table: Sequence: Searched: Run on:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database :

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
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/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/pcvuS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/pcvuS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    |        | on.          | -               | À (          | <b>1</b> | ó            | ò            | 7           | 32           | 20,      | 'n           | 32,          | 3        | m          | 'n       | , -       | , ,       | , c          | ý (                  | 7 (         | ٠<br>ر       | 7 4                                     | 7        | 2, 4            | 22,           | 28,          | 26.      |                  | ì          | ', Appli             | ,           | 2, Appli    |
|----|--------|--------------|-----------------|--------------|----------|--------------|--------------|-------------|--------------|----------|--------------|--------------|----------|------------|----------|-----------|-----------|--------------|----------------------|-------------|--------------|---|----------|-----------------|---------------|--------------|----------|------------------|------------|----------------------|-------------|-------------|
|    |        | Description  | 00404000        |              | eduence  | Sednence     | eauence      | Sednence    | Sednence     | Sednence | Seguence     | Seguence     | Seguence | Sequence   | Sequence | Segmente  | Section   | ooughboo     | acinentac<br>Somonos | acionhac    | ecuentes     | ednence                                 | Sednence | Sednence        | Sednence      | Sequence     | Sequence | Segmenter        | Secretions | eognonos<br>eognonos | acrientes   | sednence    |
|    |        | qı           | US-09-121-425-1 | -09-121-425- | -07-923- | -08-609-4263 | -08-374-6520 | 00 3/4-032C | 00-147 404 0 | -08-140- | -08-63-709-2 | -08-419-448- | -08-819- | -09-163-64 | -09-155- | -155-855- | -155-855- | -08-819-825- | -04-163-642-         | -08-993-359 | -08-993-350- | 7 | 177-60   | -08-384-398A-   | -08-333-359-2 | -08-993-329- | -08-     | US-07-627-539G-2 | S          | -07-623-724-         | -08-609-40- | W07* C00 00 |
|    |        | DB           | 4               | Ψ            | -, ٠     | ۱,           | 1 0          | ٦ -         | - ۲          | ٦,       | ٠, ر         | 71 (         | 7        | 4          | 4        | 4         | 4         | 7            | 4                    | ٠,          | ۰, ۰         | , (                                     | י ר      | ი ი             | າ ເ           | 'n           | m        | Н                | Ч          | -                    | 0           | ı .         |
|    |        | Match Length | 441             | 467          | 467      | 467          | 467          |             | 707          | 40.4     | 104          | /05          | 46/      | 467        | 467      | 443       | 443       | 475          | 475                  | 443         | 439          | 430                                     | 100      | 4. 4.<br>U. 11. | 0.4           | 7 4 4 7      | 442      | 468              | 446        | 479                  | 479         | 1           |
| фP | Query  | Match        | 92.7            | 92.2         | 76.3     |              | ٠            | ٠.          |              |          |              |              |          |            | 75.5     |           | 73.6      | 54.2         |                      |             |              |   |          | ٠               | 0.10          | i,           | 31.6     |                  |            | 14.1                 | 14.1        | !           |
|    |        | Score        | 2282            | 2270         | 1879     | 1879         | 1879         | 1875        | 1875         | 1075     | 1075         | 1070         | 0/01     | 18/5       | 1860     | 1818      | 1813      | 1334         | 1334                 | 802.5       | 798.5        | 798.5                                   | 708 5    | 707             |               | 197          | 8//      | 363              | 358.5      | 347.5                | 347.5       |             |
|    | Result | No.          | 1               | 7            | ٣        | 4            | 2            | ٧           | 7            | - α      | 0            | , ,          | 7.       | 7:         | 12       | 13        | 14        | 15           | 16                   | 17          | 18           | 19                                      | 200      | 2 6             | 1 0           | 7 (          | 57       | 74               | 25         | 26                   | 27          |             |

| US-08-680-506-7 Sequence 7, Appli US-08-993-359-32 Sequence 32, Appl US-08-241-853-8 Sequence 8, Appli Sequence 8, Appli | Sequence 32,<br>Sequence 8, | Sequence 8, | , o ));;;;;;; | 8 endemons |                | Sequence 3 | Segment 10       | Segmence 10 | Seguence 1     | Section 18       | Segmence 18      | Seguence 2      | Segment 2      | Seguence 2      | Sequence 10      |                 | Sequence 43,     |  |
|--|-----------------------------|-------------|---------------|------------|----------------|------------|------------------|-------------|----------------|------------------|------------------|-----------------|----------------|-----------------|------------------|-----------------|------------------|--|
| 9 2 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  | US-08-680-506-7             | US-08-993   | US-08-241     | US-08-820  | US-08-374-652C | US-08-680  | US-08-241-853-10 | US-08-850   | US-08-758-213- | US-08-692-787-48 | US-09-097-199-48 | US-09-146-283-2 | US-08-579-823A | US-09-344-195-2 | US-08-570-311-10 | US-08-353-485-1 | US-07-923-724-43 |  |
| 7  | m                           | m           | Н             | ~          | 7              | e          | Н                | 7           | Н              | 7                | 4                | 7               | m              | 4               | 7                | ~               | 1                |  |
| 4/9  | 449                         | 92          | 113           | 113        | 24             | 318        | 113              | 113         | 386            | 386              | 386              | 515             | 515            | 515             | 1732             | 1732            | 20               |  |
| 14.1   | 6.9                         | 0.9         | 5.0           | 5.0        | 4.8            | 4.8        | 4.5              | 4.5         | 3.9            | 3.9              | 3.9              | 3.9             | 3.9            | 3.9             | 3.9              | 3.9             | 3.8              |  |
| 347.5  | 170.5                       | 148.5       | 122           | 122        | 119            | 118        | 111              | 111         | 96.5           | 96.5             | 96.5             | 96.5            | 96.5           | 96.5            | 95.5             | 95.5            | 93.5             |  |
| D 0  | 67                          | 30          | 31            | 32         | 33             | 34         | 32               | 36          | 37             | 38               | 39               | 40              | 41             | 42              | 43               | 44              | 45               |  |

ALIGNMENTS

TITLE OF INVENTION: CONSENSUS Phytases FILE REFERENCE: CONSENSUS phytases 13239 CURRENT APPLICATION NUMBER: US/09/121,425 CURRENT FILING DATE: 1998-07-23 BARLIER APPLICATION NUMBER: EPO 97112688.3 EARLIER FILING DATE: 1997-07-24 NUMBER OF SEQ ID NOS: 20 ; Sequence 1, Application US/09121425 ; Patent No. 6153418 ; GENERAL INFORMATION: SOFTWARE: Patentin Ver. 2.0 APPLICANT: Lehmann, Martin US-09-121-425-1 LENGTH: 441 SEQ ID NO 1

. 0 Score 2282; DB 4; Length 441; Pred. No. 1.1e-230; 3; Mismatches 7; Indels ( 92.78; Query Match
Best Local Similarity 97.73
Matches 431; Conservative

OTHER INFORMATION: Description of Artificial Sequence:consensus; OTHER INFORMATION: sequence US-09-121-425-1

ORGANISM: Artificial Sequence

TYPE: PRT

; 0 87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 146 147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGY 206 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 266 DIVARISDATELSPFCALFIHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 326 Gaps 27 NSHSCDIVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARY 86 181 267 241 δλ q ŏ g  $^{\circ}$ ρp δŏ qq Qγ QQ δy

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461 NWAECFA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KLADPGSQPHQASPVIN-------VIIPEGSGYNNTLDHGTCTAFED 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TYN 100
                                                          301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360
                                       ESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:consensus OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
92.2%; Score 2270; DB 4; Length 467;
Best Local Similarity: 89.7%; Pred. No. 2.1e-229;
Matches 437; Conservative 3; Mismatches 7; Indels 40
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                                                                                                                                                                                                                                                                                                                   ATTLE OF INVENTION: Consensus Phytasses
FILE REFERENCE: consensus Phytasses
FILE REFERENCE: consensus Phytasses 13239
CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                               Sequence 2, Application US/09121425 Patent No. 6153418
                                                                                                                       DDFVEGLSFARSGGNWAECFA 467
                                                                                                                                          DDFVEGLSFARSGGNWAECFA 441
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LENGTH: 467
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61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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                                                                                                                                                                            APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.3%; Score 1879; DB 1; Length 467; 75.6%; Pred. No. 2.1e-188; Live 41; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                   STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
THEFEROMANICATION INFORMATION:
                                                                                                             Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
Torkkeli, Tuula K.
Cantrell, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/496,155 FILING DATE: 19-MAR-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/044,077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
                                                                                           Nevalainen, Helena K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UK 8610600
RESULT 3
US-07-923-724-8
Sequence 8, Application US/07923724
; Patent No. 5780292
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.69
Matches 353; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-07-923-724-8
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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: U.S.A.
                                                                       GENERAL INFORMATION:
APPLICANT: Nevala
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                                                                                                                                                                    APPLICANT:
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                                                                                                                                                    APPLICANT:
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241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
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                                                                                                                                                                                                                              HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                    181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Palohaimo, Marja T.
APPLICANT: Mietichen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Gantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Purunen, Marja K.
APPLICANT: Truunen, Marja K.
APPLICANT: Tegerset m. Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                    LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 New York Avenue, Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/609,426A FILING DATE: 01-MAR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-WAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/044,077 FILING DATE: 29-APR-1987 PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600 FILING DATE: 30-APR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08609426A Patent No. 5830733
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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RAMBOSEK, JOHN A.
PIDDINGTON, CHRISTINE S.
HOUSTON, CHRISTINE S.
CANTRELL, MICHAEL A.
NVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
NVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
NVENTION: ENZYMES IN DESIRED RATIOS
                                                                                                                                                                                                                                                                                                                                                                                         SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                                                                                                                                                                                                                                                                                                                                                                                                            121 YILGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
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                                                                                                                                                                                                                                                                                                                                              361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP
                                                                                                                                                                                                                                                          Length 467;
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                                                                                                                                                                                                                                                    76.3%; Score 1879; DB 2; 75.6%; Pred. No. 2.1e-188; tive 41; Mismatches 73;
REFERENCE/DOCKET NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALCHEIMO, MARJA T.
FAGERSTROM, RICHARD B.
MIETTINEN-OINONEN, ARJA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEVALAINEN, HELENA K.M.
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; Patent No. 5834286
                                                            TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                      Matches 353; Conservative
                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-609-426A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                  TOPOLOGY:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YILGADDLIPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.3%; Score 1879; DB 2; Length 467; 75.6%; Pred. No. 2.1e-188; tive 41; Mismatches 73; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
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                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION A435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41,264
NFR: 1050.071001
                                                                                                                                                                                        APPLICATION NUMBER: US/08/374,652C FILING DATE: 24-MAY-1995
                                                                                 3: Floppý disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFREENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 467 amino acids amino acid
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not relevant
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Matches 353; Conservative
                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
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                      COUNTRY:
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STATE:
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241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Indels
                                                            APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Hertus An Van Paridon
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Robert Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Pest Local Similarity 75.6%; Pred. No. 5.6e-188;
Matches 353; Conservative 41; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24615-20026.00
                                                                                                                                                                                                                                                                                               STREET: 545 Middlefield Road, Suite 200 CITY: Menlo Park STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07/688,578
Sequence 32, Application US/08151574 Patent No. 5436156
                                                                                                                                                                                                                                                                                  ADDRESSEE: Morrison & Foerster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murashige, Kate H. REGISTRATION NUMBER: 29,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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MEDIUM TYPE: Floppy
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                                          GENERAL INFORMATION:
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301 KYYGYGAGNPLGPAQGYGFANELIARLTHSPYQDHTSTNHTLDSNPATFPLNATLYADFS 360
                361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
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                                                                                                                                                                                                                                                                                                 APPLICANT: RIETVELD, KRIJN
APPLICANT: HORKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: PEN, JAN
THUE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
CORRESPONDENCE: 31
CORRESPONDENCE ADDRESS:
                                                                                                                        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
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3ER: 44615-20011.24
                                                                                                                                                                                                                                                                                      VAN OOLJEN, ALBERT J. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/146,424
FILING DATE: 02-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   E: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                      Sequence 20, Application US/08146424 Patent No. 5593963 GENERAL INFORMATION:
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NAME: KENNEDY, BILL
REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: 4461:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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California
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ZIP: 94304-1018
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KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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                                                                                                                                                                                                                                                                   361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
                                                                                                                       241 ARLEADLPGVTLIDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
                                                                                                                                          421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAN OOLJEN, ALBERT J.J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWORED, TEUNIS C.
TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE: US/08/693,709
FILLING DATE: 07-AUG-1996
CLASSIFICATION: 800
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STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08693709
Patent No. 5770413
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 246
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/11
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Murashige, Kate H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 amino acids
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MEDIUM TYPE: Diskette
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FRAGMENT TYPE: internal
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
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                                                                                                                                                  Gaps
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                                                                                                                76.2%; Score 1875; DB 1; Length 467; 75.6%; Pred. No. 5.6e-188; tive 41; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
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                NAME/KEY: Signal Sequence
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                      Matches 353; Conservative
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                            ; LOCATION: 1...23
; OTHER INFORMATION:
US-08-693-709-2
                                                                                                                   Query Match
Best Local Similarity
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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; Patent No. 5866118
                                    ATTORNET/AGENT INFORMATION:
NAME: MOTSALIGG, KALE H.
REGISTRATION NUMBER: 24519
REFERENCE/DOCKET NUMBER: 24611;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1503
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Berka, Randy M. APPLICANT: Ray, Michael W. APPLICANT: Klotz, Alan V. TITLE OF INVENTION: Polypept TITLE OF INVENTION: And Nucleus NUMBER OF SEQUENCES: 5
10-APR-1995
                                                                                                                                                                                                    : 467 amino acids amino acids
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                 linear
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Best Local Similarity
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  FILING DATE: 10
CLASSIFICATION:
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61 SAISPDVPDDCRVTFYQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 4758.200-US
REFECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
                                                                           APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                         LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
 Diskette
                                                                                                                                                                                                                           TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO:
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US-08-819-825-3
MEDIUM TYPE:
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CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

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E: No. 62216440 No. 6221644disk of No. 6221644th America, Inc. 405 Lexington Avenue, Suite 6400
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                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DAY:
APPLICATION NUMBER: US/09/163,642
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 4758.200-US TELECOMUNICATION INFORMATION: TELEPHONE: 212 867 0123 TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
                                                                                                                                                                                                                                                                                              FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                               MEDIUM TYPE: Diskette
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Best Local Similarity 75.6%
Matches 353; Conservative
                                                                      COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
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                                                       New York
                                                                                                                                                            OPERATING SYSTEM
                                   New York
                                                                                                                                                                                                                                   FILING DATE:
   ADDRESSEE:
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US-09-155-855-3
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Patent No. 6221644
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION:
APPLICANT: And V.
TITLE OF INVENTION: And Nucleic Acids Encoding Same
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                                              GENERAL INCOMENTATION:
GENERAL INCOMENTATION:
GENERAL INCOMENTATION:
APPLICANT: KANEKO, Syunichi
APPLICANT: TANEKO, Syunichi
APPLICANT: TANEKO, Syunichi
APPLICANT: TANEKO, TATESUA
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124
CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: UP 084314
EARLIER FILING DATE: 1996-04-05
BARLIER PILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VOYE: 2.0
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APPLICANT: KONDO, Hidemasa
APPLICANT: ANAZAWA, Hideharu
APPLICANT: RANEKO, Syunichi
APPLICANT: NGASHIMA, Tadashi
APPLICANT: NGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
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Patent No. 6139902
Sequence 3, Application US/09155855 Patent No. 6139902
                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-155-855-3
                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 346;
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 467
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LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 DTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENOMVNSGIKFYRR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 NSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: KONDO, Hidemasa
APPLICANT: KANEKO, Syunichi
APPLICANT: TANEKO, Tatsuya
APPLICANT: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124;
CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1996-04-04
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALCHIIN VOS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                    Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       73.8%; Score 1818; DB 4; 75.7%; Pred. No. 4.8e-182;
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER SEQ ID NOST: 7
; SOFTWARE: PATENTIN PATE: 1996-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09155855
; Patent No. 6139902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 DSFVKGLSFARSGGDWGECFA 443
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                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Aspergillus niger
US-09-155-855-1
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.8%
Best Local Similarity 75.7%
Matches 334; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-155-855-2
                                                                                                                                                                                                                                                         LENGTH: 443
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Search completed: October 26, 2001, 16:40:47 Job time: 4958 sec
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                                                                       ; OTHER INFORMATION: Xaa at positions 2 & 3 may be any amino acid or unknown US-09-155-855-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: No. 58661180 No. 5866118disk of No. 5866118th America, Inc. 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                  90 SASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRYKA 149
                                                                                                                                                                                                                                                                 6 SKGKKYSALIEBIQONATIFEGKYAFLKTYNYSLGADDLTPFGGGELVNSGVKFYQRYES 125
                                                                                                                                                                                                                                                                                                         150 LARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYNNT 209
                                                                                                                                                                                                                                                                                                                        210 LDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTV 269
                                                                                                                                                                                                                                                                                                                                                                                  270 ARTSDATELSPFCALFTHDEWIQYDYLGSLGKYYGYGAGNPLGPAQGYGFANELIARLTH 329
                                                                                                                                                                                                                                                                                                                                                                                                                                             390 EETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDF 449
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                          0;
                                                                                                                                       Length 443;
                                                                                                                                                                  59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Rlotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                 73.6%; Score 1813; DB 4;
76.0%; Pred. No. 1.6e-181;
tive 46; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTROL OF THE CONTROL OF THE CONTROL OF THE CALL OF THE CALLON OF THE CASSIFICATION (435)
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 VEGLSFARSGGNWAECFA 467
                            TYPE: PRT
ORGANISM: Aspergillus niger
                                                                                                                                                            Matches 333; Conservative
                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
SEQ ID NO 2
LENGTH: 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-819-825-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 TYNYTLGADDLTPFGENOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 QSAKLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVE-ANFTALFA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 PAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDAT----ELSPFCALFTHDEWIQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 NATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVE--SIEETDGYSASWTVPFAARAYV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 EMMQC-----QAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGVF-VVLLSIATLFGSTSGTALGP--RGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LGSFLVLLLQFSALL--TASPAIPPFWRKKHPNVD------IARHWGQYSPFFSL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 YDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLT-HSPVQDHTSTNHTLDSNPATFPL
                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                   Length 475;
                                                                                                                                                                                                                                                                                                                                                          Ouery Match 54.2%; Score 1334; DB 2; Length 47 Best Local Similarity 56.1%; Pred. No. 3e-131; Matches 273; Conservative 62; Mismatches 114; Indels
                                                            4758.200-US
                  NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                  TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 2:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
                                                                                                                                                                                                                                                        MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 GNWAECF 466
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                                                                                                                                                                                                                                            TOPOLOGY:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

October 26, 2001, 17:47:03 ; Search time 3927.32 Seconds (without alignments) 5529.654 Million cell updates/sec Run on:

US-09-488-265-30

Title: Perfect score:

l atgggcgtgttcgtcgtgct......gggaagaatgtttcgcttaa 1404 IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

1344157 seqs, 7733874588 residues Searched:

2688314 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

: gb\_ba1:\*
: gb\_ba2:\*
gb\_ba3:\*
gb\_in1:\*
gb\_in2:\*
gb\_in3:\*
gb\_om:\*
gb\_ow:\*
gb\_pat1:\* gb\_p11:\* gb\_p12:\* gb\_p13:\* gb\_p14:\* em\_bal:\* em\_ba2:\* em\_fun:\* dp\_ph:\*

em\_htg\_hum7:\*
em\_htg\_hum8:\*
em\_htg\_inv1:\*
em\_htg\_inv2:\*
em\_htg\_other:\*
em\_htg\_rod:\*
em\_htg\_rod:\* em\_htgo\_hum: \*
em\_htgo\_inv: \*
em\_htgo\_rod: \*
em\_htg\_hum1: \*
em\_htg\_hum2: \* em\_htg\_hum3:\* em\_htg\_hum4:\* em\_htg\_hum5:\* em\_htg\_hum6:\* 112... 1143... 115... 116... 117... 1

em\_hum2:\* em\_hum3:\* em\_hum4:\*

em\_hum5:\*
em\_hum6:\*
em\_hum7:\*
em\_in:\*

gb\_htg13:\* gb\_htg14:\* gb\_htg15:\* gb\_htg16:\*
gb\_htg17:\*
gb\_htg18:\*
gb\_htg19:\* gb\_htg20:\*
gb\_htg21:\*
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gb\_htg24:\*
gb\_htg25:\* gb\_sts2:\* gb\_sts3:\* gb\_htg6:\* gb\_htg7:\* htg10:\* gb\_htq11:\* gb\_htg12:\* gb\_sts1:\* gb\_un:\* gb\_vil:\* gb\_vi2:\* em\_sts:\* em\_sy:\* gb\_htg1:\* gb\_htg8:\* gb\_htg4:\* gb\_htg5:\* gb\_ro1:\*
gb\_ro2:\*
gb\_in4:\*
gb\_pr10:\*
em\_ba3:\* em\_pl:\* gb\_pr7:\* gb\_pr8:\* gb\_pr9:\* em\_ov:\* em\_ph: \* gb\_pr2:\* em\_un:\* gb\_sy:\* gb\_pr4:\* em\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AX021809 Sequence AF295325 Synthetic A19452 phytase cDN I13430 Sequence 33 I33881 Sequence 19 ZIG414 A. niger phy AR018076 Sequence AR051916 Sequence Description 9 AX021809 56 AF295325 9 A19452 10 I13430 10 I33881 13 ANDHYAG 9 AR018076 9 AR051916 Query Match Length DB ID 1426 1350 1404 1404 1404 2000 2363 93.8 555.8 443.7 443.7 443.5 Score 1317.6 783.6 614.2 614.2 614.2 610.2 610.2 Š. Result

| 4        |           | 0     |        | Sequenc |          | U59804 Aspergillus | AF218813 Aspergill | AB022700 Aspergill | AY013315 Aspergill | 2       | AX000630 Sequence | U59803 Emericella | A46793 Sequence 11 | AX000632 Sequence | Talaromy | A46783 Sequence 1 | U59805 Aspergillus | AX000636 Sequence | U60412 Aspergillus | AX085191 Sequence |        | 2 Sequenc  | 7       |          |       | AX085208 Sequence | A46785 Sequence 3 | U59806 Myceliophth |            | 3           | s<br>S     | Хe        |       | Z35962 S.cerevisia | 80 Ye     | X78993 S.cerevisia |        |
|----------|-----------|-------|--------|---------|----------|--------------------|--------------------|--------------------|--------------------|---------|-------------------|-------------------|--------------------|-------------------|----------|-------------------|--------------------|-------------------|--------------------|-------------------|--------|------------|---------|----------|-------|-------------------|-------------------|--------------------|------------|-------------|------------|-----------|-------|--------------------|-----------|--------------------|--------|
| AR053934 | ASNPHYTAS |       | A19451 |         | AX000634 |                    |                    |                    |                    | AB04280 | AX000630          |                   | Ø                  | AX000632          |          |                   |                    | AX000636          | ATU604             |                   | AX0851 | 0 AX085192 | AX08520 | AR031151 |       | 0 AX085208        | A46785            |                    | 0 AX085210 | 4 MGR299239 | 4 SCU19789 | 4 SCPHO5A |       | 5 SCYBR093C        | 4 SCPH035 |                    |        |
| 2379 9   | Н         |       | -      |         | -        |                    |                    |                    |                    |         | 1931 9            |                   | 1912 9             | _                 | 1845 15  |                   |                    | 1567 9            | Н                  | Н                 | Н      | 1584 10    | П       | -        | Т     | Н                 | 3995 9            | Ä                  | Н          | Н           | 1          | 1404 14   | 904 1 | 934 1              |           | 748 1              | )      |
| 43.5     | 43.5      | 43.5  | 43.5   | 43.5    | 43.4     | 43.4               | 43.1               | 42.1               | 42.0               | 41.8    | 41.1              | 41.1              | 39.7               | 38.4              | 38.4     | 37.6              | 37.6               | 37.5              | 37.5               | 36.4              | 36.4   | 36.4       | 29.5    | 24.6     | 20.4  | 20.0              | 18.3              | 18.3               | 9.5        | 9.9         | 4.6        | 4.6       | 4.6   | 4.6                | 4.6       | 4                  |        |
| 610.2    | 610.2     | 610.2 | 610.2  | 610.2   | 610      | 610                | 605.4              | 591.6              | 589.6              | 587.2   | 576.8             | 576.8             | 558                | 539.4             | 539.4    | 528.6             | 528.6              | 527               | 527                | 511.2             | 510.6  | 510.6      | 414.2   | 346      | 286.2 |                   | 257.2             |                    |            |             |            | 64        | 64    | 64                 | 64        | 44                 | ;      |
| 6        | 10        | ::    | 12     | 13      | 14       | 15                 | 16                 | 17                 | . 6                | 51.     | 20                | 1.0               | 22                 | 23                | 24       | 25                | 26                 | 27                | 28                 | 29                | 30     | 31         | 32      | 33       | 34    | 35                | (*)               | 37                 | 38         | c 39        | 7          | 41        | 42    | 43                 | - 7       | 7                  | י<br>י |

## ALIGNMENTS

| 07-SEP-2000   | ·   |                                   |
|---|---|-----------------------------------|
| PAT   |   | truct"<br>'t                      |
| AX021809 1426 bp DNA<br>Sequence 3 from Patent EP0897985.<br>AX021809.1 GI:10045052 | synthetic construct. synthetic construct artificial sequence. 1 (bases 1 to 1426) Lehmann,M. Consensus phytases Pattent: EP 08997885-A 3 24-FEB-1999; |                                   |
| RESULT 1 AXO21809 LOCUS DEFINITION ACCESSION VERSION                                | REFERENCE<br>ORGANISM<br>REFERENCE<br>AUTHORS<br>TITLE<br>JOURNAL   | FEATURES SOURCE BASE COUNT ORIGIN |

|   | QY       | 61   | geettgggteetegtggtaacteteesetettgtgaeactgttgaeggtggttaecaatgt 120                   |    |
|---|----------|------|---|----|
|   | QQ       | 7    | CCTTGGGTCCTCGTGGTATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 13                       |    |
|   | ΟŊ       | -    | cccagaaatttctcacttgtggggtacatactctccattcttctctttggc                                 |    |
|   | Dp       | 132  | TCCCAGAAATTICTCACTTGTGGGGTCAATACTCTCCATACTTCTCTTTGGAAGACGAA 19                      |    |
|   | QY       | -    | tgctatttctccagacgttccaaaggttgtagagttactttcgttcaagttttgtct 24                        |    |
|   | οp       | 2    | CIGCTATITCICCAGACGIICCAGACGACIGIAGAGIIACIIICGIICAAGIITIGICI 25                      |    |
|   | δλ.      | 4 1  | agacacggtgctagatacccaacttcttctgcgtctaaggcgtactctgctttgattga                         |    |
|   | <b>q</b> | ń    | GACACGGIGCIAGAIACCCAACIICIICIAAGICIAAGACCIIIAACAGIGGIGCIIAAGAGAGAG                  |    |
|   | QY       | 301  | gctattcaaagaacgctactgctttcaagggtaadtacgctttcttgaaggctLacaac sou<br>                 |    |
|   | g<br>T   | 4 1  | CIAITCAAAAGAAACGCIACIGCIIICOGGGGGGGGGGGGGGGGG                                       |    |
| • | Oy<br>Dp | 361  | Facactriggfggrgadgagactrigatrocartocygysgacaraatascsggr-<br>                        |    |
|   | Qγ       |      | ttaagttotacagaagatacaaggotttggotagaaagattgttocattcattagagot 48                      |    |
|   | qq       | 432  |   |    |
|   | Qy       | 481  | tgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct 54                             |    |
|   | qu       | 492  | CIGGITCIGACAGAGITATIGCITCIGCIGAAAGIICATIGAAGGITTCCAAICTGCI 55                       |    |
|   | δλ       | 541  | occagtgctaacccacaccaagctctccagttattaacgttattatt 60                                  |    |
|   | QD       | 552  | STIGGCIGACCCAGGITCICAACCACACAAGCITCICCAGITAITGACGITAITAIT 61                        |    |
|   | QY       | 601  | tggttacaacacactttggaccacggtttgtgtactgctttcgaagaa 66                                 |    |
|   | qq       | 612  | CAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTCCTTTCGAAGAC 67                      |    |
|   | Qy       | 661  | <pre>sgacgttgaagctaacttcactgctgttttcgct                                      </pre> | _  |
|   | qq       | 672  | ctgaattgggtgacgacgttgaaggtaacttcactggttggt  |    |
|   | δλ       | N    | gctcacttgccaggtgttaacttgactgacgaagacgttgttaacttg 78                                 | _  |
|   | qq       | 732  | CTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGAC   |    |
|   | ΟŅ       | 781  | ttgctagaacttctgacgctactcaattgtctcca 84  | _  |
|   | qq       | 792  | TGGACATGTGTCCATTGGAAACTGTTGCTAGAACTTCTGACGTACTGAATTGTCTCCA 85                       |    |
|   | οy       | 841  | 0   | _  |
|   | QQ       | 852  | TCTGTGCTTTGTTCACTCACGACGAATGGAGACAATACGACTACTTGCAATCTTGGGT 91                       | _  |
|   | QY       | 901  | t 96<br>  | _  |
|   | qq       | 912  | STACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 97                       | _  |
|   | Qγ       | 961  | gaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020                      |    |
|   | qa.      | 972  | AATTGATTGCTAGATTGACTAGATCTCCAGTTCAAGACCACTTCTACTAACCAC 103                          |    |
|   | Qy       | 1021 | ttggactetaacccagctactttcccattgaacgctactttgtacgctgacttctt 108                        | 90 |
|   | qq       | 1032 | CTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 109                     |    |
|   | Qy       | 1081 | caacactatggtttctattttctttcgttttgggtttgtacaacggtactaagcca 114                        | 0  |
|   | qa       | 1092 | ACGACAACTCTATGATTTCTATTTTTCTTCGCTTTGGGTTTGTACAACGGTACTGCTCCA 115                    | 21 |

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STKLKOPRAOPGOSSEKIDVYISEASSSNNTLDPGTCTVFEDSELADTVEARFTATFV
STRORLENDLSGVTLTDTEVTYLMOMCSFOTISTSTVDTKLSPFCDLFTHDEWINVD
YLOSIKKYYGHGAGNPLGFTGGVGYANBLIARLITASPVHDDTSSNHTLDSSPAFFPLN
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MMQCQAEQBFLVRVLYNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA
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Yang, L., Bei, J., Liao, L. and Wang, X.
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/note="Aspergillus niger sequence modified for expression
in Pichia pastoris"
1201 gitccaitcgctgctagagcitacgitgaaatgatgcaatgtgaagcigaaaggaacca 1260
                                                                                            1261 tiggitagagittiggitaacgacagagitgitccattgcacggitgiggigitgacaag 1320
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synthetic construct
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1 (bases 1 to 1350)
Yang, L., Chen, Z., Bei, J., Liao, L. and Wang, X.
Synthetic sequence of phytase gene for expression in Pichia
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/product="phytase"
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Gaps

Score 783.6; DB 56; Length 1350; Pred. No. 2e-198; 0; Mismatches 334; Indels 0;

55.8%;

Best Local Similarity 74.7 Matches 984; Conservative

Query Match

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EDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDT
KLSPFCDLFFFHDEWINYDYLOSLKKYTYGGAGORDEPPQGVTANELTARLTHESPUHD
DTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTYRUITOT
DGFSSAWTYPPASKLYVEMMQCQAEQEPLVRVLVNDRVVPLHGCPVDALGRCTRDSFV
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QQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRS
SGSSRVIASGKKFIEGFQSTKLKDFRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVF
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ilarity 64.9%; Pred. No. 3.3e-153;
Conservative 0; Mismatches 493;
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|---|--|---|
| ttggttagagftttggttaacgacagagttgttccattgcacggttgtggtgttgacaag                      | 113430 1404 bp DNA Sequence 33 from patent US 5436156. 113430. 113430. GI:910771 Unknown. Unclassified. Unclassifi | Match Local Similarity 64.9%; Score 614.2; DB 10; Length 1404; les 910; Conservative 0; Mismatches 493; Indels 0; G 1 atgggegttogtegtegteattohes 493; Indels 0; G 2 atgential 1   1   1   1   1   1   1   1   1   1 |
| Oy 1261  Db 1261  Oy 1321  Db 1321  Oy 1381                                       | RESULT 4 113430 LOCUS LOCUS ACCESTION VERSION VERSION VERYWORDS SOURCE ORGANISM REFERENCE REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE BASE COUNT   | Ouery Match Best Local Matches 91  Qy 1 atg  Qy 1 21  Qy 121 ttcc  Qy 121 ttcc  Qy 121 tcc  Qy 181 tctc  Qy 241 agac  Qy 361 tacc  Qy 421 attac   |

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                               601 ccagaaggtgctggttacaacacctttggaccacggtttgtgtactgctttcgaagaa 660
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06-FEB-1997

PAT

Sequence 19 from patent US 5593963. I33881

I33881.1 GI:1824672

Unknown. Unclassified. Unknown

ORGANISM

SOURCE

1404 bp

133881

LOCUS

RESULT 133881 DEFINITION ACCESSION

VERSION KEYWORDS

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1 (bases 1 to 1404)
Van Ooijen,A.J.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C.
and Verwoerd,T.C.
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                                                      Expression of phytase in plants
Patent: US 5593963-A 19 14-JAN-1997;
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van Hartingsveldt,W., Van Zeijl,C.M.J., Harteveld,M.G., Gouka,R.J., Suykerbuyk,M.E.G., Luiten,R.G.M., Van Paridon,P.A., Selten,G.C.M., Van Sarktra,A.E., Van Gorcom,R.F.M. and Van Den Hondel,C.A.M.J.
Veenstra,A.E., Van Gorcom,R.F.M. and Van Den Hondel,C.A.M.J.
Cloning, molecular characterization and overexpression of the phytase gene (phyta) of Aspergillus niger
Gene (1992) In press
2 (bases 1 to 2000)
van Hartingsveldt W.
Direct Submission
Submitted (G5-OCT-1992) Van Hartingsveldt W., TNO Medical
Submitted (G5-OCT-1992) Lange Klelweg 139, Rijswijk, the Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Fungi: Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 2000)
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/strain="Van Tieghem strain"
/db_xref="taxon:5061"
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369. .1712
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804 CGCGTGATCGCCTCCGGCAAGAATTCATCGAGGGCTTCCAGAGCACCAAGCTGAAGGAT 863
                                            ccaggtgctaacccacaccaagcttctccagttattaacgttattattccagaaggtgct 612
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TGTTTTGCTTA 1714
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05-DEC-1998

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| REFERENCE<br>AUTHORS         | ORS         | 1 (bases 1 to 2363)<br>Nevalainen, H.K.M., Paloheimo, M.T., Miettinen-Oinonen, A.S.K.,<br>Torkkeli, T.K., Cantrell, M., Piddington, C.S., Rambosek, J.A.,                                       | QY                               | 853 t<br>1358 T                  | ttcactcacgae<br>            <br>TTCACCCATGAE   |
|------------------------------|-------------|---|----------------------------------|----------------------------------|--|
| TITLE<br>JOURNAL<br>FEATURES | NAL<br>KES  | Turunen,M.K. and Fagerstrom.R.B.<br>Production of phytate degrading enzymes in trichoderma<br>Patent: US 5780292-A 7 14-JUL-1998;<br>Location/Qualifiers  | Qy                               | 913 t                            | tacggtgctgg<br>          <br>CATGGCGCAGG   |
| BASE C                       | SOULC       | e 1. 2363<br>/organism="unknown"<br>559 a 732 c 510 g 562 t   | Qy<br>D                          | 973 9                            | gctagattgac<br>  |
| ORIGIN                       | · .         | د<br>د<br>۱۹  | Oy                               |                                  | aacccagctac  |
| Best<br>Matc                 | Loc         |   | qa &                             | 1538 2                           | AACCCAGCTAC<br>atggtttctat   |
| VO do                        | 13          | gtegtgetaetgteeattgeeacettgtteggtteeacateeggtaeegeettgggteet 72<br>   | 7 A                              |                                  | ATCATCTCTAT  |
| G GX                         |             | cgtggtaactctcactttgtgacactgttgacggttgttaccaatgtttcccagaaatt 132 cgtggtaactctcactttggacactgttgacggttgttaccaatgtttcccagaaatt 132 TCGAGAAATCAATCCACTTGCGATACGGTCGATCAAGGGTATCAATGCTTCTCCGAGACT 637 | oy da                            | 1153 1 1658 2                    | tetgttgaate<br>          <br>ACCGTGGAGAA   |
| QY                           | 133         | teteactigigggiàcatactetecattetetetiggetgacgaatetgetattet 192<br>  | g 6                              | 1718                             | TCGCGTCTGTA  |
| O.Y<br>Db                    |             | ccagacgttccaaagggttgtagagttactttcgttcaagttttgtctagacacggtgct 252<br>  | da d                             |                                  | ttggttaacga<br>              <br>TTGGTTAATGA   |
| λο qa                        |             | agatacccaacttettetgegtetaaggegtaettegetttgattgaagetatteaaaag 312<br>  | qa<br>a                          |                                  | aagagagacga<br>        <br>ACCCGGGATAG   |
| Qy<br>Db                     |             | aacgctactgctttcaagggtaagtacgcttcttgaagacttacaactacactttgggt 372 allii i   | QV<br>Dp                         | 1393                             | tgttcgctta<br>   |
| Qy<br>Db                     | 373         | gctgacgacttgactccattcggtgaacaacaaatggttaactctggtattaagttctac 432<br>  | RESULT<br>AR051916<br>LOCUS      | LT 8<br>1916<br>S                |  |
| Qy<br>Dp                     | 433<br>938  | agaagatacaaggctttggctagaaagattgttccattcatt  | ACCESSION<br>VERSION<br>KEYWORDS | ACCESSION<br>VERSION<br>KEYWORDS | AR051916.  |
| Oy<br>Db                     | 493<br>998  | agagttattgcttctgctgaaaagttcattgaaggtttccaatctgctaagttggttg  | SOURC                            | SCURCE<br>ORGANISM<br>REFERENCE  |  |
| Qy                           | 553<br>1058 | ccaggtgctaacccaccaccaagcttctccagttattaacgttattattccagaaggtgct 612<br>   | LI LI                            | TITLE                            | Torkkell, Turunen, Nucleic a   |
| Qy                           | 613         | ggttacaacaacatttggaccacggtttgtgtactgctttcgaagaatctgaattgggt 672<br>   | FEAT                             | FEATURES<br>Sourc                | F4 CGII.:  |
| Qy                           | 673<br>1178 | gacgacgitgaagctaacttcactgctgttttcgctccaccaattagagctagaitggaa 732<br>  | BASE                             | BASE COUNT<br>ORIGIN             | ָּהָ בְּיִהְ ב |
| VO 4                         | 733         | geteactigecaggigitaactigacigaegaagaegtigitaactigaigaeaigigt 792<br>   | W B C                            | Best Loc<br>Matches              | Local Similari<br>nes 903; Cons  |
|                              | 793         |   | Qy<br>Dp                         | 13                               | gtcgtgctact  |
| g .                          | 1298        |   | QY                               | 73                               | cgtggtaact   |

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nen,H.K.M., Paloheimo,M.T., Miettinen-Oinonen,A.S.K.,
1,T.K., Cantrell,M., Piddington,C.S., Rambosek,J.A.,
"M.K., Pagerstrom,R.B. and Houston,C.S.
acid molecules encoding phytase and pH2.5 acid phosphatase
US 5830733-A 7 03-NOV-1998;
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rity 64.9%; Pred. No. 4e-152;
nservative 0; Mismatches 488; Indels 0;
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|-----|---|--|---|--------------------------------------|---|---------------------------------|--|---|--|--|---|--|---|--|---|--|---|--|
| E   | +> E+   |  | tacc<br>    <br> ATC  | aacgctact<br>        <br>AACGTGACC   | gctgacgac<br>            <br>GCAGATGAC                          | agaagatac<br>     <br>CAGCGATAC | 5-5  | ccaggtgct<br>          <br>                                     | ggttacaac<br>       <br>TCATCCAAC  | gacgacgtt<br>  <br> SATACCGTC                                      | gctcacttg<br>     <br>AACGACCTG                                     | ccattcgaca<br>        <br>TCCTTCGACA                                 | ttcactcace  | tacggtgetg<br>          <br> CATGGCGCAC                            | gctagattga<br>  | aacccagcta<br>   | atggtttcta<br>         <br>ATCATCTCTA                               | tctgttgaat<br>   |
| 578 | 133   | 193  | 253<br>758  | 313                                  | 373<br>878  | 433                             | 493<br>998   | 553<br>1058   | 613<br>1118  | 673<br>1178  | 733   | 793  | 853<br>1358   | 913  | 973   | 1538   | 1093  | 1153   |
| QQ  | QV  | O <sub>Y</sub>   | QY<br>Db  | OY<br>Db                             | QY<br>Db  | Qy<br>Db                        | Qy<br>Db   | Qy<br>Db  | QY   | Qy<br>Db   | QY<br>Db  | Qy<br>Db   | Qy  | Qy<br>Dp   | Qy  | Qy<br>Db   | Qy<br>Dp  | Οy   |

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Nevalainen, H.K. M., Palohelmo, M.T., Fagerstrom, R.B., Miettinen-Oinonen, A.S.K., Turunen, M.K., Rambosek, J.A., Midtinen-Oinonen, A.S.K., Turunen, M.K., Rambosek, J.A., Houston, C.S., Houston, C.S. and Cantrell, M.A. Recombinant cells that express phytate degrading enzymes in desired ratios
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                          1213 gctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaaccattggttagagtt 1272
                                          1333 aagagagacgacttcgttgaaggtttgtctttcgctagatctggtggtaactgggaagaa 1392
                                                                                                                                                 1838 ACCCGGGATAGCTITGTGAGGGGTTGCTAGATCTGGGGGGTGAITGGGGCGAG 1897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 610.2; DB 9; Length 2379;
Pred. No. 4e-152;
0; Mismatches 488; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: US 5834286-A 1 10-NOV-1998;
                                                                                                                                                                                                                                                                                 Sequence 1 from patent US 5834286.
AR053934
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/LTAIRS 14 LION-"MOYSAVILDELYLLAGVTSGLAVPASRNOSTCDTVDOGVQCFSET
SHLMGOYAPPESLAMESAISPDVPAGCRVTPRQVLSRHGARYPTESGKKYKSALIBEI
QOVVTPEDGKYREKTYRYSLGADDLTPFGEQELVNSGIKFYQRYSELTRNIIPETRS
GOSSRYLASGEKVEIKTYRYSLGADDLTPFGEQELVNSGIKFYQRYSELTRNIIPETRS
SGSSRYLASGEKFFFANIALPETRAFAPSTRQRGSSPK.IDVYISSASSSNNTLADGGTCTVF
EDSELADTVERNFTARFAPSTRQRLENDLSGVTLTDTFGVYTLADMGSFDTISTSTVDT
KLSPFCOLFFTHDEWIHYDYLOSIKKYTYGHGAGNPLGPTGVGVGYANELIATTHSPVHD
DGFSSAWITLDSRPAFFFLNSTLYVEMMQCQAEQEPLVRYLNDLSFTYFFNITQF
DGFSSAWIVPFASRLYVEMMQCQAEQEPLVRYLNUDKRVVPLHGCPIDALGRCTRDSFY
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                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                         piddington,C.S., Houston,C.S., Paloheimo,M., Cantrell,M.,
Miettinen-Oinonen,A., Nevalainen,H. and Rambosek,J.
The cloning and sequencing of the genes encoding phytase (phy) and
pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2379)
Carter,J.R., Franden,M.A., Aebersold,R.H. and McHenry,C.S.
Molecular cloning, sequencing and overexpression of the gene encoding the psi subunit of E. coli DNA polymerase III holoenzyme Unpublished (1992)
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                                                                                                                   Aspergillus niger (strain ALK0243, sub_species awamori) DNA
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                              awamori phytase gene, complete cds
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/db_xref="taxon:5061"
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/EC_number="3.1.3.8"
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/protein_id="AAA16898.1"
/db_xref="G1:166519"
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/citation=[2]
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Eukaryota; Fungl; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurofiales; Trichocomaceae; Aspergillus. 1 (bases; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillus. 1 (bases; Trichocomaceae; Aspergillus. Positive identication of a lambda gt11 clone containing a region of fungal phytase gene by immunoprobe and sequence verification of Appl. Microbiol. Biotechnol. 35, 611-614 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHIMGOYAPFFSLANESYISPEYPAGCRVTFAQVLSHGARYPTDSKGKKYSALIEEI
QONATTEDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYORYESLTRNIYPFIRS
SGSRYLASGKKFIEGFGYSTKKDPRAOPGOSSRYIDVYSTSASSSNNTLDGGTCTVF
EDSELADTYPNNFTATFVPSIRQRLENDLSGYTLTDTEVTYTMDMCSFDTISTSTVDT
KLSPFCOLFTHDBWINTDYLQSLKKYYGHGAGNFLGFTQGYGYATTLDDGTTSTSTVDT
DTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTVENITQT
DGFSSAMTVPFASRLYVENMQCQAEQEPLVRYLYUNDKYVPLHGCPVDALGRCTRDSFV
                                                                                                                                                                                                                                                       ASNPHYTASE 2665 bp DNA PLN 27-APR-1993
Aspergillus niger myo-inistol hexaphosphate phosphohydrolyase gene,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AaA32705.1"
/db_xref="G1:166521"
/translation="MGVSAVLLP1YLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSET
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/product="myo-inositol hexaphosphate phosphohydrolyase"
808 c 574 g 650 t
1333 aagagagactccgttgaaggtttgtctttcgctagatctggtggtaactgggaagaa 1392
                         1854 ACCCGCGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGGGGGTGATTGGGGCGAG 1913
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Mullaney,E.J.
Sequence of the Aspergillus niger (ficuum) phytase gene
Unpublished (1992)
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Aspergillus niger
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/tissue_lib="EMBL 3; NRRL 3135"
<683. .726
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/note="phytase gene"
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/EC_number="3.1.3.8"
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SGSSRVIASGKKFIEGFOSTKLKDPPRAQPGGSSPKIDVVISFASSSNNTLDPGTCTVF
EDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDT
KLSPFCOLFTHDEWINYDYLOSLKKYYGHGAGNPLGFPGGVGYANELLTATHSFNHD
DTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGINNGTKPLSTTAVFNHT
DGFSSANTVPFASRLYVEMMQCQAEQEPLVRVLNDRYVPLHGCPVDALGRCTRDSFV
RGLSFARSGGDWAECFA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSET
SHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEI
                                                                                                                                                                                             1937 ACCGIGGAGAATAICACCCAGACAGAIGGATICICGICTIGGACGGIICCGITIGCI 1996
                                        gctagagcttacgttgaaatgatgcaatgtgaagctgaaaggaaccattggttagagtt 1272
                                                                         2057 TIGGITAAIGAICGCGITGICCCGCIGCAIGGGIGCCGGIIGAIGCTIIGGGGAGAIGI 2116
                                                                                                                                                                                                                                                                                                                                                                                                           phytase gene locus of plasmids pAF 2-3, pAF 2-6, pAF 2-7. A19451
                                                                                                                      1273 ttggttaacgacagaqttqttccattgcacggttgtggtgttgacaagttgggtagatgt
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1 (bases 1 to 6756)
van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A., Venstra,A.E., Luiten,R.G.M. and Selten,G.C.M.
Cloning and expression of microbial phytase
Patent: EP 0420358-A 40 03-APR-1991;
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join(210. 254,357. 1715)
/gene="phytase gene"
join(210. 254,357. 1715)
/gene="phytase gene"
join(210. 254,357. 1712)
/gene="phytase gene"
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/gene="phytase gene"
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/db_xref="GI:583194"
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357. .1715
/gene="phytase gene"
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| 0; Gaps 0                              |                                   | 13.  | 119   |   | tattcaaaag 312<br>              <br>GATCCAGCAG 623 | 37.   | taagttctac 432<br>         <br>CAAGTTCTAC 743                    | tggttctgac 492<br>        <br>TGGCTCCAGC 803                     | 55<br>86   | agaaggtgct 612<br>    <br>CGAGGCCAGC 923                         | tgaattgggt 672<br>        <br>CGAATTGGCC 983                   | tagattggaa 732<br>        <br>ACGTCTGGAG 1043                    | ggacatgtgt ·792<br>          <br> GACATGTGC 1103                 | otgtgacttg 852<br>  |   | gaattgatt 972<br>         <br> GAGCTCATC 1283                    | ttggactct 1032<br>         <br> TrGGACTCG 1343                   | :gacaacact 1092<br>   |
| . No. 4.3e-152;<br>smatches 488; Indel | gtaccg<br> <br> <br>GACTGG        | CGTGGTaactctcactcttgtgacactgttgacggtggttaccaatgtttcccagaaatt | teteacttgtggggtacatactctccattcttctctttggctgacgaatctgctattct | ccagacgttccaaagggttgtagagttactttcgttcaagttttgtctagacacggtgt<br> | agatacccaacttcttctgcgtctaaggcgtactctgctttgattga    | aacgctactgctttcaagggtaagtacgcttcttgaagacttacaactacactttgggt<br> | gctgacgacttgactccattcggtgaacaacaaatggttaactctggtattaagttctac<br> | agaagatacaaggetttggetagaaagattgttecatteattagagettetggttetgae<br> | agagttattgcttctgctgaaaagttcattgaaggtttccaatctgctaagttggctgac<br> | ccaggtgctaacccacaccaagcttctccagttattaacgttattattccagaaggtgct<br> | ggttacaacaacactiggaccacggtttgtgtactgctttcgaagaatctgaatlggt<br> | gacgacgttgaagctaacttcactgctgttttcgctccaccaattagagctagattggaa<br> | gctcacttgccaggtgttaacttgactgacgaagacgttgttaacttgatggacatgtgt<br> | ccattcgacactgttgctagaacttctgacgctactcaattgtctccattctgtgactt<br> | ttcactcacgacgatggattcaatacgactacttgcaatctttgggtaagtactacggt<br> | tacggtgctggtaacccattgggtccagctcaaggtgttggtttcgttaacgaattgatt<br> | gctagattgactcactctccagttcaagaccacacttctactaaccacactttggactct<br> | aacccagctacttcccattgaacgctactttgtacgctgacttctctcacgacaacact |
| 64.9%; Pred. N<br>ative 0; Mism        | cattgccaccttgttcggttccacatccg<br> | otcttgtgacactgttg:<br>                <br> CAGTTGCGATACGGTCG | tacatactctccattct!<br>                <br>TCATACGCACGTTCTI  | 999ttgtagagttacttt<br>  | ttctgcgtctaaggcgta<br>                             | caagggtaagtacgcttt<br>                   <br>TGACGGAAATAIGCCTI  | tccattcggtgaacaaca<br>                  <br> TCCTTCGGAGAACAGGA   | tttggctagaaagattgt<br>                  <br>GCTCACAAGGAACATCGT   | tgctgaaaagttcattga<br>   | acaccaagettetecagt<br>             <br>GGGCAATCGTCGCCCAA         | tttggaccacggtttgtg<br>               <br> CTCGACCCAGGCACCTG    | caacttoactgctgtttt<br>   | gttaacttgactgacga<br>  | gctagaacttctgacgc<br>   | ltggattcaatacgacta(<br>                <br> TGGATCAACTACGACTA(  | ccattgggtccagetca:<br>   | tctccagttcaagaccad<br>  -  -  -  -  -  -  -  -  -  -  -  -  -    | ccattgaacgctacttte  |
| Local Similarity<br>les 903; Conserv   |                                   | 73 cgtggtaactetca<br>  11<br>84 TCGAGAAATCAATC               |   |   |  |   | e 4+   | m 4  |  |  |  |  |  |   |   |  |  |   |
| Best L                                 | Oy 13<br>Db 324                   | Qy 7<br>Db 38  | Oy 133<br>Db 444  | Oy 193<br>Db 504  | Qy 253<br>Db 564                                   | Oy 313<br>Db 624  | Qy 37.<br>Db 68  | Qy 43:   | Qy 493<br>Db 804   | Qy 553<br>Db 864   | Qy 613<br>Db 924   | Qy 673<br>Db 984   | Oy 733<br>Db 1044  | Oy 793<br>Db 1104   | Qy 853<br>Db 1164   | Qy 913<br>Db 1224  | Qy 973<br>Db 1284  | Qy 1033   |

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1344 AGCCCGGCTACCTTTCCGCTCAACTCTACCCGGACTTTTCGCATGACAAGGGC 1403
                                                                         1153 tctgttgaatctattgaagaaactgacggttactctgcttcttggactgttccattcgct 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

( Dases 1 to 6756)

Van Gorcom, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A., Veenstra, A.E., Luiten, R.G.M. and Selten, G.C.M.

Cloning and expression of phytase from aspergillus
Patent: US 5436156-A 31 25-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%; Score 610.2; DB 10; Length 6756; 64.9%; Pred. No. 4.3e-152; Live 0; Mismatches 488; Indels 0;
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SPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFNNELIARLTRSPVQDHT
STNSTLVSNPATFPLANTMYVDFSHDNSMVSIFFALGLYNGTBPLSRTSVESAKELDG
YSASWWYPFGARAFTPETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLNDFVKG
LSWARSGGNWGBCFS"
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ANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRAS
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66.7%; Pred. No. 4.4e-152;
Live 0; Mismatches 440;
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/note="unnamed protein product"
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Van, L.A. and Wyss, M.
Modified phytases
Patent: EP 0897010-A 5 17-FEB-1999;
HOFFMANN LA ROCHE (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB77103.1"
/db_xref="G1:7241016"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="unidentified"
                                                                                                               Sequence 5 from Patent EP0897010.
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                                                                                                                                                                        675 cgacgitgaagctaacttcactgcttttcgctccaccaattagagctagattggaagc 734
                                                                                                                                                                                                  768 TGAGGITGCGGCCAATTTCACTGCGCTCTTTGCACCGGACATCCGAGCTCGCGCGGGAA 827
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                                                       555 aggtgctaacceacaccaagcttctccagttattaacgttattattccagaaggtgctgg
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        SFU59804
        1812 bp
        DNA
        PLN
        17-JAN-1998

        LOCUS
        SFU59804
        1812 bp
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        PLN
        17-JAN-1998

        LOCUS
        ACCESTION
        VS9804
        ACCESTION
        U59804-1
        GI:2108353

        KEYMORDS
        ASPERGILLUS fumigatus.
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HIWGOYSPFESLEDELGYSSKLPKDORITLVOYLSREGARYPTSSKEKKYKKLUTAIO
ANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRAS
GSDRYLASGEKFIEGFOQAKLADPGATURAAPAISV1 IPESETFNNTLDHGVCTKFEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVTLTFLLSAAYLLSGRVSAAPSSAGSKSCDTVDLGYQCSPATS
                  Eukaryota; Fungl; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. I (bases I to 1800)
Pasamontes, L., Halker, M., Wyss, M., Tessier, M. and van Loon, A.P. Gene cloning, purification, and characterization of a heat-stable phytase from the fungus Aspergillus fumigatus
Appl. Environ. Microbiol. 63 (5), 1696-1700 (1997)
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                                                                                                                                                                                                                                                           Submitted (02-JUN-1996) Luis Pasamontes, VFCB, F.Hoffmann-La Roche AG., Basel 4070, Switzerland
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                                                                                                                                                                                                                                                                                                                                                 /organism="Aspergillus fumigatus"
/db_xref="taxon:5085"
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join(<284. .330,388. .>1738)
join(284. .330,388. .1738)
/EC_number="3.1.3.8"
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/db_xref="GI:2108354"
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Pasamontes, L.
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aggtgctaacccacaccaagcttctccagttattaacgttattattccagaaggtgctgg 614
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gb\_gss25:\*

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em\_gss\_pro:\*

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em\_gss\_hum9:\* em\_gss\_inv1:\*

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em\_gss\_hum6:\*
em\_gss\_hum7:\*
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em\_gss\_hum3:\*

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gb\_est111:\*
gb\_htc:\*
em\_gss\_fun:\*
em\_gss\_hum1:\*
em\_gss\_hum2:\*

em\_gss\_rod1:\*
em\_gss\_rod3:\*
em\_gss\_rod4:\*
em\_gss\_rod5:\*
em\_gss\_vrt1:\*
em\_gss\_vrt2:\*
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em\_gss\_vrt3:\*

gb\_gss2:\* gb\_gss3:\* gb\_gss4:\* \*:9ss6\_dp

\*:8ss6\_dp

gb\_gss5:\*

253: em\_gss\_rod6:\*
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255: qb\_gss35:\*
256: qb\_gss35:\*
258: qb\_gss35:\*
258: qb\_gss37:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_inv4:\*

95-9525 95-9525 95-95831:\*\* 95-988331:\* 95-988332:\* 95-9883333:\* JOURNAL

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|           |               |             | _                  | _           |             | _   |     | _   |          | _       |   | -         |            |          |          |          |          |          |          |            |          | _        |          |                   |                   |                    |                      |                   |          |                   |              |             |      |                   |       |          |     |         |          |            |         |         |           |          |   |
|-----------|---------------|-------------|--------------------|-------------|-------------|-----|-----|-----|----------|---------|---|-----------|------------|----------|----------|----------|----------|----------|----------|------------|----------|----------|----------|-------------------|-------------------|--------------------|----------------------|-------------------|----------|-------------------|--------------|-------------|------|-------------------|-------|----------|-----|---------|----------|------------|---------|---------|-----------|----------|---|
|           |               | Describtion | AQ324539 mqxb0019C | mgxb0014    |             |     | _   |     | mgxb0004 | mgxpuou | AD20/439 IELIAOUON<br>AV054552 AV054552 | RPC 111-4 | 17 HS 3124 | AV129427 | -        | AV05471  | V293643  | AV0027   | AV07712  | V114552    | AV08195  | AV0601   | AV05388  | AV118366 AV118366 | AV047696 AV047696 | BF637070 NF049F02L | AV4.23.43 AV4.23.243 | AV04996Z AV04996Z | 0777     | AV161297 AV161297 | V05600       | V091        | V049 | AV079904 AV079904 | .vo/8 | AVIOU    | ~ ~ | AVUSSIO | . <      | RE AVORGAG | AV02040 | 4405078 | 136 AV054 | AV118481 |   |
| SUMMARIES | Q.            |             | A032               | AQ25545     | AJ274       |     |     |     |          |         | AV054552                                |           |            | AV129427 | AV064132 | AV054718 | AV293643 | AV002/59 | AV0//122 | AVI14552   | AV081956 | AV060181 | AV053884 | AVII8366          | AVU4 / 696        | BF 03 / U / U      | AV049962             | AV212676          | AU039641 | AV161297          | AV056003     | AV091633    |      | AV07990           |       | AV120593 |     | AV05389 | AV151459 | AV05848    | AV05079 | 5767    | 54        | 48       |   |
|           | DB            | 1           | 227                | 226         | 104         | 227 | 225 | 227 | 227      | 221     | 109                                     | 225       | 224        | 25       | 109      | 109      | 82,5     | 100      | 201      | 77         | 100      | 7 O T    | 103      | 27                | בים ר<br>הם ר     | 30 T               | 109                  | 26                | 107      | 25                | 109          | 109         | 109  | 100               | 100   | 25       | 109 | 109     | 25       | 109        | 109     | 109     | 109       |          |   |
| , "·      | Length        |             | 802                | 837         | 752         | 600 | 810 | 769 | 699      | 1016    | 4                                       | 481       | 545        | 231      | 234      | 230.     | 747      | #07<br>C | 200      | 2/2        | 202      | 767      | 000      | 343               | 247               | 4 8 2              | 265                  | 295               | 512      | 227               | 249          | 266         | 202  | 280               | 285   | 289      | 289 | 290     | 291      | 296        | 297     | 298     | 300       | .303     | - |
| or        | ery           |             | 10.9               | ю г<br>4. с | » · v       |     | 5.4 | 5.3 | 5.2      | 3.1     | 3.0                                     | 3.0       | 0.6        | 9.0      | 2.0      | , c      |          | , c      | 4 c      | <i>y</i> c | , c      | , c      | , 0      | , c               | , 0               | . 6                | 2.9                  | 5.9               | 2.9      | 2.8               | α, α<br>α, α | м с<br>20 о | 4 C  | . 6               | 2     | 2.8      | 2.8 | 2.8     | 2.8      | 2.8        | 2.8     | 2.8     | 2.8       | 2.8      | • |
|           | Score         |             | 152.6              | , ,         | <u> ۱</u> « | · - |     | 4   | m        | ω.      | $\ddot{-}$                              | ᡤ.        | ∹,         | ٠,       |          | -        | 7.1.7    |          | :<br>-   | -          | ;<br>-   | -        | ; -      | 41.2              |                   |                    | 0                    | o.                | 40.2     | 9.                |              | ס ת         | 70   | 39.6              | σ     | 6        | 9   | g       | g)       | S)         | σ       | 9       | 39.6      | о<br>О   |   |
|           | Result<br>No. |             | ci<br>Ci           | N 0         | 0 <b>4</b>  |     | 0 0 |     | <b>8</b> | 6       | 10                                      | Η,        | 0<br>15    | ÷.       | T -      | 7 F      | 7 -      | a<br>T   | 0 0      | 200        | 2,5      | 22       | 1 6      | 240               | 2.5               | 26                 | 27                   | 28                | c 29     | 30                | J.C.         | 3 6         | 9.6  | 35                | 36    | 37       | 38  | 39      | 40       | 41         | 42      | 43      | 44        | 45       |   |

ALIGNMENTS

A0324539 802 bp DNA GSS 08-JAN-1999 mgxb0019C01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0019C01r, DNA sequence. (bases 1 to 802)
Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. AQ324539.1 GI:4116391 Magnaporthe grisea. Magnaporthe grisea AQ324539 RESULT 1 AQ324539/C DEFINITION ORGANISM ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE SOURCE

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/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome with an average insert size of 130
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."
1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     864 cgaatggattcaatacgactacttgcaatctttgggtaagtactacggttacggtgctgg 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 CGTGGCAGATCCNCAAGCAC-----CCTGTCGCAGTTCTGCACGCTGTTTACGCAACG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%; Score 152.6; DB 227; Length 802; 55.3%; Pred No. 1.4e-33;
               Contact: Dean RA (
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Beani: rdean@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                /organism="Magnaporthe grisea"/strain="70-15"
                                                                                                                                                                                                                                                                                      /db_xref="taxon:148305"
                                                                                                                                                                                      High quality sequence stop: 408.
Location/Qualifiers
Unpublished (1998)
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Matches 343; Conservative
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// lab_host="Froplasts"
// lab_host="E. coli DH10B"
// lab_host="E. coli DH10B"
// lab_host="E. coli DH10B"
// lab_host="E. coli DH10B"
// lab_host="Vector: pBACWICID; Site_1: HindIII; Site_2: HindIII;
// Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n-7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request.

48 a 154 c 188 g 243 t 4 others
                                                                                                                                                                                                                                                                                                       AQ255459 837.bp DNA GSS 23-OCT-1998 mgxb0014M15r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0014M15r, DNA sequence.
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Yu.Y., Zhu.H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,

Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                              1278 taacgacagagttgttccattgcacggttgtggtgttgacaagttgggtagatgtaagag 1337
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                                                                                   80 CAACGACAGGGTGACGCCGCTGCAGAACTGCGATGCCGACACAAAGTATGGGTCGTTGCACGCT 21
140 GATGTTTGTTGAAAAAATGACTTGCGCAGGGCAGAACGAGGAGCTTGTGAGAATCCTGGT 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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/clone_lib="CUGI Rice Blast BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
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High quality sequence stop: 277.
Location/Qualifiers
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="70-15"
                                                                                                                                            1338 agacgacttcgttgaaggtt 1357
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Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Metarhizium.
1 (bases 1 to 581)
Screen, S.E., Mathur, P. and St. Leger, R.J.
EST analysis of the insect pathogenic fungus Metarhizium anisopliae (Dnpublished (1999)
Contact: Screen SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: Unizap; Metarhizium anisopliae was grown on
insect cuticle for 24 hours. A cDNA library was
constructed in the unidirectional Lambda vector, Unizap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ274007 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae
                                                                                                                                                                                                                                                                                   977 gattgactcactctccagttcaagaccacacttctactaaccacatttggactctaacc 1036
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                                                                                                                                                                           380 GATTAACCCGGAAGCCCAGTCCAAGATCAAACCATGTCCAATACGACACTTGACATGAACC 439
200 TGGAAACAACGCGAACTTTGAAAAACTGGCCAACTTTCACCGCTTTGCAATCTGTTA 259
                                                                                                                        260 CGGAAGCAGATTGGGTAAAATATGGTTACTTGTCCAGCGTGCAAAAATGGTACAGATACG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                440 CGGAAACCTTACTCCTACAAGGCAAATTGTATGCTGATTTTATCCATACGGACGATATTA 499
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                                                                      857 ctcacgacgaatggattcaatacgactacttgcaatctttgggtaagtactacggttacg 916
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4112 Plant Sciences Building, College Park, MD 20742, USA.
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Metarhizium anisopliae
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Matches 234; Conservative
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/clone="magnature" /
/clone="magnature" /
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//Lisb.host="brotoplasts"
//Lab.host="E. coli DH10B"
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Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomprete with a haploid genome (n=7) of approximately 40 Mpp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request. "3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ163004 753 bp DNA GSS 09-SEP-1998
mgxb0021D19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                         442 aaggetttggetagaa---gattgttecatteattagagettetggttetgacagagtt 498
322 gotttoaagggtaagtaogotttottgaagacttacaactacactttgggtgctgacgac 381
                                                                                                                                                                                                                460 CAGAAGTTAGCGGAGGATTCGACCATCCCTTTGTTCGAGCCTCGGGCTCTGAAAGAGTC 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
                                                                                                                                                                                                                                                                                 499 attgottotgotgaaaagttcattgaaggtttccaatctgotaag 543
                                                                                                                                                                                                                                                                                                               520 GTCATGTCAGGGCAAGATTTTGTTCATGGCTTCTACAAGCCAAG 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Magnaporthe grisea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dean RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone mgxb0021D19r, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:148305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 448.
Location/Qualifiers
1.,753
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
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Gaps

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Query Match

6.0%; Score 83.8; DB 225; Length 753;
Best Local Similarity 50.7%; Pred. No. 2e-13;
Matches 227; Conservative 0; Mismatches 215; Indels 6;

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AQ162040 699 bp DNA GSS 09-SEP-1998
mgxb0010F06r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
alone mgxb0010F06r, DNA sequence.
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                  90 ttgtgacactgttgacggtggttaccaatgtttcccagaaatttctcacttgtggggtac 149
                      249 GTAIGCACCATITITCGTIGCACCGICAGCACCATCGGATIAIGAITCCTCTGCIACCIT 308
                                                                                                                                                                                                                                                       264 ttcttctgcgtctaaggcgtactctgctttgattgaagctattcaaaagaacgctactgc 323
                                                                                                                                                                                                                                                                                                369 GGCTCAAACCGGGGGGAAATTCTCGAACACGATTCACCGACTCCAAACCTCACGTACCGG 428
                                                                                                                                                                                                                                                                                                                                           324 tttcaagggtaagtacgctttcttgaagacttacaactacactttgggtgctgacgactt 383
                                                                                                                                                                                                                                                                                                                                                                    384 gactccattcggtgaacaacaatggttaactctggtattaagttctacagaagatacaa 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          549 AAATCTGGCCAGAAGGAACGAACCATTTATTCGCTATGATGACAAANAACGCGTGTTTGA 608
                                                                                 150 atactetecattetetetttggetgaegaatetgetatttetecagaegttecaa----
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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/clone="maxb0010F06r"
/clone=lb="Cug1 Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. col1 DH10B"
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Clemson University Genomics Institute
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Location/Qualifiers
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             609 TAGCGCAGAACTCTGGGCTAGGGGTTTC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 ttctgctgaaaagttcattgaaggtttc 531
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AQ161556 810 bp DNA GSS 09-SEP-1998 mgxb0008K02r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008K02r, DNA sequence.
AQ161556
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/tissue_type="Protoplasts"
/lab host="E. coli DH10B"
/note="Vector: pBACWICH; Site_l: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
              blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In corder to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Y.Y. Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1178 acggitactctgcttcttggactgttccattcgctgctagagcttacgttgaaatgatgc 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1238 aatgtgaagctgaaaaggaaccattggttagagttttggttaacgacagagttgttccat 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 TGCAGAACTGCGATGCCGACAGTATGGGTCGTTGCACGCTGAGCAAGTTCGTTGAGAGCT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 CTTGCGCAGGCCAGAACGAGCGTGTGAGAATCCTGGTCAACGACAGGGTGACGCCGC 532
                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
haploid genome (n=7) of approximately 40 Mbp.
                                                                                                                                                                                                                                                                                                                                        Length 699;
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5.8%; Score 81.4; DB 225; Length
Best Local Similarity 59.9%; Pred. No. 9.7e-13;
Matches 136; Conservative 0; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1358 tgtctttcgctagatctggtggtaactgggaagaatgtttcgcttaa 1404
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Clemson University Genomics Institute
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Class: BAC ends
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Fax: 864 656 4293
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a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     590 TIGCGCAGGGCAGAACGAGCTTGTGAGAATCCTGGTCAACGACGACGACGCCGCT 531
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                                                                                                                                                                                                                                                                                                            Query Match 5.4%; Score 75.6; DB 225; Length 810; Best Local Similarity 58.4%; Pred. No. 5.1e-11; Matches 132; Conservative 0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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/clone_lib="CUGI Rice Blast BAC Library"
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/lab_host="E. coli DH10B"
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Contact: Dean RA
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of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request. 3 others
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                             87 ctcttgtgacactgttgacggtggttaccaatgtttcccagaaatttctcacttgtgggg 146
                                                                                                                                                                                                                                                                                                                                                                                                                                     273 CIGITITGAIGCGCCAGCCCGCGGTTTTCAATTIAAAGCAGCAATCACTCATAATTGGGG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 tacatactctccattcttcttttggctgacgaatctgctatttctccagacgttccaa- 205
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Clemson University Genomics Institute
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634 Tel: 864 656 5737

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/note="Vector: Dargaments Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request." I others
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/clone_lib="CUGI Rice Blast BAC Library"
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                                                                                                                                                                                                                                                                                                      /tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                   /strain="70-15"
/db_xref="taxon:148305"
                                                                                                High quality sequence stop: 465.
Fax: 864 656 4293
Bmall: rdcan@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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1 (bases 1 to 1016)

2 (bases 1 to 1016)

3 (bases 1 to 1016)

4 (bases 1 to 1016)

6 (bases 1 to 1016)

7 (bases 1 to 1016)

8 (bases 1 to 1016)

9 (bases 1 to 1016)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Tetraodon nigroviridis genome survey sequence T7 end of clone 105015 of library G from Tetraodon nigroviridis, genomic survey
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Best Local Similarity 48.0%; Pred. No. 0.13;
Matches 122; Conservative 1; Mismatches 131; Indels 0;
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/db_xref="taxon:99883"
/clone="105015"
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       1033 aacccagctactttcccattgaa 1055
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Thermostabilization and thermoactivation of thermolabile enzymes by Thermostabilization and thermoactivation of tuli length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 34)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, M., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/dev_stage="adult"
60 c 101 g 9
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YV054552 Mus musculus pancreas C:
Clone 1810031C08, mRNA sequence.
AV054552
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Contact: Chie Owa
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1 (bases 1 to 481).

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Sub, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Other_GSSS: RPCIII-48J14:TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
class: BAC ends.
                                           AQ202816 481 bp DNA GSS 20-APR-1999
RPCIl1-48J14.TK RPCI-11 Homo sapiens genomic clone RPCI-11-48J14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966 attgattgctagattgactcactctccagttcaagaccacacttctactaaccacacttt 1025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41.8; DB 225; Length 481;
Pred. No. 0.35;
0; Mismatches 177; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mark Adams
Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="RPCI-11-48J14"
/clone_lib="RPCI-11"
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                                                                                     DNA sequence.
AQ202816
                                                                                                                                                                                                    Homo sapiens
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 545)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                           AQ140737 545 bp DNA GSS 24-SEP-1998 HS_3124_A2_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=20 Row=G, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and scanning the \ensuremath{\mathsf{human}} genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 actotgotttgattgaagotattcaaaagaacgotactgotttcaagggtaagttgctt 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 AATCTGATTTGGTTTTAATAGTAAAAGTACACTGGTGGGAGCATGAGCATTCTT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 caaatggttaactctggtattaagttctacagaagatacaaggctttggctagaaagatt 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 TACAAGGTTAAGTAAACCATTATTTTCTATCTGTGAAACAAG--AATAACTAGATATTTA 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TT: (206) 616-3618
Eax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 t
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Location/Qualifiers
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Matches 129; Conservative
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                                    AUTHORS
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                                                                                                                                                               Akahira, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatau, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigamoto, Y., Shiraki, T., Soqabe, Y., Suqahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., RIKEN Mouse ESTs
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-resettc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation for the synthesis of full length cDNA
Transcriptional sequencing: A method for DNA sequencing using RNA
Ploase visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 231)
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/clone_lib="Mus musculus C57BL/6J 11-day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watch 2.9%; Score 41.2; DB 25; Length 231; Local Similarity 52.3%; Pred. No. 0.41; les 91; Conservative 0; Mismatches 83; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="11-day embryo"
51 c 66 q 55 t
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                  AV129427.1 GI:5315662
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                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chie Owa
                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 234)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara, A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Cardinci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mus musculus small intestine C57BL/6J adult"
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/clone="2010009L02"
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45 c 72 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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Tel: Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-9145
Fax: 81-298-36-9098
Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., RIKEN Mouse ESTS

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/clone_lib="Mus musculus pancreas C57BL/6J adult"
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/tissue_type="pancreas"
/dev_stage="adult"
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/strain="C57BL/6J"
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COMMENT
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0; Gaps 0; Ouery Match 2.9%; Score 41.2; DB 109; Length 236; Best Local Similarity 52.3%; Pred. No. 0.42; Matches 91; Conservative 0; Mismatches 83; Indels 0;

1154 ctgttgaatctattgaagaaactgacggttactctgcttcttggactgttccattcgctg 1213 g

1214 ctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaaccattggttagagttt 1273 â

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1274 tggttaacgacagagttgttccattgcacggttgtggtgttgacaagttgggta 1327 δ

Search completed: October 26, 2001, 18:33:06 Job time: 6796 sec

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Mappli. work

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

October 26, 2001, 17:50:32; Search time 210.38 Seconds (without alignments) 4190.388 Million cell updates/sec Run on:

US-09-488-265-30

Perfect score:

l atgggcgtgttcgtcgtgct......gggaagaatgtttcgcttaa 1404 Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

730101 seqs, 313950809 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:\*
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/SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                 | Consensus phytase- Consensus phytase- DNA encoding a mut Consensus phytase Consensus phytase Consensus phytase Consensus phytase- Consensus phytase |
|-----------------------------|---|
| ID                          | AAZ31521<br>AAAZ3234<br>AAZ3233<br>AAAZ323<br>AAZ3232<br>AAZ3292<br>AAZ31520<br>AAAZ31520<br>AAZ31520<br>AAZ3153  |
| DB                          | 20<br>21<br>21<br>21<br>20<br>21<br>21<br>21  |
| Query<br>Match Length DB ID | 1404<br>1404<br>14064<br>1426<br>1426<br>1404<br>1404<br>1404   |
| Query<br>Match              | 100.0<br>100.0<br>100.0<br>98.9<br>98.9<br>98.6<br>94.5   |
| Score                       | 1404<br>1404<br>1404<br>1404<br>1388<br>1388<br>1384 8<br>1327 2<br>1327 2  |
| Result<br>No.               | 110<br>110<br>110   |
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WPI; 1999-591030/50. P-PSDB; AAY43170.

Petersen S;

| o >  | us phyta<br>oding phyatus phy<br>llus fun<br>oding a<br>llus fic<br>omal phy                                       | Phytase gene. Asp<br>Phytase gene. Asp<br>A. niger phytase g<br>Sequence, from ove<br>Aspergillus ficuum<br>Aspergillus fumiga<br>A. fumigatus phyta<br>Aspergillus niger<br>Aspergillus niger<br>Aspergillus niger | hyta<br>ric<br>herm<br>us p<br>As<br>ytas<br>erre<br>ase<br>ase<br>ase       |
|--|--|---|--|
| AAA7329<br>AAZ2742<br>AAX2302<br>AAA7323<br>AAZ5963<br>AAZ5963 | 11 AAA73236<br>00 AA231522<br>11 AAZ31522<br>11 AAZ317<br>12 AAA73235<br>13 AAA73235<br>12 AAQ11175<br>00 AAZ27421 | AAQ1387<br>AAQ5694<br>AAQ1117<br>AAT6513<br>AAX0314<br>AAZ2742<br>AAT9670   | 32324131441  |
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## ALIGNMENTS

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Phytase; animal feed preparation; thermostable phytase; transgenic plant; consensus sequence; ds.
                                                      Consensus phytase-10-thermo(3)-Q50T-K91A coding sequence.
       AAZ31521 standard; DNA; 1404 BP
                                                                                                                                                                      98DK-0000806.
98DK-0001176.
99DK-0000091.
99DK-0000093.
                                                                                                                                                99WO-DK00154.
                                                                                                                                                               98DK-0000407
                                       06-JAN-2000 (first entry)
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                                                                                                                                               22-MAR-1999;
                                                                                                                                                                       19-JUN-1998;
18-SEP-1998;
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22-JAN-1999;
                                                                                                                               30-SEP-1999
                                                                                                Synthetic.
                        AAZ31521;
AAZ31521
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                                             This sequence encodes the consensus phytase-10-thermo(3)-050T-K91A. The invention relates to a process for preparing animal feed by saglomerating feed ingredients with a thermostable phytase, which a added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed
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                                                                                                                                                                                                                     DB 20; Length 1404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                      ingredient and a feed additive (phytase) simultaneously.
                                                                                                                                                                              Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;
animal feed using a thermostable phytase
                                                                                                                                                                                                                    100.0%; Score 1404; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                            0; Mismatches
                           Example 3; Fig 10; 71pp; English.
                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 1404; Conservative
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                   121
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99DK-0000092.

22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS

21-JAN-2000; 2000WO-DK00025

WO200043503-A1

Synthetic.

27-JUL-2000

Lehmann M;

WPI; 2000-491161/43

P-PSDB; AAB20527

ytases with improved properties such as temperature stability, ity and substrate specificity, for use in pharmaceuticals and Novel phytases with improved compound foods and feeds stabi

Claim 10; Fig 8a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, substrate binding, position specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds rhe feed can be used to reduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present

Sequence 1404 BP; 329 A; 309 C; 308 G; 458 T; 0 other;

ö goottggggtootcgtggtaactctcactcttgtgacactgttgacggtggttaccaatgt 120 121 ttcccagaaatttctcacttgtggggtacatactctccattcttcttttggctgacgaa 180 gccttgggtcctcgtggtaactctcactcttgtgacactgttgacggtggttaccaatgt 120 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 420 420 480 480 9 1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc ttoccagaaatttotcacttgtggggtacatactctccattcttotctttggctgacgaa tacactttggggggcgacttgactccattcggtgaacaacaggttaactctggt attaagttetacagaagatacaaggetttggetagaaagattgtteeatteattagaget attaagttotacagaagatacaaggotttggotagaaagattgttocattoattagagot tctggttctgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct DB 21; Length 1404; 0 Indels 0; Ouery Match
100.0%; Score 1404;
Best Local Similarity 100.0%; Pred, No. 0;
Matches 1404; Conservative 0; Mismatches 61 121 181 241 241 301 361 181 301 481 481 361 421 421 δ Dp δλ d рp δ g g ð δ g δ g ŏ δ 셤 ò g

961 aacgaattgattgctagattgactcactctccagttcaagaccacattctactaaccac 1020 961 aacgaattgattgetagattgactcactctccagttcaagaccacacttctactaaccac 1020 1021 actitggactetaacccagetactiteccattgaacgetactitgtacgetgaettett 1080 Cacgacaacactatggtttctattttcttcgctttgggtttgtacaacggtactaagcca 1140 gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca 1260 ttggttagagttttggttaacgacagagttgttccattgcacggttgtggtgttgacaag 1320 ttggttagagttttggttaacgacagagttgttccattgcacggttgtggtgttgacaag 1320 tigictactacticigitigaatctatigaagaaacigacggitactcigcitcitiggact 1200 gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaggaacca 1260 840 ccagaaggtgctggttacaacaacactttggaccacggtttgtgtactgctttcgaagaa tctgaattgggtgacgacgttgaagctaacttcactgctgttttcgctccaccaattaga 841 ttctgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttgggt 901 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt atggacatgtgtccattcgacactgttgctagaacttctgacgctactcaattgtctcca 901 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgtttggtttcgtt 1021 actttggactctaacccagctactttcccattgaacgctactttgtacgctgacttctct ccagaaggtgctggttacaacaacactttggaccacggtttgtgtactgctttcgaagaa 1381 aactgggaagaatgtttcgcttaa 1404 1381 aactgggaagaatgtttcgcttaa 1404 601 601 661 661 781 1081 1141 1261 1201 1201 1261 οy qq QQ δ ŏ g qq δχ δ ga Ωÿ g ð Db g ö ŏ δy g δy g δ g ò g

RESULT AAZ59716

AA259716 standard; DNA; 1404

BP.

AAZ59716;

19-APR-2000 (first entry)

DNA encoding a mutant phytase-10, phytase-10-thermo[3]-Q50T-K91A.

Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; ds. 

Aspergillus terreus cbs16.46. Aspergillus terreus 9A1

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The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phytase) and one or more stabilishing agents including phytase (myo-inositol hexakisphosphate) physphothylene glycols with a molecular weight of to 4000 ba, preferably 1000 to 350 ba; the disodium salts of malonic, to 4000 ba, preferably 1000 to 350 ba; the disodium salts of malonic, and succinic acid; carboxymethyleellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a red composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal ced in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed of such animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved enzyme. The phytase formulation of the invention has an improved contained the proposition of the invention of the particle of participal entring long-term storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and pelleting. The present sequence represents DNA encoding a mutant phytase-10 consensus sequence, phytase-10-thermo[3]-050T-K91A, which has a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAY69566). Its specific activity with phytate as a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New stabilized enzyme formulation, useful for feed compositions for
                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Phytase-10-thermo[3-Q50T-K91A"
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                                                                                                                                                                Talaromyces thermophilus ATCC20186
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Aspergillus niger var. awamori. Aspergillus niger str. NRLA135. Aspergillus fumigatus ATCC13722. Aspergillus fumigatus ATCC3722. Aspergillus fumigatus ATCC58128. Aspergillus fumigatus ATCC32339.
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Paxillus involutus NN005693.
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Agrocybe pediades NN009289.
Peniophora lycii NN006113.
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Mismatches

Query Match 100.0%; Score 1404; Best Local Similarity 100.0%; Pred. No. 0; Matches 1404; Conservative 0; Mismatches

DB 21; Length 1404;

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AAA73293 standard; DNA; 1404 AAA73293; AAA73293 RESULT

05-DEC-2000 (first entry)

Consensus phytase 10 thermo 5 Q50T K91A polynucleotide SEQ ID NO:96.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds.

WO200043503-A1

27-JUL-2000

21-JAN-2000; 2000WO-DK00025

99DK-0001340. 99DK-0000092 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS

Lehmann M;

WPI; 2000-491161/43. P-PSDB; AAB20534.

temperature stability, in pharmaceuticals and phytases with improved properties such as ability and substrate specificity, for use compound foods and feeds stability Novel

Disclosure; Fig 25a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce 

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pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
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                                                                                                                10; Indels
                                                             Sequence 1404 BP; 329 A; 312 C; 304 G; 459 T; 0 other;
                                                                                           Score 1388; DB Pred. No. 0; 0; Mismatches
                                                                                        Query Match 98.9%;
Best Local Similarity 99.3%;
Matches 1394; Conservative
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                                                               gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca 1260
          aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt
                                                    aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac
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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present
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                                                     The present invention describes improved phytases, preferably with
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                          Claim 8; Fig 5a-c; 240pp; English.
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Matches 1394; Conservative
compound foods and feeds
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Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
thermostable; animal feed; monogastric animal; phytate phosphorus;
phosphate availibility; consensus; phytase-10; ds
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                                                                                                                  aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt 960
                                                                                     792 atggacatgtgtccattcgacactgttgctagaacttctgacgctactcaattgtctcca
                                                                           841 ttctgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttgggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding phytase-10, a consensus phytase.
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Aspergillus terreus cbs16.46.
Aspergillus niger var. awamori.
Aspergillus niger str. NRR13135.
Aspergillus fumigatus ATCC13073.
Aspergillus fumigatus ATCC32722.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC32239.
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formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilisting agents including phosphohydrolase) and one or more stabilisting agents including thosphohydrolase) and one or more stabilisting agents including to yield or tribitol; pulyethylene glycols with a molecular weight of 600 to 4000 Da, preferably loud to 3550 Da; the disodium salts of malonic, attabilised phytase formulation is used in a method for preparing a read stabilised phytase formulation is used in a method for preparing a provides a monogastric animals (e.g., pigs, poultry) and provides a monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphate is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate cot the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus animals of the inorganic phosphate liberated from phytate phosphorus animals of animal can make use of the inorganic phosphate liberated from phytate phosphorus animal can make use of the inorganic phosphate liberated from phytate phosphorus animal can make an animal can withstand feed processing methods such as extrusion, expansion and animals of an withstand feed processing methods and with a solution of each an animal can withstand feed processing methods and can withstand feed processing methods are animals of an animal can make animals animals and animals animals animals and animals animals and animals and animals and animals and animals and animals animals and animals animals and animals animals and animals and animals animal
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/note= "Signal peptide from Aspergillus terreus cbs16.46"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New stabilized enzyme formulation, useful for feed compositions for monogastric animals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a novel stabilised dry or liquid enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents DNA encoding a
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/product= "Mature phytase-10"
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/product= "Phytase-10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                        Location/Qualifiers
Talaromyces thermophilus ATCC20186. Myceliophthora thermophila.

Paxillus involutus NN005693.
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                                                                                           Agrocybe pediades NN009289.
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Gaps

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Pred. No. 0; 0; Mismatches

Best Local Similarity 99.3 Matches 1394; Conservative

Emericella nidulans.

Query Match

98.9%; Score 1388; 99.3%; Pred. No. 0;

DB 21; Length 1426; Indels 8

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cacgacaacatatggtttctattttcttcgctttgggtttgtacaacggtactaagcca 1140
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AAA73292 standard; DNA; 1404

AAA73292;

(first entry) 05-DEC-2000 Consensus phytase 10 thermo 5 Q50T polynucleotide SEQ ID NO:94.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate.binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds.

Synthetic

WO200043503-A1

27-JUL-2000 

21-JAN-2000;

22-JAN-1999;

99DK-0000092. 99DK-0001340. 21-SEP-1999;

(NOVO ) NOVO NORDISK AS

Ξ Lehmann WPI; 2000-491161/43. P-PSDB; AAB20533. temperature stability, in pharmaceuticals and Novel phytases with improved properties such as pH stability and substrate specificity, for use compound foods and feeds -

Disclosure; Fig 24a-c; 240pp; English.

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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaccutical compositions or compound food or feeds. The feed can be

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ito reduce levels of phytate in animal manure, by converting it blower inositol phosphates and/or inositol and inorganic phosphate. Present sequence encodes a phytase sequence from the present
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                                                                       Score 1384.8;
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98DK-0000806.
98DK-0001176.
99DK-0000091.
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P-PSDB; AAY43169.
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19-JUN-1998;
18-SEP-1998;
22-JAN-1999;
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This sequence encodes the consensus phytase-1-thermo(8)-050T-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced morre efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed
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tteccagaaattteteaettgtggggtacataeteteeattettetetttggetgaegaa 180 240 240 300 360 360 480 480 540 540 600 gccttgggtcctcgtggtaactctcactcttgtgacactgttgacggtggttaccaatgt 120 tacactttgggtgctgacgacttgactccattcggtgaacaacaaatggttaactctggt 420 tacactttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggt 420 0; Gaps 1 atgggcgtgttcgtcgtcgtctactgtccattgccacttgttcggttccacatccggtacc 60 9 coagaaggtgctggttacaacaacactttggaccacggtttgtgtactgctttcgaagaa ccagaaggatccggttacaacaacactttggaccacggtacttgtactgctttcgaagac atggacatgtgtccattcgacactgttgctagaacttctgacgctactcaattgtctcca atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc totgetatttetceagacgttecaaagggttgtagagttactttegtteaagtttgtet tetgetatttetecagaegttecagaegaetgtagagttaetttegtteaagttttgtet gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac aagttggctcaggtgctaacccacaccaagcttctccagttattaacgttattatt aagttggctgacccaggttctcaaccacaccaagcttctccagttattaacgtgatcatt totgaattgggtgacgacgttgaagctaacttcactgctgttttcgctccaccaattaga 94.5%; Score 1327.2; DB 20; Length 1404; 96.6%; Pred. No. 0; 48; Indels ingredient and a feed additive (phytase) simultaneously. Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other; 0; Mismatches Best\_Local Similarity 96.6
Matches 1356; Conservative Query Match 121 241 421 61 61 181 181 301 301 361 361 421 481 481 541 541 601 601 199 199 721 721 781 g g QQ g g δ g Qγ ρp δy g Op q Db ò ŏ ŏ QY ò ò QΥ QΥ ò

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aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020
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ttetgtgaettgttcaetcaegaegaaatggattcaataegaetaettgeaatetttgggt 900
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Lehmann M;

2000-491161/43 P-PSDB; AAB20526

temperature stability, in pharmaceuticals and such as t for use i Novel phytases with improved properties stability and substrate specificity, compound foods and feeds -

Claim 10; Fig 7a-c; 240pp; English

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present

Sequence 1404 BP; 329 A; 319 C; 304 G; 452 T; 0 other;

; ttoccagaaatttctcacttgtggggtacatactctccattcttctttggctgacgaa 180 tetgetatttetecagaegttecaaagggttgtagagttaetttegtteaagtttgtet 240 360 480 tacactttgggtgctgacgacttgactccattcggtgaacaacaatggttaactctggt 420 540 540 aagttggctgacccaggtgctaacccacaccaagcttctccagttattaacgttattatt 600 0; Gaps 1 atgggcgtgttcgtcgtgctactgtccattgccacttgttcggttccacatccggtacc 60 1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60 tctgctatttctccagacgttccagacgactgtagagttactttcgttcaagttttgtct gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac Score 1327.2; DB 21; Length 1404; Pred. No. 0; 48; Indels 0; Mismatches 94.5%; 96.6%; Matches 1356; Conservative Best Local Similarity Query Match 61 61 121 181 301 181 361 301 361 121 481 541 541 601 601 481 q δλ ó Q δŽ g öλ Ωp δ g δλ QQ QQ ŏ QΥ q αq ò ŏ

1260 aacgaattgattgctagattgactcactctccagttcaagaccacattctactaaccac 1020 961 aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020 cacgacaacactatggtttctatttttttcgctttgggtttgtacaacggtactaagcca 1140 1261 tiggitagagittitggitaacgacagagitigitccattgcacggitgigcigitgacaag 1320 841 ttctgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttgggt 900 096 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgct 960 tctgaattgggtgacgttgaagctaacttcactgctgttttcgctccaccaattaga atggacatgttccattcgacactgttgctagaacttctgacgctactcaattgtctcca 841 ttctgtgctttgttcactcacgacgaatggatccaatacgactacttgcaaagcttgggt 901 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt 1201 gttccattcgctgctagagcttacgttgaaatgatgcaatgtcaagctgaaaaggaacca actttggactctaacccagctactttcccattgaacgctactttgtacgctgacttctct 1201 gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca 1261 ttggttågagttttggttaacgacagagttgttccattgcacggttgtggtgttgacaag 1321 ttgggtagatgtaagaagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1381 aactgggaagaatgtttcgcttaa 1404 721 1021 661 721 901 961 1081 g δ pp Dp à ŏ g δ q δ qq ò Dp δy g qq 셤 a ò ŏ ŏ g

DNA encoding a mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A. AAZ59715 standard; DNA; 1404 19-APR-2000 (first entry) AAZ59715; RESULT 10 AAZ59715 

Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; ds. Aspergillus terreus cbs16.46.
Aspergillus niger var. awamori.
Aspergillus niger str. NRRL3135.
Aspergillus fumigatus ATCC130735. Aspergillus terreus 9Al

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formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol or ribitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal to utilise this form of phystate phosphorus, amongastric animals are unable to utilise this form of phosphate, resulting in the addition of extra phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for additional phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phytase-1 consensus sequence, phytase-1-thermo(8]-050T-K91A, which has a temperature optimum and melting point 7 degrees Celsius higher than that of phytase-1 (AAY69558).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and pelleting. The present sequence represents DNA encoding a mutant phytase-1 consensus sequence, phytase-1-thermo[8]-Q50T-K91A, which has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can withstand feed processing methods such as extrusion, expansion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New stabilized enzyme formulation, useful for feed compositions for monogastric animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel stabilised dry or liquid enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Phytase-1-thermo[8]-Q50T-K91A"
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                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                             Talaromyces thermophilus ATCC20186.
Myceliophthora thermophila.
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                              fumigatus ATCC58128.
fumigatus ATCC26906.
fumigatus ATCC32239.
fumigatus ATCC32722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brugger R, Lehmann M, Wyss M;
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                                                                                                                                                  Emericella nidulans.
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                                                                     Aspergillus
Aspergillus
Aspergillus
Aspergillus
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ttggttagagttttggttaacgacagagttgttccattgcacggttgtggtgttgacaag 1320
                                     ttgggtagatgtaagagagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1380
   Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds.
   Consensus phytase 3 thermo 11 Q50T K91A polynucleotide SEQ ID NO:92
   aactgggaagaatgtttcgcttaa 1404
   AAA73291 standard; DNA; 1404
  05-DEC-2000 (first entry)
  AAA73291;
   1261
  1321
                              1261
   1381
   RESULT
   g
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 δλ
              g
                             δy
  Db
  ò
   δ
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such as temperature stability, for use in pharmaceuticals and Novel phytases with improved properties pH stability and substrate specificity, 21-JAN-2000; 2000WO-DK00025 99DK-0001340. 99DK-0000092 (NOVO ) NOVO NORDISK AS 2000-491161/43. P-PSDB; AAB20532 WO200043503-A1. 22-JAN-1999; 21-SEP-1999; 27-JUL-2000. Lehmann M; Synthetic.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present research research and phytase sequence from the present Disclosure; Fig 23a-c; 240pp; English.

compound foods and feeds

C; 303 G; 452 T; 0 other; A; 321 Sequence 1404 BP; 328

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240
  aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020
  gccttgggtcctcgtggtaactctcactcttgtgacactgttgacggtggttaccaatgt 120
  300
  420
   480
   900
   900
   099
  720
   780
                       Gaps
   901 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgct 960
   aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt 960
  09
  atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc
  1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc
  gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt
  tacactttgggtgctgacgacttgactccattcggtgaacaacaaaggttaactctggt
   361 tacactttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggt
   781 atggacatgtgtccattcgacactgtcgctagaacttctgacgctactgaattgtctcca
  541 aagttggctgacccaggtgctaacccacaccaagcttctccagttattaacgttattatt
   ccagaaggtgctggttacaacaacactttggaccacggtttgtgtactgctttcgaagaa
   781 atggacatgtgtccattcgacactgttgctagaacttctgacgctactcaattgtctcca
   ttotgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttggggt
   totgotatttctccagacgttccaaagggttgtagagttactttcgttcaagttttgtct
  totggttctgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct
   totgaattgggtgacgacgttgaagctaacttcactgctgttttcgctccaccaattaga
   DB 21; Length 1404;
   ö
  51; Indels
 Score 1322.4;
            Pred. No. 0;
0; Mismatches
          96.48;
                  Matches 1353; Conservative
          Similarity
Query Match
Best Local
  481
  61
   121
   121
  181
   181
  241
   301
   301
  361
   601
  196
   721
   841
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Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds.
   The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile,
  1320
actttggactctaacccagctactttcccattgaacgctactttgtacgctgacttctct 1080
                           1021 actitiggactetaacceagetactiteceatigaacgetactitigtacgetgactietet 1080
   cacgacaacactatggtttctatttttttcgctttgggtttgtacaacggtactaagcca 1140
  ttgtctactacttctgttgaatctattgaagaaactgacggttactctgcttcttggact 1200
  gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca 1260
   ttggttagagttttggttaacgacagagttgttccattgcacggttgtggtgttgacaag 1320
   ttgggtagatgtaagagagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1380
   Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
  gttccattcgctgctagagcttacgttgaaatgatgcaatgtcaagctgaaaaggaacca
   ttggttagagttttggttaacgacagagttgttccattgcacggttgtgctgttgacaag
   Consensus phytase 3 thermo 11 Q50T polynucleotide SEQ ID NO:90.
   Disclosure; Fig 22a-c; 240pp; English.
   1381 aactgggaagaatgtttcgcttaa 1404
   BP.
   AAA73290 standard; DNA; 1404
   21-JAN-2000; 2000WO-DK00025
   99DK-0000092
  99DK-0001340
   (first entry)
  compound foods and feeds
   (NOVO ) NOVO NORDISK AS
   WPI; 2000-491161/43.
   P-PSDB; AAB20531.
   WO200043503-A1.
   22-JAN-1999;
  21-SEP-1999;
   05-DEC-2000
  27-JUL-2000
  Lehmann M;
  Synthetic.
  AAA73290;
  1141
   1321
  1261
   1261
  1081
   1201
  1321
   1081
   1141
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   AAA73290
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substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present
  360
   540
  099
  999
   720
  720
   780
  780
  840
   840
  121 ttoccagaaatttotoacttgtggggtacatactotocattcttottttggctgacgaa 180
   240
  300
   360
  tacactttggggtgctgacgacttgactccattcggtgaacaacaacaatggttaactctggt 420
   420
   480
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  009
   900
   geettggggteetegtggtaaeteteaetettgtgaeaetgttgaeggtggttaecaatgt 120
   geettgggteetegtggtaatteteactettgtgacaetgttgaeggtggttaecaatgt 120
specific activity, substrate specificity, substrate cleavage pattern,
  Gaps
   9
   181 tctgctatttctccagacgttccaaagggttgtagagttactttcgttcaagttttgtct
   gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac
  301 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac
  totiggttotigacagagttattigcttotigctigaaaagttoattigaaggtttocaatctigct
   ccagaaggtgctggttacaacaacactttggaccacggtttgtgtgtactgctttcgaagaa
|||||||||
  601 ccagaaggatccggttacaacaacactttggaccatggtctttgtactgctttcgaagac
   tetgaattgggtgacgacgttgaagetaacttcactgetgttttcgetecaccaattaga
   getagattggaageteaettgecaggtgttaaettgaetgaegaagaegttgttaaettg
   atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc
  1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc
  DB 21; Length 1404;
   53; Indels
   Sequence 1404 BP; 330 A; 320 C; 302 G; 452 T; 0 other;
   Score 1319.2;
Pred. No. 0;
0; Mismatches
   94.0%;
  Best Local Similarity 96.2 Matches 1351; Conservative
   invention.
   Query Match
Best Local 3
  361
  481
   481
   199
  781
   601
  781
  421
  721
   721
  61
  19
   301
  qq
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   pp
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   ttggttagagttttggttaacgacagagttgttccattgcacggttgtggtgttgcaag 1320
   ttggttagagttttggttaacgacagagttgttccattgcacggttgtgctgttgacaag 1320
         aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt 960
   841 ttctgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttgggt
  1381 aactgggctgaatgtttcgcttaa 1404
  aactgggaagaatgtttcgcttaa 1404
   1141
   1261
  1201
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  1381
                qq
                                 δλ
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  δ
  g
  δ
  g
   g
   qq
  Qγ
  ð
  ò
   qq
   Qγ
  g
  ó
   q
  ŏ
   Dp
```

Ascomycete consensus phytase coding sequence. BP AAZ27423 standard; cDNA; 1426 (first entry) 07-DEC-1999 AAZ27423; AAZ27423 XXX XX 
Phytase; variant; enzyme; phosphorus liberation; phytase substrate; phytate level reduction; animal manure; food preparation; soy processing; inositol manufacture; ss.

Synthetic.

W09949022-A1

99WO-DK00153 22-MAR-1999; 30-SEP-1999

98DK-0000407. 98DK-0000806. 98DK-0001176 99DK-0000091 23-MAR-1998; 19-JUN-1998; 18-SEP-1998; 22-JAN-1999;

(NOVO ) NOVO-NORDISK AS

Svendsen A;

WPI; 1999-580444/49.

ccagaaggtgctggttacaacaacacttggaccacggtttgtgtactgctttcgaagaa 660

601

P-PSDB; AAY39906

New variant phytase enzymes, used for liberating phosphorus from a phytase substrate, for reducing phytate levels in animal manure and in feed and food preparations -

Disclosure; Fig 9f-g; 141pp; English.

This sequence encodes the consensus Ascomycete phytase sequence.
The invention relates to variant phytase enzymes with specific amino acid substitutions for improved properties. The phytase variants can be used for liberating phosphorus from a phytase substrate. They can be used for reducing phytate levels in animal manure. They can be used in feed or food preparations. The phytase DNA can also be used to produce transgenic plants which can be used in feeds or foods. The phytase variants can also be used in soy processing and in the manufacture of inositiol or be used in soy processing and in the manufacture of inositiol or stability, temperature stability, phy profile, temperature profile, specific activity (in particularly in relation to pH and temperature), substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytase degradation rate and end level of released phosphate reached.

Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;

g

δ

g

ŏ q

g Q

δ

δ q q δ qq ŏ g ŏ qq δy

δy

; 0 61 gccttgggtcctcgtggtaactctcactcttgtgacactgttgacggtggttaccaatgt 120 251 tacactttgggtgctgacgacttgactccattcggtgaacaacaaatggttaactctggt 420 gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360 attaagttotacagaagatacaaggotttggotagaaagattgttocattoattagagot 480 tctggttctgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct 540 Gaps aagttggctgacccaggtgctaacccacaccaagcttctccagttattaacgttattatt 600 611 1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60 71 181 tctgctatttctccagacgttccaaagggttgtagagttactttcgttcaagttttgtct aagttggctgacccaggttctcaaccacaccaagcttctccagttattgacgttattatt DB 20; Length 1426; ; 0 54; Indels 93.8%; Score 1317.6; 96.2%; Pred. No. 0; 11ve 0; Mismatches Query Match 93.8 Best Local Similarity 96.2 Matches 1350; Conservative 312 372 492 541 301 361 481 421

```
ttgggtagatgtaagagagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1380
   actttggactctaacccagctactttcccattgaacgctactttgtacgctgacttctct 1080
   ttggttagagttttggttaacgacagagttgttccattgcacggttgtggtgttgacaag 1320
   1272 ttggttagagttttggttaacgacagagttgttccattgcacggttgtgctgttgacaag 1331
   aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020
  cacgacaacactatggtttctattttcttcgctttgggtttgtacaacggtactaagcca 1140
  1212 gttccattcggtgctagagcttacgttgaaatgatgcaatgtcaagctgaaaaggaacca 1271
   aacgaattgattgctagattgactagatctccagttcaagaccacacttctactaaccac 1031
   900
   780
  911
   aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgtttggtttcgtt 960
   tetgaattgggtgaegaegttgaagetaaetteaetgetttgttegeteeagetattaga 731
  791
   Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical; ds.
ccagaaggatccggttacaacaacactttggaccacggtacttgtactgcttcgaagac 671
   gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca
                     tctgaattgggtgacgattgaagctaacttcactgctgttttcgctccaccaattaga
   atggacatgtgtccattcgacactgttgctagaacttctgacgctactcaattgtctcca
  ttetgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttgggt
   Location/Qualifiers
  1392 aactgggctgaatgtttcgcttaa 1415
   1381 aactgggaagaatgtttcgcttaa 1404
   Fungal phytase gene consensus DNA.
  BP.
  AAX23022 standard; DNA; 1426
  (first entry)
   12..1415
   /*tag=
  11-JUN-1999
  Fungi.
   14
  1321
   672
  792
   852
  106
  961
  972
   1021
  1081
  1092
  1141
   1152
  1201
  1261
   612
  721
  732
                         199
  781
   841
  Key
  AAX23022
   g
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   g
  ò
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   g
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This invention describes a novel process for the preparation of a consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or pharmaceutical compositions. This sequence encodes the consensus phytase protein used in the method of the invention.
  tctggttctgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct 540
   ttoccagaaattteteaettgtggggtacatacteteceattettettttggetgaegaa 180
  300
   gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360
   tacactttgggtgctgacgacttgactccattcggtgaacaacaactggttaactctggt 420
   tacactttgggtgctgacgacttgactccattcggtgaaaaccaaatggttaactctggt 431
  geettgggteetegtggtaaeteteaetettgtgacaetgttgaeggtggttaeeaatgt 120
   191
  getattcaaaagaaegetactgetttcaagggtaagtacgetttettgaagaettacaae 371
  72 gccttgggtcctcgtggtaattctcactcttgtgacactgttgacggtggttaccaatgt 131
   9
  71
   0; Gaps
  DB 20; Length 1426;
   54; Indels
   Preparation of a consensus protein, especially a phytase programs to compare evolutionary similarity of sequences
   Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;
   11arity 96.2%; Score 1317.6; Score 1317.6; Conservative 0; Mismatches
/product= "phytase"
  Claim 8; Fig 2; 30pp; English.
   (HOFF ) HOFFMANN LA ROCHE AG
  98EP-0113176
  97EP-0112688
   WPI; 1999-134647/12.
  Best Local Similarity
Matches 1350; Conserv
   P-PSDB; AAW93380
  24-JUL-1997;
   15-JUL-1998;
                           EP897985-A2
   24-FEB-1999
   Lehmann M;
  Query Match
   121
  132
   181
  241
  252
  301
   312
  361
   372
  432
  481
  61
   192
   421
   QQ
   δλ
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  ò
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  qq
  g
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  ŏ
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  ò
   δŽ
   δy
    ŏ
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961 aacgaattgattgctagattgactcactctccagttcaagaccacattctactaaccac 1020
   aacgaattgattgctagattgactagatctccagttcaagaccacacttctactaaccac 1031
  1140
  gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca 1260
  ttggttagagttttggttaacgacagagttgttccattgcacggttgtggtgttgacaag 1320
   ttgggtagatgtaagagagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1380
                      492 totggttotgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgct 551
  ccagaaggtgctggttacaacaacacttggaccacggtttgtgtactgctttcgaagaa 660
  tctgaattgggtgacgacgttgaagctaacttcactgctttgttcgctccagctattaga 731
   840
  ttctgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttgggt 900
  aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt 960
   912 aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgtttggct 971
   tctgaattgggtgacgacgttgaagctaacttcactgctgttttcgctccaccaattaga
   ttctgtgctttgttcactcacgacgaatggagacaatacgactacttgcaatctttgggt
  atggacatgtgtccattcgacactgttgctagaacttctgacgctactcaattgtctcca
   actttggactctaacccagctactttcccattgaacgctactttgtacgctgacttctct
   ttggttagagttttggttaacgacagagttgttccattgcacggttgtgctgttgacaag
   cacgacaacactatggtttctattttcttcgctttgggtttgtacaacggtactaagcca
  1392 aactgggctgaatgtttcgcttaa 1415
   aactgggaagaatgtttcgcttaa 1404
  BP.
  DNA; 1426
   AAA73231 standard;
   972
  601
   612
  661
  672
   732
  792
  841
  901
  1092
   721
   781
   852
  1021
   1032
   1321
  1081
  1141
  1152
   1201
  1272
  1332
   1212
  1261
   1381
  g
                       Qγ
   d
  ö
   ò
  g
   δλ
   QQ
  δ
  Db
   δy
   pp
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   δ
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   ò
   δy
   qq
   δλ
   qq
   ŏ
   g
   QQ
  δ
  g
   ŏ
```

```
Consensus phytase polynucleotide sequence SEQ ID NO:15.
   (first entry)
  05-DEC-2000
  AAA73231;
RESULT 15
          AAA73231
                    XX AC AC
```

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile: temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure; ds.

Synthetic.

WO200043503-A1 27-JUL-2000 21-JAN-2000; 2000WO-DK00025

99DK-0000092. 22-JAN-1999; 21-SEP-1999; 

(NOVO ) NOVO NORDISK AS

Lehmann M;

WPI; 2000-491161/43 P-PSDB; AAB20515 'el phytases with improved properties such as temperature stability, stability, and substrate specificity, for use in pharmaceuticals and compound foods and feeds Novel

Example 9; Fig 2a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce used to reduce levels of phytate in animal manner, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence encodes a phytase sequence from the present invention

Sequence 1426 BP; 338 A; 311 C; 308 G; 469 T; 0 other;

ö

gccttgggtcctcgtggtaactctcactcttgtgacactgttgacggtggttaccaatgt 120 ttoccagaaatttotcacttgtggggtacatactctccattcttctctttggctgacgaa 180 240 0; Gaps 1 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 60 12 atgggcgtgttcgtcgtgctactgtccattgccaccttgttcggttccacatccggtacc 71 totgctatttctccagacgttccaaagggttgtagagttactttcgttcaagttttgtct 192 totgetattteteceagaegttecagaegaetgtagagttaetttegtteaagttttgtet Length 1426; 54; Indels DB 21; 93.8%; Score 1317.6; 96.2%; Pred. No. 0; 0; Mismatches Best Local Similarity 96.2 Matches 1350; Conservative Query Match 61 121 181 252 δy g ò g ά g ŏ qq δ ga

gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360

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1151
  actttggactctaacccagctactttcccattgaacgctactttgtacgctgacttctct 1080
  aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020
   960
   aagttggctgacccaggtgctaacccacaccaagcttctccagttattaacgttattatt 600
   ccagaaggtgctggttacaacaacactttggaccacggtttgtgtactgctttcgaagaa 660
  780
   atggacatgtgtccattcgacactgttgctagaacttctgacgctactcaattgtctcca 840
   851
  aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgct 971
                            431
  611
  ccagaaggatccggttacaacaacactttggaccacggtacttgtactgctttcgaagac 671
   791
  attaagttetacagaagatacaaggetttggetagaaagattgtteeatteattagaget 480
   gotattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 371
  aagtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgtt
   cacgacaacactatiggtttctattttcttcgctttgggtttgtacaacggtactaagcca
              tetggttetgaeagagttattgettetgetgaaaagtteattgaaggttteeaatetget
  aactgggaagaatgtttcgcttaa 1404
   1152
   732
  852
   912
  972
   1021
  1032
  1081
  1141
  1201
   1212
   1381
  672
   792
  841
  901
   1092
   492
   961
 312
   552
  601
  612
   661
  721
  781
   421
   481
   541
  g
   QQ
   δy
   g
  δλ
  g
   δy
   g
  QΥ
   a
  οy
  q
   Qγ
   g
  g
   qq
   οy
   δ
  q
  ò
               δy
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  οy
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  CD
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  g
  οy
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   Qγ
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October 26, 2001, 17:50:47 5048 sec Search completed: Job time: 5048 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

October 26, 2001, 15:20:18 Run on:

% Search time 87.5 Seconds
(without alignments)
3037.632 Million cell updates/sec

US-09-488-265-30

1 atgggcgtgttcgtcgtgct......gggaagaatgtttcgcttaa 1404 Perfect score: Sequence:

Scoring table:

IDENTITY\_NUC Gapor 10.0 , Gapext 1.0

649198 Total number of hits satisfying chosen parameters:

324599 seqs, 94655562 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | Sequence 3. Appli |                  | Segmence 19, Appr | 177             | 7 6              | 1               | - 1              | -                | 7 6              | , -              | ,<br>ה          | Segmence 3, Appli | ř -             | ì               | -i -            | ì.               | 1 0              |                  | Segmence 21, Appr | , ,              | 000              | , , ,            | , c              | 7 .               | <b>⊣</b> L | U I      | 'n   | Sequence 2, Appli |
|-----------|-----------------------|-------------------|------------------|-------------------|-----------------|------------------|-----------------|------------------|------------------|------------------|------------------|-----------------|-------------------|-----------------|-----------------|-----------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------|----------|------|-------------------|
| SUMMARIES | ID                    | US-09-121-425-3   | US-08-151-574-33 | US-08-146-424-19  | US-08-693-709-1 | US-08-419-448-33 | US-07-923-724-7 | US-08-609-426A-7 | US-08-374-652C-1 | US-08-151-574-31 | US-08-419-448-31 | US-09-155-855-5 | US-09-155-855-4   | US-08-819-825-1 | US-09-163-642-1 | US-09-221-654-1 | US-08-989-358A-1 | US-08-993-359-23 | US-08-993-359-21 | US-08-993-359-25  | US-08-993-359-27 | US-08-993-359-29 | US-08-232-463-14 | US-08-151-574-12 | TIS-08-419-448-12 | 54C-86V-   | -677-064 | 200  | J9-014-58         |
|           | n DB                  |                   |                  |                   | 1               |                  |                 |                  |                  |                  |                  |                 |                   |                 |                 | · m             | е<br>С           |                  |                  |                   |                  |                  |                  |                  |                   |            |          | •    |                   |
|           | Lengt                 | 1426              | 1404             | 1404              | 1404            | 1404             | 2363            | 2363             | 2379             | 675              | 675              | 151             | 1332              | 2200            | 220(            | 1320            | 1320             | 1593             | 150              | 1522              | 1647             | 1536             | 7218             | 6                | 6                 | 1631       | 1631     | 1631 | 7 7 7             |
| dР        | Query<br>Match Length | 93.8              | 43.7             | 43.7              | 43.7            | 43.7             | 43.5            | 43.5             | 43.5             | 43.5             | 43.5             | 42.1            | 42.1              | 24.6            | 24.6            | 9.4             | 4.6              | 9.4              | 8.0              | 7.1               | 6.5              | 6.2              | 3.4              | 3.3              | 3.3               | 3.0        | 3.0      | . ~  | )<br>)            |
|           | Score                 | 1317.6            | 614.2            | 614.2             | 614.2           | 614.2            | 610.2           | 610.2            | 610.2            | 610.2            | 610.2            | 591.6           | 590.6             | 346             | 346             | 131.4           | 131.4            | 131.4            | 112.2            | 100               | 8.06             | 87.6             | 48.4             | 46.8             | 46.8              | 42.4       | (.4      | 42.4 | ,                 |
|           | Result<br>No.         | -                 | 7                | m                 | 4               | 2                | 9               | 7                | ω                | δ                | 10               | 11              | 12                | 13              | 14              | 15              | 16               | 17               | 18               | 19                | 20               | 21               | 22               | 23               | 24                | 25         | 26       | 27   | ì                 |

| Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 28, Appli<br>Sequence 37, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 1, Appli | seduence I, Appil |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------|
| US-07-772-087-1<br>US-08-235-836C-75<br>US-08-222-289-1<br>US-08-222-289-1<br>US-08-861-083-37<br>US-08-961-083-37<br>US-08-993-359-31<br>US-09-993-359-31<br>US-09-039-773A-2<br>US-08-061-083-9<br>US-09-004-225-1<br>US-09-004-346-11<br>US-09-004-346-11<br>US-09-11-574-11                                                                                                                                                                         | T. 010 000 60 60  |
| H 4 6 H 8 M 8 M 8 M 8 M 8 M 8 M 8 M 8 M 8 M 8                                                                                                                                                                                                                                                                                                                                                                                                           | ۲                 |
| 1867<br>2126<br>2126<br>2165<br>2165<br>2165<br>2367<br>8367<br>8367<br>8367<br>276<br>726<br>726<br>726<br>7364<br>3084<br>3084<br>3084<br>3084<br>3084                                                                                                                                                                                                                                                                                                | 1                 |
| $\alpha$                                                                                                                                                                                                                                                                                                                                                               |                   |
| 35.2<br>34.3<br>32.8<br>32.6<br>31.2<br>31.2<br>31.2<br>31.2<br>31.3<br>30.8<br>30.8                                                                                                                                                                                                                                                                                                                                                                    | )                 |
| 22888888888888888888888888888888888888                                                                                                                                                                                                                                                                                                                                                                                                                  | :                 |
| υυυ                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ,                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                   |

## ALIGNMENTS

| US-09-121-425-3  US-09-121-425-3  Sequence 3, Application US/09121425  Sequence 3, Application US/09121425  Sequence 3, Application US/09121425  GENERAL INFORMATION:  APPLICANT: Lehmann, Martin  TITLE OF INVEWINON: Consensus Phytases  FILE REFERENCE: consensus phytases  TITLE OF INVEWINON WUMBER: US/09/121,425  CURRENT APPLICATION NUMBER: EPO 97112688.3  EARLIER FILING DATE: 1997-07-24  NUMBER OF SEQ ID NOS: 20  SOFTWARE: Patentin Ver. 2.0  SOFTWARE: Patentin Ver. 2.0  SOFTWARE: DNA  ORGANISM: Artificial Sequence  FEATURE: INFORMATION: Sequence  FEATURE: COTHER INFORMATION: Sequence |                              |                                     |                    |                      |                            |                                        |                                          | •                                         |                                 |                                            |                                 |                          |                             |             |              |           |                               |          | Sequence consensus                          |                             |  |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|-------------------------------------|--------------------|----------------------|----------------------------|----------------------------------------|------------------------------------------|-------------------------------------------|---------------------------------|--------------------------------------------|---------------------------------|--------------------------|-----------------------------|-------------|--------------|-----------|-------------------------------|----------|---------------------------------------------|-----------------------------|--|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | KESULT 1<br>TIG-08-131-435-3 | Sequence 3, Application US/09121425 | Patent No. 6153418 | GENERAL INFORMATION: | APPLICANT: Lehmann, Martin | TITLE OF INVENTION: Consensus Phytases | FILE REFERENCE: consensus phytases 13239 | CURRENT APPLICATION NUMBER: US/09/121,425 | CURRENT FILING DATE: 1998-07-23 | EARLIER APPLICATION NUMBER: EPO 97112688.3 | EARLIER FILING DATE: 1997-07-24 | NUMBER OF SEQ ID NOS: 20 | SOFTWARE: PatentIn Ver. 2.0 | SEQ ID NO 3 | LENGTH: 1426 | TYPE: DNA | ORGANISM: Artificial Sequence | FEATURE: | OTHER INFORMATION: Description of Artificia | OTHER INFORMATION: sequence |  |

0; Gaps 1 atgggcgtgttcgtcgtgtctactgtccattgccaccttgttcggttccacatccggtacc 60 DB 3; Length 1426; 54; Indels Score 1317.6; Pred. No. 0; 0; Mismatches 93.8%; 96.2%; Best Local Similarity 96.2 Matches 1350; Conservative Query Match q δλ δ qq q qq ŏ δ ŏ g

gctattcaaaagaacgctactgctttcaagggtaagtacgctttcttgaagacttacaac 360

301

δ

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δ

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gttccattcgctgctagagcttacgttgaaatgatgcaatgtgaagctgaaaaggaacca 1260
   ttgggtagatgtaagagagacgacttcgttgaaggtttgtctttcgctagatctggtggt 1380
   aacgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccac 1020
  actitiggactotaacccagctactiticcattgaacgctactitigtacgctgactictct 1080
   cacgacaacactatggtttctattttcttcgctttgggtttgtacaacggtactaagcca 1140
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STRAIN: NRRL 3135
  Score 614.2; DB 1;
Pred. No. 4.6e-173;
   PatentIn Release #1.0, Version #1.25
  0; Mismatches 493;
   STREET: 545 Middlefield Road, Suite 200 CITY: Menlo Park
  24615-20026.00
   APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
   US/08/151,574
   APPLICANT: Annemarie E. Veenstra APPLICANT: Rudolf G.M. Luttin APPLICANT: Gerardus Solten TITLE OF INVENTION: Cloning and EXF TITLE OF INVENTION: Phytase NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS:
   OPERATING SYSTEM: PC-DOS/MS-DOS
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                 Sequence 33, Application US/08151574 Patent No. 5436156
  NAME: Murashige, Kate H
REGISTRATION UNDRER: 29,959
REFERENCE/DOCKET 126,159
RELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEO ID NO: 33:
SEQUENCE CHARACTERISTICS:
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  43.7%;
64.9%;
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TYPE: nucleic acid
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US-08-151-574-33
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02-NOV-1993
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STREET: 755 Page Mill Road
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  USA
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   APPLICANT: VAN OOIJEN, ALBERT J. J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PLW, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
  Indels
  Score 614.2; DB 1;
Pred. No. 4.6e-173;
0; Mismatches 493;
   Version #1.
   REFERENCE/DOCKET NUMBER: 44615-20011.24 TELECOMMUNICATION INFORMATION:
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| đ       | Oy<br>Dp                                                          | QV<br>Db                                                             | Q<br>D                                                      | oy<br>G                                                              | Q<br>P                                                              | QY<br>Db                                                             | Qy<br>Dp                                                             | QV<br>Dp                                                         | Qy<br>Dp | Qy<br>Db                                                        | QY<br>Db                                   | OY<br>Db                                                              | oy<br>D                                                             | Qy                                                               | QY<br>Dp                                                               | QV<br>Db                                                         | Qy<br>Dp                                                              | οy                                                                    |

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   GENERAL INFORMATION:
APPLICANT: VAN OOLJEN, ALBERT J.J.
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: PEN, JAN
APPLICANT: JUNONS, PETER C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
   ZUDNITE: 04304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: DESCRIPE: DOS
SOFTWARE: FASIERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,709
FILING DATE: O7-AUG-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/146,424
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
   NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFRENCE/POCKET NUMBER: 24615-20011.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFRAX: 415-494-0792
  ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
   US-08-693-709-1; Sequence 1, Application US/08693709; Patent No. 5770413
   TELERAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
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OTHER INFORMATION:
NAME/KEY: mat_peptide
LOCATION: 70...1401
OTHER INFORMATION:
   TOPOLOGY: linear
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  CA
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  STATE:
   δλ
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NAME: MUTSABLIGG, Kate H.
REGISTRATION NUMBER: 29,959
REPRENCE/DOCKET NUMBER: 24615
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS: Phytase 10-APR-1995 N: 435 CURRENT APPLICATION DATA: TITLE OF INVENTION: CITILE OF INVENTION: Ph NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: CITY: Washington 20006-1888 CLASSIFICATION: FILING DATE: ADDRESSEE: US-08-419-448-33 COUNTRY: STREET: SOFTWARE 1021 1201 1261 1321 961 Op g g δy qq Óλ Op δy g g g ŏ δŽ δý ò ; 0

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Matches 910; Conservative
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US-08-419-448-33
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   Phytase Degrading Enzymes
  Ų
   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
   E: Sterne, Kessler, Goldstein & 1100 New York Avenue, Suite 600
  Miettinen-Oinonen, Arja S.K.
Torkkeli, Tuula K.
Cantrell, Michael
   s.
   APPLICATION NUMBER: US/07/923,724 FILING DATE: 31-JUL-1992
   Piddington, Christopher
Rambosek, John A.
  APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of ITILE OF INVENTION: in Trichoderma
   Nevalainen, Helena K.M.
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   US-07-923-724-7

Sequence 7, Application US/07923724

Patent No. 5780292

GENERAL INFORMATION:

APPLICANT: Nevalainen, Helena K
  Paloheimo, Marja T.
   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
  CURRENT APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  NUMBER OF SEOUENCES:
  STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
  Washington
   ADDRESSEE:
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APPLICANT:
  STREET:
CITY: Wa
  APPLICANT:
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APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
  UK 8610600
  NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 86
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
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   Production of Phytase Degrading Enzymes
  Nevalainen, Helena K.M.
Paloheimo, Marja T.
Miettinen Oinonen, Arja S.K.
Torkkeli, Tuula K.
Cantrell, Michael
Piddington, Christopher S.
Rambosek, John A.
  Fagerstr m, Richard B. Houston, Christine S.
   ; Sequence 7, Application US/08609426A; Patent No. 5830733
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   TITLE OF INVENTION:
   GENERAL INFORMATION:
  US-08-609-426A-7
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   43.5%; Score 610.2; DB 2; Length 2363; 64.9%; Pred. No. 9e-172; tive 0; Mismatches 488; Indels 0;
  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
  REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  ADDRESSEE: Sterne, Kessler, Goldstein & STREET: 1100 New York Avenue, Suite 600
   CLASSIFICATION: 435

RELOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
  join(404..447, 550..1906)
  APPLICATION NUMBER: US/08/609,426A FILING DATE: 01-MAR-1996 CLASSIFICATION: 435
TITLE OF INVENTION: in Trichoderma
  PC-DOS/MS-DOS
  FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
  NAME: Reed, Grant E. REGISTRATION NUMBER: P-41,264
  Eloppy disk
IBM PC compatible
  FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION:
  Matches 903; Conservative
              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  OPERATING SYSTEM:
   Query Match
Best Local Similarity
  Washington
   STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
  TOPOLOGY: both
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US-08-609-426A-7
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   APPLICANT: NEVALAINEN, HELENA K.M.
APPLICANT: PALOHEINO, MARJA T.
APPLICANT: PALOHEINO, MARJA T.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: TOUSTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
  1050.071001
  join(404..447, 550..1906)
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
   APPLICATION NUMBER: US/08/374,652CFILING DATE: 24-MAY-1995
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 1, Application US/08374652C Patent No. 5834286 GENERAL INFORMATION:
  REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
  ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
   MOLECULE TYPE: DNA (genomic)
   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
   LENGTH: 2379 base pairs
   COMPUTER READABLE FORM:
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Length 2379;

43.5%; Score 610.2; DB 2; Length 64.9%; Pred. No. 9e-172; ... tive 0; Mismatches 488; Indels

Matches 903; Conservative

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Best Local Similarity

Query Match

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Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Willem Van Hartingsveldt
APPLICANT: A. Van Earlân
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerards Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
  Aspergillus ficuum (Aspergillus niger)
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin. Release #1.0, Version #1.25
SOFTWARE:
  ADDRESSEE: Morrigon & Foerster
STREET: 545 Middlefield Road, Suite 200
  24615-20026.00
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
   NAME: MITASHIGO, KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 2461;
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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  Sequence 31, Application US/08419448
Patent No. 5863533
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Annemarie E. Veenstra
APPLICANT: Randolf G.M. Luttin
APPLICANT: Recardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
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STRAIN: NRRL 3135
ADDRESSEE: Morrison & ruelace.
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
  Patentin Release #1.0, Version #1.25
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TELEPHONE: 202-887-1500
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  /codon_start= 210
/product= "Phytase"
   LOCATION: 381..1712
IDENTIFICATION METHOD: experimental
  join(210..253, 356..1715)
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,448
FILING DATE: 10-APR-1995
CLASSIFICATION: 435
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   LIBRARY: lambda Ar
CLONE: pAF2-3, pAF2-6, pAF2-7
  ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 6756 base pairs
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  Query Match
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   APPLICANT: KONDO, Hidemasa
APPLICANT: KONDO, Hidemasa
APPLICANT: KANZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
APPLICANT: RANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124
CURRENT FILING DATE: 1998-10-05
EARLIER FILING DATE: 1997-04-04
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER PILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 2.5e-166;
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   42.18;
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ORGANISM: Aspergillus niger
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Best Local Similarity 64.6'
Matches 882; Conservative
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CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER APPLICATION NUMBER: JP 084314
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEQ ID NOS: 7
  GENE
  APPLICANT: ANAZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
APPLICANT: NGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND
FILE REFERENCE: 81356/124
  Sequence 4, Application US/09155855 Patent No. 6139902
  TYPE: DNA
ORGANISM: Aspergillus niger
  SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 4
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  APPLICANT: KONDO, Hidemasa
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ITLE OF INVENTION: And Nucleic Acids Encoding

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Sequence 1, Application US/08819825 Patent No. 5866118 GENERAL INFORMATION:

US-08-819-825-1

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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
   405 Lexington Avenue, Suite 6400
   No. 5866118disk
  JMBER: US/08/819,825
18-MAR-1997
   NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,728
   TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
  TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
  Query Match 24.6%;
Best Local Similarity 57.2%;
Matches 753; Conservative
  ADDRESSEE: No. 58661180
  ATTORNEY/AGENT INFORMATION:
   REFERENCE/DOCKET NUMBER;
  SEQUENCE CHARACTERISTICS:
LENGTH: 2200 base pairs
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
  CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
   ; TOPOLOGY: linear
US-08-819-825-1
  CLASSIFICATION:
   FILING DATE:
   a
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   APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
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   APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Ray, Michael W.
APPLICANT: Rlotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62216444 o. 62216444 isk of No. 62216444
  Sequence 1, Application US/09163642
Patent No. 6221644
GENERAL INFORMATION:
  ZIP: 10174-6401
COMPUTER READABLE FORM:
   New York
   U.S.A.
   New York
   COUNTRY:
   US-09-163-642-1
  STREET:
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  967 rececededererreceregeagaerrerreaaceecedearrecaagaraceaaagae 1026
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  totgacagagttattgcttctgctgaaaagttcattgaaggtttccaatctgctaagttg 546
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  727 GGAGCTCGGTATCCTACTGCTCACAAGAGTGAAGTCTACGCCGAGTTGCTTCAAAGGATC 786
   547 getgacecaggtgetaacecacaccaagettetecagttattaacgttattattecagaa
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  24.6%; Score 346; DB 4; Length 2200;
57.2%; Pred. No. 3.1e-93;
Live 0; Mismatches 515; Indels 48;
   SYSTEM: DOS
FastSEQ for Windows Version 2.0
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
   2200 base pairs
  TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 753; Conservative
   TYPE: nucleic acid_
STRANDEDNESS: single
   linear
   CLASSIFICATION:
   FILING DATE:
  TOPOLOGY:
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  US-09-163-642-1
   LENGTH:
   Query Match
   187
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SEE: No. 60543060 No. 6054306disk of No. 6054306th America, Inc.: 405 Lexington Avenue
New York
1204 ATCACTAAACACATGCGGGTGTGAACCTCCACCTTGGAGGATGTCCCGTTGTTCATGGAT 1263
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  787 atgtgtccattcgacactgt----tgctagaacttctgacgctactcaattgtctcca 840
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   SOFTWARE: FASTERN: DOS SOFTWARE: FASTESEO for Windows Version 2.0 CURRENT APPLICATION DATA:
   APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Ohmann, Anders
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
   Sequence 1, Application US/09221654 Patent No. 6054306 GENERAL INFORMATION:
   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
  COMPUTER READABLE FORM:
  TITLE OF INVENTION: Pe
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
   U.S.A.
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   ADDRESSEE:
   COUNTRY:
   US-09-221-654-1
  STREET:
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1023 tttggactctaacccagctactttcccattgaacgctactttgtacgctgacttctctca 1082
  963 cgaattgattgctagattgactcactctccagttcaagaccacacttctactaaccacac 1022
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  663 igaatigggigacgacgitgaagctaacticacigcigitticgciccaccaatiagage 722
   903 gtactacggttacggtgctggtaacccattgggtccagctcaaggtgttggtttcgttaa 962
  594 TGAAGTGGATGGTGACGAATCCACAACGTGGCGTGTTTTGCGCCCGAACATCACCGC 653
   654 GCGATTGAACGCTGCTGCCGAGTGCCAACCTCTCAGACAGCGACGCGCTCACTCTCAT 713
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  843 ctgtgacttgttcactcacgacgaatggattcaatacgactacttgcaatctttgggtaa 902
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56.9%; Pred. No. 1.5e-29;
ive 0; Mismatches 191; Indels 12;
  1083 cgacaacactatggtttctattttcttcgctttgggtttgtacaacggtac 1133
  REFERENCE/DOCKET NUMBER: 5101.200-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123 TELEPAX: 212-878-9655 TELEX:
APPLICATION NUMBER: US/09/221,654
   APELICATION NUMBER: 0529/97
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,358
"TI.ING DATE: 12-DEC-1997
"TI.ING DATE: 0529/97
   Query Match 9.4%;
Best Local Similarity 56.9%;
Matches 268; Conservative
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   TYPE: nucleic acid_
STRANDEDNESS: single
  ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-221-654-1
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Search completed: October 26, 2001, 15:20:39 Job time: 595 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein

Search time 48.78 Seconds ٠. 2001, 15:10:29 October 26, Run on:

(without alignments)
729.264 Million cell updates/sec

US-09-488-265-31 Title: Perfect score:

Sequence:

2468 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWEECFA

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|        | Description    | 1 - C CO C C C C C C C C C C C C C C C C | 3-phytase (EC 3.1. | -phytase (EC 3 | pilytuse (EC 3. | 3 70     | cid phosphatas | 7   | 7        | -nhvtase /FC 3 | cid phosphat | 7 7      |     |          | cutamin-lepiessid | pilospilatas<br>Ginospilatas | _     | nypornerical prote |     |       | cid | hosphat          | 1.1 | acid phosphatase ( | acid phosphatase ( | hypothetical prote |          | exo-poly-alpha-aal | himothetical prote | hynothetical prote | alucose-1-procept | מינולייטיול + ייייטייות |
|--------|----------------|------------------------------------------|--------------------|----------------|-----------------|----------|----------------|-----|----------|----------------|--------------|----------|-----|----------|-------------------|------------------------------|-------|--------------------|-----|-------|-----|------------------|-----|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|-------------------|-------------------------|
|        | B ID           | 1 JN0889                                 | JN0656             | 1 JN0482       | PABYC           | 2 S53476 |                |     | 2 S52495 | 1 JN0715       | 1 JN0890     | 2 JC4285 |     | 2 T39929 |                   |                              |       |                    |     |       |     | 214/47<br>317003 |     | CTOHO              | 20616              | ₽                  | 2 T21241 | A3671              | T205               | T1634              | JV008             |                         |
|        | Length DB      | 467                                      | 7                  | 41             |                 |          |                |     |          | 479            |              |          |     |          |                   |                              |       |                    |     |       |     | 7 000            |     |                    |                    |                    |          |                    |                    |                    | 13                | ,                       |
| ap (   | Query<br>Match | 75.0                                     | 74.9               | •              | 9               | 16.0     | 9              | 5   | 15.0     | 14.6           | •            | •        | •   | 12.6     |                   |                              |       |                    | •   | •     |     | ο α<br>* •       | •   | •                  | •                  | 4 . 4              | 4.3      | 4.3                | 4.2                | 4.2                | 4.1               |                         |
|        | Score          | 1852                                     | 1848               | 1787           | 405             | 394      | 394            | 391 | 369      | 360.5          | 354.5        | 350      | 328 | 311.5    | 303.5             | 153                          | 149.5 | 142                | 130 | 127.5 | ά,  | 110              | 4   | 114.5              | 1001               | C . 60 T           | $\sim$   | 106.5              | 103                | 102.5              | 101.5             |                         |
| 11:000 | NO.            | .7                                       | 7                  | Э              | 4               | S        | 9              | 7   | 80       | 0              | 10           | 11       | 12  | 13       | 14                | 15                           | 16    | 17                 | 18  | 10    | 20  | 2.5              | 22  | 1 0                | 57                 | # I                | 72       | 56                 | 27                 | 28                 | 29                |                         |

| periplasmic glucos<br>probable formate C<br>hunchholical marte | hypothetical prote<br>hypothetical prote<br>acid phosphatase ( | acid phosphatase (hypothetical prote | probable peptide s | ATP Synthase hydr | probable formate Caldehyde dehydroge | probable LTR retto | copper resistance |
|----------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------|--------------------|-------------------|--------------------------------------|--------------------|-------------------|
| B85636<br>E69144<br>T20893                                     | S77346<br>JH0610                                               | S64682<br>T08601                     | T50176<br>T37690   | S61067<br>H82928  | H69430<br>T44987                     | A71444<br>T27570   | KSPSCY            |
| 0.00                                                           | 17                                                             | 77                                   | 2 2                | 7                 | 7                                    | 0 0                | -                 |
| 413<br>642<br>408                                              | 630<br>386                                                     | 438<br>1021                          | 4924               | 693<br>464        | 776<br>496                           | 1433               | 609               |
| 4 4 4<br>L.T.L                                                 | 4.0                                                            | 4.0                                  | 4.0<br>4.0         | 9.6<br>9.6        | w w                                  | ო ო<br>თ. თ.       | 3.9               |
| 101.5<br>101.5<br>101                                          | 100.5                                                          | 0<br>0<br>0                          | 98.5<br>98         | 97.5<br>97        | 97<br>96.5                           | 96.5<br>96         | 95.5              |
| 30<br>31<br>32                                                 | 33<br>34                                                       | 32<br>30                             | 37<br>38           | 39                | 41                                   | 43                 | 45                |
|                                                                |                                                                |                                      |                    |                   |                                      |                    |                   |

## ALIGNMENTS

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3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori N'Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein C;Species: Aspergillus awamori C;Date: 14-Jul-1994 #sequence\_revision 19-oct-1995 #text\_change 11-Jun-1999

C;Accession: JN0889 11-Jun-1999 C;Accession: JN0889 L1-Jun-1999 C;Accession: JN0889 L2-Jun-1999 R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A. Gene 133, 55-62, 1993 and sequencing of the genes encoding phytase (phy) and pH 2.5-op A;Reference number: JN0889; MJID:94040796

A; Accession: JN0889

A; Molecule type: DNA A; Residues: 1-467 <PID>

A) Experimental source: Strain ALK0243
A) Experimental source: strain ALK0243
A) Note: part of the sequence, including the amino end of the mature protein, was conf C; Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic

C;Genetics: A;Gene: phyA

A.Introns: 15/2 C.Superfamily: yeast acid phosphatase C.Superfamily: yeast acid phosphatase C.Keywords: extracellular protein: glycoprotein; phosphohistidine; phosphoprotein; ph F:1-19/Domain: signal sequence #status predicted <SIG> F:20-467/Product: 3-phytase A #status experimental <MAT> F:27,59,105,120,207,230,339,352,376,388/Binding site: carbohydrate (Asn) (covalent) # F:81,361/Active site: Arg, His #status predicted F:82/Active site: His (phosphohistidine intermediate) #status predicted

Gaps .; 0 75.0%; Score 1852; DB 1; Length 467; 74.3%; Pred. No. 1.1e-137; ative 42; Mismatches 78; Indels ( Conservative Query Match Best Local Similarity Matches 347;

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1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60 g

SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 61 δλ

61 g

YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 οy qq

181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240 ò

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241 ARLEAHLPGVNLTDEDVVNLAMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

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J-pnytase (tc. 3.1.3.8) A - Aspergillus flocum
N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
C;Species: Aspergillus ficuum
C;Species: Aspergillus ficuum
C;Date: 30.5ep-1993 #sequence_revision 19-oct-1995 #text_change 07-May-1999
C;Accession: JN0482; PN0023
R;Ullah, A.H.J.; Dischinger Jr., H.C.
R;Ullah, A.H.J.; Dischinger Jr., H.C.
A;Feference number: JN0482; MUID:93249451
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A;Residues: 1-441 < ULL.
A;Residues: 1-441 < ULL.
A;Note: authors state that the 9 Asn followed by Thr or Ser after an intervening resi
R;Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
B;Ochem. Biophys: Res. Commun. 178, 45-53, 1991
A;Title: Cyclohexanedione modification of arginine at the active site of Aspergillus
A;Accession: PN0023
A;Accession: PN0023
A;Accession: PN0023
A;Accession: PN0023
A;Accession: Appertance catalyzes the hydrolysis of inorganic orthophosphate from phyt
C;Superfamily: yeast acid phosphatase
C;Gewpords: extracellular protein; glycoprotein; phosphopistidine; phosphoprotein; ph
F;4,36 &2.97,184,207,316,329,353,365/Binding site: carbohydrate (Asn) (covalent) #sta
F;58,338/Active site: His (phosphohistidine intermediate) #status predicted
F;58/Active site: His (phosphohistidine intermediate)
   87 PISSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
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   DTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
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   NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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  447 DDFVEGLSFARSGGNWEE 464
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  Best Local Similarity
Matches 332; Conserv
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  387
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  C; Spectlas: Aspergillura niger
C; Spectlas: Aspergillura niger
C; Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C; Accession: JN0656; S28456
E; van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M. A.M.J. J.
Gene 127, 87-94, 1993
A; Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyh A; Reference number: JN0656; MUD: 9355284
A; Reference number: JN0656
A; Molecule type: DNA
A; Residues: 1-467 < VANA
A; Residues: 1-467 < VANA
A; Residues: 1-467 < VANA
A; Residues: 1-67 <
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N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein
C;Species: Aspergillus niger
  ö
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  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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   KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
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   421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
   LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  Local Similarity 74.3
nes 347; Conservative
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  301
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Gaps 86

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R;Silve, S.; Monod, M.; Hinnen, A.; Haguenauer-Tsapis, R.
Mol. Cell. Biol. 7, 3306-3314, 1987
A;Title: The yeast acid phosphatase can enter the secretory pathway without its N-ter
A;Reference number: A27774; MUID:88038886
  A;Gene: SGD:PHO5; MIPS:YBR093c
A;Cross-references: SGD:S0000297; MIPS:YBR093c
  A;Cross references: GB:M17306
C;Genetics:
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Matches 125; Conservative
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A; Residues: 1-51,'S',53-60
  A; Accession: A2777
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   ×
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   RESULT
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  C; Species: Saccharomyces cerevisiae
C; Date: 19-Feb-1984 #sequence_revision 30-Sep-1991 #text_change 12-Nov-1999
C; Accession: S05795; A38792; S48860; S45961; A00777; A38793; S41855; B25241; A25367; A27
R; Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A; Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeas
   acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (Saccharomyces cerevisiae)
N.Alternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093c
   A,Cross-references: EMBL:235962; NID:9536364; PIDN:CAA85046.1; PID:9536365; GSPDB:GN0000 Nucleic Acids Res. 11, 1657-1672, 1983
A)Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repress A; Reference number: A00777; MUD:83168913
   A,Molecule type: DNA
A,Residues: 1-35,Y',37-129,'G',131-293,'O',295-445,'V',447-461,'DT',464-465,'K',467 <AR
A,Cross-references: BMBL:V01320; NID:94158; PIDN:CAA24630.1; PID:94159
   R;Bergman, L.W.
Mol. Cell. Biol. 6, 2298-2304, 1986
A;Title: A DNA fragment containing the upstream activator sequence determines nucleosome
A;Reference number: A25367; MUID:87064526
  A:Residues: 1-30, 77, 32-51, 5, 53-75 <MEY>
A:Cross-references: EMBL:M24178; NID:g172156; PIDN:AAA34868.1; PID:g172157
A:Cross-references: EMBL:M24178; NID:g172156; PIDN:AAA34868.1; PID:g172157
B:Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.Mol. Cell. Biol. 6, 1855-1865, 1986
A:Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within A:Reference number: A93074; MUID:87064474
   A:Cross-references: EMBL:X78993; NID:q476045; PIDN:CRA55598.1; PID:q476051
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
Submitted to the Protein Sequence Database, August 1994
A:Reference number: S45927
   A; Molecule type: protein
A; Molecule type: B-45 CBA12>
R; Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A; Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A; Reference number: $48255; MUID:95208357
A; Rccession: $48260
  A;Cross-references: EMBL:X01079; NID:94162; PIDN:CAA25555.1; PID:9758282 A;Note: the authors translated the codon TAC for residue 272 as Thr
  A; Status: nucleic acid sequence not shown; translation not shown
  A; Molecule type: DNA
A; Residues: 1-2,'Y',4-43,'T',45-51 <BER>
424 DSFVRGLSFARSGGDWAE 441
  A; Residues: 1-467 <BAJ>
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   A; Residues: 1-467 <FE2>
  A; Residues: 1-44 <TAI>
   A; Molecule type: DNA
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  A; Molecule type: DNA
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   A; Molecule type: DNA
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   A; Accession: S45961
  A; Accession: B25241
  A; Molecule type:
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A,Map position: ZR
A,Ndp position: ZR
A,Note: YBR093c
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C,Superfamily: yeast acid phosphohistidine; phosphoprotein; phosphoric monoester hydr
E;1-17/Domain: signal sequence #status predicted <SIG>F;1-17/Domain: signal sequence #status predicted <SIG>F;1-17/Domain: signal sequence #status predicted *status appearable #status experimental <MAT>F;15/Active site: His (phosphohistidine intermediate) #status predicted
E;97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (co
   C; Accession: $53476; JCi018
R; Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Ka submitted to the EMBL Data Library, February 1994
A; Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of th
  N;Alternate names: protein YAR071w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Apr-2000
  66 DVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK-TYNYTLG 124
  59 DLPEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIR 118
   125 ADD------LTPF-GEQQMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIA 168
   119 DDDDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHD 178
   169 SAEKFIEGFQSAKLADPGANPHQASPVINVII----PEGAGYNNTLDHGLCTAFEESEL 223
   179 TAQYFIDG-----LGDQ------FNITLQTVSEAESAGANTLSACNSCPAW-DYDA 222
   223 NDDIVNEYDTTYLDDIAKRLNKENKGLNLTSTDASTLFSWCAFEV----NAKGYSDVCD 277
  278 IFTKDELVHYSYYQDLHTYYHEGPGYDIIKSVGSNLFNASVKLLKQSELQDQ----- 329
   404 AARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF-----VEGLSFA 456
   378 GARVYTEKFQC--SNDTYVRYUINDAVVPIETCSTGPGFSCEINDFYDYAEKRVAGTDFL 435
  284 LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLD 343
   344 SNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPF 403
   330 -----KVWLSFTHDTDILNFLTTAGIIDDKNNLTAEYVPFMGNT--FHRSWYVPQ 377
   Gaps
  6 VLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISP 65
   5 VVYSILAASLANAGTI--PLGKLADVDKIGTQKDIFPFL----GGAGPYYSFPGDYGISR 58
   acid phosphatase (EC 3.1.3.2) precursor - yeast (Saccharomyces cerevisiae)
  224 GDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCD
   78;
   DB 1; Length 467;
  16.4%; Score 405; DB 1; Length 467
26.0%; Pred. No. 5e-24;
Live 62; Mismatches 216; Indels
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acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (Saccharomyces cerevisination constitution - yeast (Saccharomyces cerevisiae C.Species: Saccharomyces cerevisiae C.Species: Saccharomyces cerevisiae C.Species: 30-Sep-1991 *sequence_revision 09-Sep-1994 *text_change 05-Nov-1999 C.Accession: S48259; 845960; S05794; A25241; S44674 *text_change 05-Nov-1999 C.Accession: S48259; R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 10, 1363-1381, 1994 *text_change of yeast chromosome II. A; Reference number: S48255; MUID:95208357
   A;Cross-references: EMBL:U00029; NID:9551322; PIDN:AAB69729.1; PID:9458917; MIPS:YHR2
R;Xu, L.
  A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g476050
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A; Residues: 1-16, L',18-81,'AR',84-149,'H',151-467 <XUL>
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  77 ERYPTVSKAKSIMTTWYKLSNYTGQFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
  129 TPF-GEQOMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPG 186
  187 ANPHQASPVINVII-----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
   242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301
   302 YYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSH 361
  362 DNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPL 421
  338 DIDILNYLTIGIIDDQNNLTAEHVPFMENT--FHRSWYVPQGARVYTEKFQC--SNDTY 393
   1 PIGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDLPESCEMKQVQMVGRHG 76
   24 PRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHG 83
   241 RINKENKGLNLTSSDANTFFAWCAYEINAR-----GYSDICNIFTKDELVRFSYGQDLET
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A;Molecule type: DNA
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   394 VRYVINDAVVPIETCSTGPGFSCEINDFYGYAEKRVAGTDFLK 436
  422 VRVLVNDRVVPLHGCGVDKLGRCKRDDF-----VEGLSFAR 457
   submitted to the EMBL Data Library, January 1995
  A;Cross-references: SGD:S0001258; MIPS:YHR215w
A;Map position: 8R
C;Superfamily: yeast acid phosphatase
C;Keywords: phosphoric monoester hydrolase
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  A;Reference number: S59658
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  A; Molecule type: DNA
A; Residues: 1-467 <MAN>
  A; Molecule type: DNA
A; Residues: 1-467 <MAC>
                                     A; Accession: S48996
   A; Gene: SGD: PHO12
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A; Reference number: S53458
A; Accession: S53476
A; Molecule type: DNA
A; Residues: 1-467 - 8805
A; Cross-references: EMBL:128920; NID:g1616966; PIDN:AAC09508.1; PID:g456155; MIPS:YAR071
R; Chel. J.Y.; Gong, Y.; Ao, S.Z.
Acta Biochim. Biophys. Sin. 21, 437-444, 1989
A; Title: The primary structure of acid phosphatase gene PH011 in S. cerevisiae and compa A; Recession: JG1018
A; Accession: JG1018
A; Molecule type: DNA
A; Residues: 1-16, 'L', 18-149, 'H', 151-353, 'Q', 355-422, 'G', 424-467 < CHE>
A; Note: this paper is in Chinese, with an English abstract
C; Genetics:
A; Mote: this paper is cid phosphatase status predicted < Signal Sequence #status predicted < Signal Sequence Signal Sequence #status predicted < Signal Sequence Signal Sequence #status predicted < Signal Sequence Signal Sequence 
  C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 22-Jun-1999
C;Accession: S48996; S59659
  191 -----FNISLQTISEAESAGANTLSAHHSCPAWDD-DVNDDILKKYDTKYLSGIAK 240
   302 YYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSH 361
  296 YYQTGPGYDVVRSVGANLFNASVKLLKESEVQDQ-------KVWLSFTH 337
  338 DIDILNYLTIIGIIDDKNNLTAEHVPFMENT--FHRSWYVPQGARVYTEKFQC--SNDTY 393
  84 ARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK------TYNYTL-----GADDL 128
  77 ERYPTVSKAKSIMTTWYKLSNYTGQFSGALSFLNDDYEFFIRDTKNLEMETTLANSVNVL 136
  129 TPF-GEQQMVNSGIKFYRRYRALARKIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPG 186
  187 ANPHQASPVINVII-----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
   242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301
  362 DNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPL 421
   24 PRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHG 83
   21 PLGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDLPESCEMKQVQMVGRHG 76
   acid phosphatase (EC 3.1.3.2) PHO12 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR215w
   16;
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  394 VRYVINDAVVPIETCSTGPGFSCEINDFYDYAEKRVAGTDFLK 436
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  submitted to the EMBL Data Library, February 1994 A; Description: The sequence of S. cerevisiae cosmid 9177.
  Query Match 16.09
Best Local Similarity 25.79
Matches 119; Conservative
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Gaps

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A;Cross_references: EMBL:274072; NID:91430996; PIDN:CAA98583.1; PID:91430997; MIPS:YD
  acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein D2815
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C.Accession: $52495; $67556
C.Accession: $52495; $6.7556
C.Accession: $52495; $6.7556
C.Accession: $52495; $6.7556
C.Accession: $52495
C.Accession: $52495
C.Accession: $52492
C.Accession: $52492
C.Accession: $52492
   3-phytase (EC 3.1.3.8) B precursor - Aspergillus ficuum
N:Alternate names: pH 2.5-optimum acid phosphatase
C;Species: Aspergillus ficuum
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
   A; Residues: 1468 (AND)
A; Cross-references: EMBL:248432; NID:g683669; PIDN:CAA88335.1; PID:g683673
A; Experimental source: strain S288C
R; Urrestarazu, L.A.; Andre, B.; Vissers, S.
submitted to the Protein Sequence Database, July 1996
   49 GTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATA 108
   --GADDLIPF-GEQOMVNSGIKFYRRYKALAR 152
   ------ DDVEANFTAVFAPPIRARLEAHLPGVNLT 253
  198 ----TLSENSSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLENISDRLNDENKGLNLS 253
   254 DEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGP 313
  -----GDGFNISLQ 197
   314 AQGVGFVN----BLIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFF 370
   309 SIGANLFNATVKLIRQSAH-------LDQKVWLSFTHDTDILNYLT 347
   371 ALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRV 430
   153 KIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD
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   15.0%; Score 369; DB 2; Length 468; 25.3%; Pred. No. 3.4e-21;
  431 VPLHGCGVDKLGRCKRDDFVE-----GLSFARSGGNWEEC 465
   404 VPIESCSSGPGFSCEEGTFYEYAKDRLRGVSF-----YEDC 439
  60; Mismatches 175;
  163 NCTNFPIFTTNSKRIYDTAQYFAEAL---
   A; Map position: 4L
C; Superfamily: yeast acid phosphatase
  A; Experimental source: strain S288C
   Best Local Similarity 25.33
Matches 117; Conservative
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  212 HGLCTAFEESELG-----
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  A; Accession: S67556
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  A; Residues:
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  A; Molecule type: DNA
A; Residues: 1-467 <FE2>
A; Residues: 1-467 <FE2>
A; Cross-references: EMBL: 235961; NID:9536362; PIDN:CAA85045.1; PID:9536363; GSPDB:GN000C
B; Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A; Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeas A; Reference number: S05794; MUID:85037940
   A; Molecule type: DNA
A; Residues: 1-218, MKT', 222-467 < BAJ1>
A; Residues: 1-218, MKT', 222-467 < BAJ1>
A; Cross-references: EMBL:X01080, NID:g4148; PIDN:CAA25557.1; PID:g758281
A; Note: the authors translated the codon AdT for residue 134 as Asp and TAC for residue 18 Tait-Kamradt, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G. A).
A; Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within A; Reference number: A93074; MUID:87064474
   C.Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola F:1-17/Domain: signal sequence *status predicted <SIG>F:1-17/Domain: signal sequence *status predicted <SIG>F:18-46/T/Product: acid phosphatse, constitutive *status predicted <WAT>F:75/Active site: His (phosphohistidine intermediate) *status predicted F:97,103,162,192,250,315,356,390,439,445,466,461/Binding site: carbohydrate (Asn) (coval F:337/Active site: His *status predicted
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994 R:Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I. submitted to the Protein Sequence Database, August 1994
   13;
   49 GTYSPFFSLADESALSPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEALQKNATA 108
  109 FKGKYAFLK-TYNYTLGADD-------LTPF-GEQQMVNSGIKFYRKKALAR 152
  153 KIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD 211
   162 NQTSFPIFAASSERVHDTAQYFIDGL------GDQFNISLQTVSEANSAGA---NTLS 210
   212 HG-LCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVA 270
   331 PVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIE 390
   270 R-----GYSDVCDIETEDELVRYSYGQDLVSFYQDGPGYDMIRSVGANLFNATLKLLKQS 324
   391 ETDGYSASWIVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF- 449
  211 AGNACPGWDE-DANDDILDKYDTTYLDDIAKRLNKENKGLNLTSKDANTLFAWCAYELNA
   RTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHS
   325 ETQD------LKVWLSFTHDTDILNYLTTAGIIDDKNNLTAEYVPFMG
   Length 467;
  15.8%; Score 391; DB 1; Length 467 27.0%; Pred. No. 6.3e-23; tive 61; Mismatches 192; Indels
  A; Cross-references: SGD:S0000296; MIPS:YBR092c
  C; Superfamily: yeast acid phosphatase
   A; Gene: SGD: PHO3; MIPS: YBR092c
   Matches 117; Conservative
  423 DYAEKRVAGTDFLK 436
   A; Reference number: S45927
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  A; Accession: S45960
   A; Accession: A25241
  A; Map position: 2R
   Query Match
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A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-op A;Reference number: JNO889; MUID:94040796 A;Accession: JNO890 A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-479 <PID>
   A;Cross-references: GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482
A;Experimental source: strain ALK0243
C;Comment: The highly similar enzyme from A. ficuum has been shown to have 3-phytase
  R; Payne, W.E.; Gannon
Gene 163, 19-26, 1995
  DNA
  A; Accession: JC4285
   218 FEESELG--
  A; Molecule type:
   C; Genetics:
   RESULT 11
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              C; Accession: JN0715; PN0594; PN0460

R; Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
Biochem Biophys. Res. Commun. 195, 53-57, 1993

A; Title: Identification and cloning of a second phytase gene (phyB) from Aspergillus nig A; Reference number: JN0715; MUID: 93371452

A; Molecule type: DNA
A; Residues: 1-479 cEHR>
A; Molecule type: DNA
A; Residues: 1-479 cEHR>
A; Cross-references: GB:L20567
A; Accession: PN0594
A; Molecule type: protein
A; Residues: 20-101;133-146;376-399 cEH2>
B; Residues: 20-101;133-146;376-399 cEH2>
B; Residues: 20-101;133-146;376-399 cEH2>
A; Residues: Commun. 192, 754-759, 1993
A; Title: Identification of active-site residues in Aspergillus ficuum extracellular pH A; Reference number: PN0460; MUID: 93249452
A; Recession: PN0460
A; Molecule type: protein
A; Residues: 65-66,68-93 cULL>
C; Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), hy
  Gigenetics:
A;Gene: phyB
A;Introns: 261/1; 300/2; 335/2
C;Genetics:
A;Gene: phyB
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Reywords: extracellular protein; glycoprotein; phosphopistidine; phosphoprotein; phosp
F;1-19/Domain: signal sequence #status predicted <SIG>
F;10-4/9/Product: 3-phytase #status experimental <MAT>
F;81,Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #statu
   R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Oinonen, A.;
Gene 133, 55-62, 1993
   16;
  C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #Sequence_revision 19-Oct-1995 #text_change 11-Jun-1999
C;Accession: JNO890
   263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
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   323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY--NGTKP 380
  381 LSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC 436
  359 L----DRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDKGTYVRLVLNEAVLPFNDC 413
   -- DDVEANFTAVFAPPIR---ARLEAHLPGVNLTDEDVVNLMD 262
   108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GEQQMVNSGIKFYRRYKAL--ARKIVPF 157
  109 EYKGDLAFLINDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
  158 IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
   Gaps
  49 GTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAY-SALIEAIQKNAT 107
   -------FGYNYSTNAALNII 201
  -----KEAGP-----LFFNLAHDTNITPILAALGVLIPNEDLP
  91;
  DB 1; Length 479;
  Mismatches 157; Indels
  acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
   14.6%; Score 360.5; DB 1
28.3%; Pred. No. 1.6e-20;
tive 53; Mismatches 157
   169 F-SSGYGRVIETARKFGEGF-----
   Conservative
  Query Match
Best Local Similarity
Matches 119; Conserv
   317 SLTLLNOGP-
   218 FEESELG---
   RESULT 10
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A;Gene: aph
A;Gene: aph
A;Introns: 261/1; 300/2; 335/2
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Superfamily: yeast acid phosphatase
C;Superfamily: yeast acid protein; glycoprotein; phosphohistidine; phosphoprotein; ph
F;1-19/Domain: signal sequence *status predicted <ANT>
F;20-479/Product: 3-phytase #status predicted <ANT>
F;81,337/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carbohydrate (Asn) (covalent) #st
  A;Gene: phol
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydr
   A.Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterizati
  acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichia pastoris)
N;Alternate names: orthophosphoric-monoester phosphohydrolase (acid optimum); Pho
C;Species: Pichia pastoris
C;Date: 14.Nov-1995 #sequence_revision 08-Feb-1996 #text_change 29-Oct-1999
C;Accession: JG4285
  15;
  263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
  262 MASFELNAR-----PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANA 316
   381 LSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC 436
  49 GTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASK-AYSALIEAIQKNAT 107
  53 GPYSERVSY----GIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINTT 108
   108 AFKGKYAFLKTYNYTL----GADDLT-PF-GEQQMVNSGIKFYRRYKAL--ARKIVPF 157
   109 EYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
  158 IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
   -----FGYNYSTNAALNII 201
   202 SESEVMGADSLIPICDIDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMV 261
   323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY--NGTKP 380
  317 SLTLLNOGPKE-------AGSLFFNFAHDTNITPILAALGVLIPNEDLP 358
  Gaps
   A;Residues: 1.468 <PAY>
A;Cross-references: GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
  -DDVEANFTAVFAPPIR---ARLEAHLPGVNLTDEDVVNLMD
   Length 479;
  Indels
   DB 1;
  53; Mismatches 159;
   14.4%; Score 354.5; DB 1
27.9%; Pred. No. 4.8e-20;
   A; Reference number: JC4285; MUID:96001238
  Gannon, P.M.; Kaiser, C.A.
   Query Match 14.48
Best Local Similarity 27.99
Matches 117; Conservative
  A; Experimental source: GS115 C; Genetics:
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Length 453;

13.3%; Score 328; DB 1; Similarity 25.8%; Pred. No. 5.4e-18;

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C;Superfamily: yeast acid phosphatase
C;Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
F;68/Active site: Arg #status predicted
F;69/Active site: His (phosphohistidine intermediate) #status predicted
  Query Match
   Best Local
  ò
   qq
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F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-468/Product: acid phosphatase #status predicted <NAT>
F;84/Active site: His (phosphohistidine intermediate) #status predicted
F;163,196,256,321,360,453/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;345/Active site: His #status predicted
   C; Species: Schizosaccharomyces pomber: 10-Sep-1999 #text_change 21-Jul-2000
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: A25326; T50405
R; Elliott, S.; Chang, C.; Schweingruber, M.E.; Schaller, J.; Rickli, E.E.; Carbon, J. J. Biol. Chem. 261, 2936-2941, 1986
A; Title: Isolation and characterization of the structural gene for secreted acid phospha A; Reference number: A25326; MUID:86140050
  acid phosphatase (EC 3.1.3.2) precursor [similarity] - fission yeast (Schizosaccharomyce
  A; Cross-references: EMBL: AL137099; PIDN: CAB68657.1; GSPDB: GN00067; SPDB: SPBP4G3.02
  21;
   61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIE-AIQKNATAFKGKYAFLKTY 119
   68 SEI----ESCTIDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVEVPTGPLSFFQDY 122
  120 NYTLG----ADDLTPFGEQQMVNSGIKF----YRRYKAL-----ARKIVPFIRASGSDR 165
  123 DYFVSDAAWYEQETTKGFYSGLNTAFDFGTTLRERYDHLINTSEEGKKL--SVWAGSQER 180
  166 VIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPE---GAGYNNTLDHGLCT----A 217
   231 YKDGDFPNDIAEREAD-----RLNTLSPGFNITADDIPTIALYCGFELNVRGE- 278
   335 HISTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTK-PLSTTSVESIEETD 393
  181 VVDTAKYFAQGFMKSNYTD------MVEVVALEEEKSQGLNSLTARISCPNYNSHI 230
  394 GYSASWTVPFAARAYVEMMQC--EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVE 451
   90; Gaps
  6 VLLSIATL---FGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPF--FSLADE 60
  10 IILALATLOSVFAVELOHVLGVNDRPYPORT-DDQYNILRHLGGL-GPYIGYNGWGIAAE 67
  A;Residues: 1.453 cmL.>
A;Residues: 1.453 cmL.>
A;Cross.references: GB:M11857; NID:g173422; PIDN:AAA35321.1; PID:g173423
R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25068
   FEESELGDDV---EANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSD
   279 ----SSFCDVLSREALLYTAYLRDLGWYYNVGNGNPLGKTIGYVYAN------
  275 ATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQD
  Match 14.2%; Score 350; DB 2; Length 468; Local Similarity 25.2%; Pred. No. 1.1e-19; les 124; Conservative 79; Mismatches 200; Indels
  Experimental source: strain 972h(-); clone p1 p4G3
  A; Gene: phol; SPDB:SPBP4G3.02
   452 GLSFARSGGNWEE 464
  434 RLEALNEDSDFAE 446
   A; Residues: 1-453 <RIE>
   A; Molecule type: DNA
   A; Accession: A25326
  Accession: T50405
  A; Map position: 2
   A; Molecule type:
  Query Match
   Matches
   218
   C; Genetics
   RESULT
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  δ
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  g
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   thiamin-repressible acid phosphatase - fission yeast (Schizosaccharomyces pombe) C:Species: Schizosaccharomyces pombe C:Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
  15;
  157 IYTAAQQRVVDSALWYGYGMF-----GEDVHNFTNYILVSENATAGSNSLSSYNACPA 209
  278 LSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTS 337
   101 AIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRRYKALARKIVPF 157
   97 SVPIDYSVSGNPLSFVPTWTPVIEAANADALSSSGRVELFDMGRQFYERYHELFNASTYN 156
   158 IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
  218 FEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQ 277
  -----QVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMKA 366
   265 YSEFCKLFNSVDFLNFEYEGDLSFSYGMGNSVKWGSIFGGAYANSLANSL--RSVENNTQ 322
   43 HKPYF----YGPSIDFPTTCKIKOVHTLQRHGSRNPT-GGNAAFDAVGIANFQQRLLNG 96
   98 ------LIEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRR 146
  89 LNNFQEKLLNGSIPVNFSYPENPLCFIKQWTPVIDAENADQLSSRGRLELFDLGRQLYQR 148
  147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEG--A 204
   46 HLWGTYS----PFFSLADESALSPDVPKGCRVTFVQVLSRHGARYPTS--SASKAYSA-- 97
  210 SDADDETTPALEAWRNVYMPPIRQRLNPYFSNYNLTNDDILNLYGICSYEIALQ----D
   338 TNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSA
      50;
   22 2
  Length 463;
60; Mismatches 187; Indels
   C,Accession: T39929
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, submitted to the EMBL Data Library, May 1998
   Indels
  51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSA-
   367 SEFVPFAGNLITELFQCEDSKY-YVRHLVNEEVFPLSDCG 405
  398 SWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCG 437
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Best Local Similarity 25.3%; Pred. No. 1.1e-16;
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   A; Accession: T39929
A; Status: preliminary; translated from GB/EMBL/DDBJ
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  69;
103; Conservative
  Matches 113; Conservative
  A; Reference number: Z21857
   A; Gene: SPDB:SPBC21H7.03c
  A; Molecule type: DNA
   A; Map position: 2
   C; Genetics:
  RESULT 13
  δ
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| nh 200 canstamyyscpvyrdnnidrnttraahtsmrnyflkpianrinkyfdsgynltysdvrs 259 | 260 LANDACPEDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSIGKYYGYGAGNPLGPAQGVGF 3   1   1   1   1   1   1   1   1   1 | QY 320 VNELIARLTHSFVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWYSIFFALGLYNGTK 379 1 | OY 380 PLSTISVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVD 439  1                                                      | Oy 440 KLG 442<br>  Db 418 PSG 420                  | RESULT 15 JE0369 histidine acid phosphatase (EC 3.1.3) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Oate: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000 | C;Accession: JE0369 R;Mullaney, E.J.; Ullah, A.H.J. Biochem. Biophys. Res. Commun. 251, 252-255, 1998 A;Tille: Identification of a histidine acid phosphatase (phyA)-like gene in Arabidops A;Tille: Identification of a histidine acid phosphatase (phyA)-like gene in Arabidops A;Reference number: JE0369; MUID:99009256 A;Accession: JE0369 | Astratus: preliminary<br>Astrolecule type: DNA<br>Astrolecules: 1.465 <mul><br/>C;Superfamily: yeast acid phosphatase<br/>C;Keywords: phosphoric monoester hydrolase</mul>                                                                       | Query Match 6.2%; Score 153; DB 2; Length 465;<br>Best Local Similarity 22.5%; Pred. No. 0.00031;<br>Matches 102; Conservative 61; Mismatches 199; Indels 92; Gaps 21;                                            | QY 35 DGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSA 91                                                                                      | OY 92 SKAYSALIEAIQKNATAFK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | QY 139 SGIKEYRRYKALAKKIVPFIRASGSDRVIASAEKFIEGFOSAK-LADPGANPHOAS 193                        | QY 194 PVINVIIPECAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLT 253  194 PVINVIIPECAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLT 253  Db 189VTSENRASDTKLRFFECC |   | n Eu                                                          | Db 279 LNYKMGVPLLEDVLHSMEEAIKAREEKLPPGSYE-KARLRFAHAETIVPPFS 329  Qy 371 A-LGLYNGTRPLSTTSVESIEETDGYSASWTVPPAARAYVEMMGCEAE 417       | Db 330 CLLGLFLDGSEFEKTQKEKPLELPPQPPKTRDFRGSTMAPFGGNNILVLXSCPAE 384 Qy 418 KEPLVRVLVNDRVVPLHGCGVPKLGRCKRDDF 449 | Db 385 SSPKYFVQVLHNEHPIAVPGCDGKDFCPLEDF 416                          |
|-------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---|---------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|
|                                                                         |                                                                                                         |                                                                           | 260 LFYICEYELAIKUHSDECSIFIFSEFLNREIDSDEDQAIGGGFVSEMASILGGGAI 320 VNELIARLTHSPVQDHISTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTK : | INNLADSL-TETD PLSTTSVESIEETD   : :   PQNPLPTDKNIYTY | Qy 440 KLGRCKRDDFVEGLSFARSGGN 461<br>    :        <br>  Db 418 PSGTSDGLCELQAYLNSPIRANSTSN 443                                                                                                                                                                 | RESULT 14 S14119 acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 10-Dec-1999 C; Accession: S14119; T40455                                                                                                      | R; Yang, J.; Schweingruber, M.E. Curr. Genet. 18, 269-272, 1990 A; Tit.le: The structural gene coding for thiamin-repressible acid phosphatase in Schizosa A; Reference number: S14119; MUID:91064763 A; Reference number: S14119; MUID:91064763 | A;Status: preilminary<br>A;Molecule type: DNA<br>A;Residues: 1-463<br>A;Cross-references: GB:X56939; NID:95006; PIDN:CAA40258.1; PID:95007<br>R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K. | Submitted to the EMBL Data Library, November 1996 A. Reference number: 221931 A. Accession: T40455 A. Status: preliminary; translated from GB/EMBL/DDBJ | A; Molecule type: DNA A; Residues: 1-463 <liva 1-463="" 972h-;="" <liva="" a;="" al034382;="" c428<="" caa22278.1;="" cosmid="" cross-references:="" embl:="" experimental="" gn00067;="" gspdb:="" pidn:="" residues:="" source:="" spbc428.03c="" spdb:="" strain="" td=""><td>C;Genetics: A;Gene: Spectal 28.03c A;Map position: 2 C;Superfamily: yeast acid phosphatase</td><td>C; Keywords: phosphoric monoester nydroidse Onerv Match 12.3%; Score 303.5; DB 2; Length 463;</td><td>9</td><td>Oy 46 HLWGTYSPPFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSA 97   </td><td>QY 98LIEALQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146  Db 89 IDIFQNKLLNGSIPVNFSYPENPLYFVKHWTPVIKAENADQLSSSGRIELFDLGRQVFER 148</td><td>QY 147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGA 204   </td><td>OY 205 GYNNTLDHGLCTAPEESELGDD-VEANFTAVFAPPIRARLEAHL-PGVNLTDEDVVN 259</td></liva> | C;Genetics: A;Gene: Spectal 28.03c A;Map position: 2 C;Superfamily: yeast acid phosphatase | C; Keywords: phosphoric monoester nydroidse Onerv Match 12.3%; Score 303.5; DB 2; Length 463;                                                                           | 9 | Oy 46 HLWGTYSPPFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSA 97 | QY 98LIEALQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146  Db 89 IDIFQNKLLNGSIPVNFSYPENPLYFVKHWTPVIKAENADQLSSSGRIELFDLGRQVFER 148 | QY 147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGA 204                                          | OY 205 GYNNTLDHGLCTAPEESELGDD-VEANFTAVFAPPIRARLEAHL-PGVNLTDEDVVN 259 |

Search completed: October 26, 2001, 15:10:30 Job time: 6336 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2001, 15:18:04; Search time 29.88 Seconds (without alignments) 535.385 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-488-265-31 2468. 1 MGVFVVLLSIATLFGSTSGT......DFVEGLSFARSGGNWEECFA 467

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | •      | Description  | P34753 |            | ~          |            | P35842 saccharomyc | P38693 saccharomyc | P24031 saccharomyc |            | P34754 aspergillus |            | P52291 pichia past | P52289 kluyveromyc |            | Q01682 schizosacch |            | P20611 rattus norv | P24638 mus musculu |          |            | _          | P19926 escherichia | P15309 homo sapien | 013712 schizosacch |            | Q10944 caenorhabdi | P38132 saccharomyc | Q23316 caenorhabdi |            |            | _          |            | _          | ٥,        |
|-----------|--------|--------------|--------|------------|------------|------------|--------------------|--------------------|--------------------|------------|--------------------|------------|--------------------|--------------------|------------|--------------------|------------|--------------------|--------------------|----------|------------|------------|--------------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|------------|------------|------------|------------|------------|-----------|
| SUMMARIES |        | QI           | YA     | PHYA_ASPNG | PHYB_EMENI | PPA5_YEAST | PPAB_YEAST         | PPAC_YEAST         | PPA3_YEAST         | PPAD_YEAST | PHYB_ASPNG         | PHYB_ASPAW | PPA1_PICPA         | PPA5_KLULA         | PPA1_SCHPO | PPA2_SCHPO         | PPAX_CAEEL | PPAL_RAT           | PPAL_MOUSE         | PPAP_RAT | PPAL_HUMAN | PEHX_ERWCH | AGP_ECOLI          | PPAP_HUMAN         | YDZ5_SCHPO         | LYS4_YEAST | PPAY_CAEEL         | CC47_YEAST         | NICA_CAEEL         | COPA_PSESM | CLOS_CLOHI | ATPX_BACFI | TRG1_ECOLI | PTND_HUMAN | GSA_STAAU |
|           |        | DB r         |        |            |            | ۲.         |                    |                    |                    |            |                    |            |                    |                    |            |                    |            |                    |                    |          |            |            |                    |                    |                    |            |                    |                    |                    |            |            |            |            |            | -         |
|           |        | Length       | 467    | 467        | 46         | 467        | 467                | 467                | 467                | 468        | 479                | 479        | 468                | 469                | 453        | . 46               | 75         | 42                 | 421                | 381      | 423        | . 602      | 413                | 386                | 844                | 69         | 411                | 84                 | 72]                | 9          | 526        | 467        | 938        | 2485       | 428       |
| dt        | Query  | Match Length | U)     | 4          | 73         | 16.4       | 16                 | 16                 | -                  | 2          | 14                 | 14         | 14                 | 13.7               | (*)        | 12.3               | 5.8        | 5.2                | 4.8                | 4.7      | 4.6        | 4.3        | 4.1                | 4.0                | 4.0                | 4.0        | 3.9                | 3.9                | 3.9                | 3.9        | 3.8        | ж<br>ж     | 3.8        | e.         | 3.8       |
|           |        | Score        | 1852   | 1848       | 1804.5     | 405        | 394                | 394                | 391                | 369        | 362.5              | 354.5      | 320                | 337.5              | 328        | 303.5              | 142        | 127.5              | 118.5              | 115.5    | 114.5      | 106.5      | 101.5              | 66                 | 86                 | 97.5       | on .               | 96.5               | σ                  | N          |            | 94         | σ          | 93.5       | 93        |
|           | Result | No.          | н      | 7          | m          | 4          | S                  | 9                  | 7                  | ω.         | 6                  | 10         | 11                 | 12                 | 13         | 14                 | 15         | 16                 | 17                 | 18       | 19         | 20         | 21                 | 22                 | 23                 | 24         | 25                 | 26                 | 27                 | 28         | 29         | 30         | 31         | 32         | 33        |

| 032611 flavobacter | P52986 synechocyst | 075001 schizosacch | 030408 b tyrocidin | 025655 helicobacte | P23984 infectious | P50126 candida mal | Q52309 providencia | P54987 mus musculu | Q02603 leuconostoc | 015438 homo sapien | P22871 erwinia her |  |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| ISOA_FLASP         | DHOM_SYNY3         | MCM7_SCHPO .       | TYCB_BACBR         | PYRD_HELPY         | VP40_ILTVT        | NCPR_CANMA         | AGP_PRORE          | IRG1_MOUSE         | BGAL_LEULA         | MRP3_HUMAN         | CRTI_ERWHE         |  |
| -                  | Н                  | П                  | Н                  | Н                  | Н                 | Н                  | Н                  | Н                  | <del>- 1</del>     | Н                  | -                  |  |
| 777                | 433                | 160                | 3587               | 351                | 286               | 680                | 417                | 646                | 626                | 1527               | 492                |  |
| 3.8                | 3.7                | 3.7                | 3.7                | 3.7                | 3.7               | 3.7                | 3.7                | 3.7                | 3.6                | 3.6                | 3.6                |  |
| 93                 | 92.5               | 92.5               | 92                 | 91.5               | 91.5              | 91.5               | 91                 | 90.5               | 06                 | 06                 | 89.5               |  |
| 34                 | 35                 | 36                 | 37                 | 38                 | 33                | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |  |

# ALIGNMENTS

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   ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
   KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
   361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
   Gaps
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   1 MGVSAVLLPLYLLAGVISGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
  01-FBE-1994 (Rel. 28, Created)
01-FBE-1994 (Rel. 28, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXARISPHOSPHATE
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
   STRAIN=NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE=93252284; PubMed=8387447;
Van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M.,
Gouka R.J., Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A.,
Selten G.C.M., Veenstra A.E., van Gorcom R.F.M.,
van den Hondel C.A.M.J.J.;
     (POTENTIAL)
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  Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
  75.0%; Score 1852; DB 1; Length 467; 74.3%; Pred. No. 2.1e-140;
   78; Indels
  N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..)
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   42; Mismatches
   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
  51075 MW;
   Matches 347; Conservative
   STANDARD;
   PHOSPHOHYDROLASE A)
  467 AA;
  Similarity
  NCBI_TaxID=5061;
   PHYA_ASPNG
P34752:
   CARBOHYD
CARBOHYD
  Query Match
       CARBOHYD
                         CARBOHYD
  CARBOHYD
  CARBOHYD
   CARBOHYD
   CARBOHYD
   CARBOHYD
  CARBOHYD
  SEQUENCE
  Best Local
  RESULT 2
PHYA_ASPNG
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  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Cloning, characterization and overexpression of the phytase-encoding gene (phyA) of Aspergillus niger."; Gene 127:87-94(1993).
   D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
-1- BIOTECHNOLOGY: IS USED AS A FOOD AND FEED ADDITIVE. IT CAN FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS USED AS FOOD FOR MONOGASTRIC ANIMALS. SOLD BY NOVO NORDISK UNDER
  Kostrewa D., Gruninger-Leitch F., D'Arcy A., Broger C., Mitchell D., van Loon A.P.;
  'Aspergillus ficuum phytase: complete primary structure elucidation
  3-PHYTASE A. NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
   "Crystal structure of phytase from Aspergillus ficuum at 2.5-A resolution.";
Nat. Struct. Biol. 4:185-190(1997).
-!- FUNCTION: CATALXZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
  "Aspergillus ficuum phytase: partial primary structure, substrate selectivity, and kinetic characterization."; Prep. Biochem. 18:459-471(1988).
  oŧ
  -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY
  -:- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 =
  active site
   PROTON DONOR (BY SIMILARITY).
  to the EMBL/GenBank/DDBJ databases
   Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr., "Cyclohexanedione modification of arginine at the Aspergillus ficuum phytase.";
   Biochem. Biophys. Res. Commun. 192:747-753(1993).
   ochem. Biophys. Res. Commun. 178:45-53(1991).
  Signal; 3D-structure.
  Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
STRAIN-NRRL 3135 / VAN TIEGHEM / FICUUM;
MEDLINE-97307250; PubMed-9164457;
   FICUUM;
  SEQUENCE OF 71-93.
STRAIN-NRR 3135 / VAN TIEGHEM / FICUUM;
  VAN TIEGHEM / FICUUM;
   CHARACTERIZATION, AND PARTIAL SEQUENCE
  Dischinger H.C. Jr.;
   STRAIN=NRRL 3135 / VAN TIEGHEM / I
MEDLINE=89160685; PubMed=2852807;
  STRAIN-NRRL 3135 / VAN TIEGHEM / 1
MEDLINE=93249451; PubMed=8387289;
  MEDLINE-91298982; PubMed-1648914;
  EMBL; Z16414; CAA78904.1; -. EMBL; M94550; AAA32705.1; -.
  NOVO.
  Glycoprotein;
   by chemical sequencing.
  23
467
82
361
   PIR; JN0482; JN0482.
PIR; PN0023; PN0023.
PIR; JN0656.
PDB; 11HP; 18-MAR-98.
InterPro; IPR000560; -
  Mullaney E.J.;
Submitted (XXX-1992)
  THE NAME PHYTASE
   SEQUENCE OF 24-464.
   SEOUENCE FROM N.A.
  FROM PHYTATE.
  24
82
361
   Ullah A.H.J.,
  Ullah A.H.J.;
   Hydrolase;
   ACT_SITE
ACT_SITE
  SIGNAL
   CHAIN
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0;
   240
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
  KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
   HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60
  Gaps
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last nunotation update)
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE
3-PHOSPHOHYDROLASE B) (3 PHYTASE B) (MYO-INOSITOL HEXARISPHOSPHATE
   KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
   .
0
   Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
   1; Pezizomycotína; Eurotiomycetes; Emericella.
  Length 467;
   Indels
   421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   88FE8F3584341D6D CRC64;
   (GLCNAC. .
   78;
  Pred. No. 4.5e-140;
   Query Match 74.9%; Score 1848; DB 1; Best Local Similarity 74.3%; Pred. No. 4.5e-140; Matches 347; Conservative 42; Mismatches 78;
  (GLCNAC.
  (GLCNAC
  (GLCNAC
   463 AA
   42; Mismatches
   Emericella nidulans (Aspergillus nidulans)
  N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
  N-LINKED
N-LINKED
  PRT;
  SEQUENCE FROM N.A.
MEDLINE=98007872; PubMed=9349716;
   MM:
  Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; En
   51086
   STANDARD;
   AA;
  PHOSPHOHYDROLASE B)
  NCBI_TaxID=5072;
  PHYB_EMENI
000093;
DISULFID
DISULFID
DISULFID
   CARBOHYD
CARBOHYD
  CARBOHYD
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                                 DISULFID
  DISULFID
  CARBOHYD
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   CARBOHYD
   CARBOHYD
  CARBOHYD
  CARBOHYD
   SEQUENCE
  PHYB_EMENI
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  296
   360
  356
  420
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  Gaps
  NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
        "Cloning of the phytases from Emericella nidulans and the thermophilic fungus Talaromyces thermophilus.";
Biochim. Biophys. Acta 1353:217-223(1997).
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE
   121 YILGADDLIPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFOSA
  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
   301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
   N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMOCEAEKEP
   -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
  (POTENTIAL)
   (POTENTIAL)
  5
  Length 463;
   BINDING SUBSTRATE
  Indels
  ECC5827DIE1C82A2 CRC64;
  DB 1;
   75;
   73.1%; Score 1804.5; DB 1
72.5%; Pred. No. 1.3e-136;
iive 48; Mismatches 75;
  N-LINKED (GLCNAC.
   (GLCNAC
   (BY SIMILARITY)
   3-PHYTASE B.
REQUIRED FOR
   Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
  POTENTIAL
   N-LINKED
  Glycoprotein; Signal.
   MM:
   EMBL; U59803; AAB96871.1; -.
  51786
   Local Similarity 72.5
nes 338; Conservative
  80
  81
26
26
41
1103
1118
203
226
331
335
372
   463
   InterPro; IPR000560;
  81
357
26
41
103
118
203
226
331
335
463 AA;
  FROM PHYTATE.
   20
80
  Hydrolase;
   CARBOHYD
CARBOHYD
CARBOHYD
   CARBOHYD
  ACT_SITE
CARBOHYD
   ACT_SITE
  ACT_SITE
  CARBOHYD
   CARBOHYD
  Query Match
   CARBOHYD
  CARBOHYD
  SIGNAL
   CHAIN
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   Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.; "Analysis of a 70 kb region on the right arm of yeast chromosome II."; Yeast 10:1363-1381(1994).
  SEQUENCE FROM N.A., AND SEQUENCE OF 18-26.
MEDLINE=83168913; PubMed=6300772;
Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.;
"The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repressible acid phosphatase contains a signal peptide.";
Nucleic Acids Res. 11:1657-1672(1983).
  Saccharomyces
   SEQUENCE FROM N.A., AND SEQUENCE OF 18-45.
BEDILINE-85037940, Pubmed-6093031,
Bajva W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.;
"Structural analysis of the two tandemly repeated acid phosphatase
   cerevisiae.";
wol. Cell. Biol. 6:1855-1865(1986).
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN ALCOHOL + ORTHOPHOSPHARE.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- INDUCTION: REPRESSED BY INORGANIC PHOSPHATE.
-!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-!- PTM: SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE PAMILY.
   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
   gene
   SEQUENCE OF 1-44 FROM N.A. MEDLINE=87064474; PubMed=3537710; Tait-Kamradt A.G., Turner K.J., Kramer R.A., Elliott Q.D., Bostian S.J., Thill G.Y. Rogers D.T., Bostian K.A., "Reciprocal regulation of the tandemly duplicated PHO5/PHO3 cluster within the acid phosphatase multigene family of Sacc
   21-JUL-1986 (Rel. 01, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (P60)
421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECF 466
                                   467 AA
  Saccharomyces cerevisiae (Baker's yeast).
   genes in yeast.";
Nucleic Acids Res. 12:7721-7739(1984).
  MEDLINE=95208357; PubMed=7900426;
   EMBL, V01320; CAA24630.1; --
EMBL; X01079; CAA2555.1; --
EMBL; X78993; CAA5558.1; --
EMBL; X35962; CAA85046.1; --
EMBL; X01080; CAA2556.1; --
PIR; S05705; PABYC.
  PHO5 OR YBR093C OR YBR0814
   STANDARD;
   P34752; 11HP.
S0000297; PHOS
  SEQUENCE FROM N.A.
  NCBI_TaxID=4932;
  STRAIN-S288C
  PPA5_YEAST P00635;
  416
  PPA5_YEAST
  Db
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15;
   59 DLPEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIR 118
   119 DDDDLEMETTFANSDDVLNPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHD 178
  SNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPF 403
  404 AARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF-----VEGLSFA 456
  DVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK-TYNYTLG 124
  58
   REPRESSIBLE ACID PHOSPHATASE.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
  6 VLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISP
  LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLD
   5 VVYSILAASLANAGTI - - PLGKLADVDKIGTQKDIFPFL - - - GGAGPYYSFPGDYGISR
  125 ADD------LIPF-GEQQMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIA
   SAEKFIEGFQSAKLADPGANPHQASPVINVII-----PEGAGYNNTLDHGLCTAFEESEL
  224 GDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCD
  223 NDDIVNEYDTTYLDDIAKRLNKENKGLNLTSTDASTLFSWCAFEV----NAKGYSDVCD
   ------KVWLSFTHDTDILNFLTTAGIIDDKNNLTAEYVPFMGNT--FHRSWYVPQ
  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
  (POTENTIAL)
   (POTENTIAL)
   (POTENTIAL)
  (POTENTIAL)
  16.4%; Score 405; DB 1; Length 467; 26.0%; Pred. No. 7.2e-25; tive 62; Mismatches 216; Indels
  DC3C9504BC2D3D0C CRC64;
   N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
         Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
   D -> Y (IN REF. 1).
A -> G (IN REF. 1).
H -> Q (IN REF. 1).
S -> V (IN REF. 1).
AS -> DT (IN REF. 1).
  N-LINKED GLCNAC.
D -> Y (IN REF. 1
  REF.
  <u>`</u>
   62;
   MM;
   463
466
52858
  Conservative
  467
3337
1103
1103
1103
1102
1103
3315
3315
4445
4456
461
461
130
294
InterPro; IPR000560;
   Local Similarity
  Matches 125;
   R 457
  ACT_SITE
ACT_SITE
CARBOHYD
   CARBOHYD
   CARBOHYD
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   CARBOHYD
   CARBOHYD
   CARBOHYD
  CARBOHYD
   Query Match
   CARBOHYD
   CARBOHYD
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   CARBOHYD
   CONFLICT
   CONFLICT
   CONFLICT
   CONFLICT
   SEQUENCE
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  SIGNAL
  CHAIN
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  284
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   436
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PPAB\_YEAST

RESULT

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  -!- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
   STRAIN=S288C / ABD/2;
MEDLINE=95249563; PubMed=7731988;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
Storms R.K.;
  NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
  Chen J.Y., Gong Y.I., Ao S.Z.;
"The primary structure of acid phosphatase gene PHO11 in S. cerevisiae and comparison with other gene families.";
Acta Blochim. Blophys. Sin. 21:437-444(1989).
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
   -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
   PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
   (POTENTIAL)
   (POTENTIAL)
   (POTENTIAL)
  (POTENTIAL)
   (POTENTIAL)
  (POTENTIAL)
  (POTENTIAL)
   (POTENTIAL)
  'The nucleotide sequence of chromosome I from Saccharomyces
  EMBLI, C. 1000004; PHOII.
SGD, SO00004; PHOII.
SGD, SO00004; PHOII.
InterPro: IPRO00260; --
PERM; PFO00208; acid_phosphat; 1.
PROSITE; PSO00708; HIS_ACID_PHOSPHAT_1; 1.
R PROSITE; PSO0778; HIS_ACID_PHOSPHAT_2; 1.
R PROSITE; PSO0778; HIS_ACID_PHOSPHAT_2; 1.
R PROSITE; PSO0778; HIS_ACID_PHOSPHAT_2; 1.
ACID_PHOSPHATASE PHOII.
ACT ACID_PHOSPHATASE PHOII.
ACT ACID_PHOSPHATASE PHOII.
  VS -> AR (IN REF. 2).

R -> H (IN REF. 2).

R -> G (IN REF. 2).

D -> G (IN REF. 2).

ABCDC1C046B326C3 CRC64;
                                    Ol-UNN-1994 (Rel: 29, Last sequence update)
Ol-NOV-1997 (Rel: 35, Last annotation update)
ACID PHOSPHATASE PHO11 PRECURSOR (EC 3.1.3.2) (P56).
  N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
   N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
  N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
A -> L (IN REF. 2).
VS -> AR (IN REF. 2).
   (GLCNAC. . .)
  Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
   467 AA
  or send an email to license@isb-sib.ch).
  N-LINKED
   PRT;
                             01-JUN-1994 (Rel. 29, Created) ;
   MW.
  ALCOHOL + ORTHOPHOSPHATE
   EMBL; L28920; AAC09508.1; -.
  U19789; AAA73479.1; -. P34752; 1IHP.
  52757
 STANDARD;
   17
83
1,50
354
423
  467
75
337
97
1162
250
  356
390
439
445
461
  17
82
150
354
423
467 AA;
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  PHO11 OR YAR071W.
   NCBI_TaxID=4932;
  461
  cerevisiae.";
 PPAB YEAST
  ACT_SITE
CARBOHYD
   CONFLICT
  CARBOHYD
  CARBOHYD
  CARBOHYD
   CARBOHYD
   CARBOHYD
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   CONFLICT
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14;
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   84 ARYPISSASKAYSALIEAIQKNATAFKGKYAFLK------TYNYTL-----GADDL 128
   129 TPF-GEQQMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPG 186
   137 NPYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSNRCHDTAQYFIDG-----LGDK- 190
   187 ANPHQASPVINVII-----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
   242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301
  -----KVWLSFTH 337
  DNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPL 421
   STRAIN-2288C / AB972; MEDLINE-94378003; PubMed-8091229; MEDLINE-94378003; PubMed-8091229; Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Mancis E.J., Mencares S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
  CONSTITUTIVE AND THE OTHER IS REPRESSIBLE BY INORGANIC PHOSPHATE.
-!- PTM: GLYCOSYLATED DURING SECRETION ACROSS THE MEMBRANE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
   21 PLGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDLPESCEMKQVQMYGRHG 76
  "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
   -!- INDUCTION: S.CEREVISIAE HAS 2 TYPES OF ACID PHOSPHATASE: ONE IS
   24 PRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHG
   302 YYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSH
  Science 265:2077-2082(1994).
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
  16;
  203; Indels
  Saccharomycetales; Saccharomycetaceae; Saccharomyces
  394 VRYVINDAVVPIETCSTGPGFSCEINDFYDYAEKRVAGTDFLK 436
  422 VRVLVNDRVVPLHGCGVDKLGRCKRDDF-----VEGLSFAR 457
16.0%; Score 394; DB 1; 25.7%; Pred. No. 5.4e-24;
   296 YYQTGPGYDVVRSVGANLFNASVKLLKESEVQDQ------
  TB-1995 (Rel. 31, Last sequence update)
SB-1995 (Rel. 31, Last annotation update)
PHOSPHATASE PHO12 PRECURSOR (EC 3.1.3.2)
   467 AA
                                       65; Mismatches
   01-FEB-1995 (Rel. 31, Created)
  ALCOHOL + ORTHOPHOSPHATE.
                                     Matches 119; Conservative
   STANDARD;
                  Best Local Similarity
   SEQUENCE FROM N.A
   PHO12 OR YHR215W.
   NCBI_TaxID=4932;
  01-FEB-1995
01-FEB-1995
   PPAC_YEAST
P38693;
  Vaudin M.;
    Query Match
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  PPAC_YEAST
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  and for commercial
the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
  84 ARYPISSASKAYSALIEAIQKNATAFKGKYAFLK------TYNYTL-----GADDL 128
   129 TPF-GEQQMVNSGIKFYRRYKALARKIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPG 186
   187 ANPHQASPVINVII-----PEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
  RLNKENKGLNLTSSDANTFFAWCAYEINAR----GYSDICNIFTKDELVRFSYGQDLET 295
  YYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSH 361
   ---KVWLSFTH 337
   DNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPL 421
   Gaps
   24 PRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHG 83
  21 PLGKLSDIDKIGTQTEIFPFL----GGSGPYYSFPGDYGISRDLPESCEMKQVQMVGRHG 76
  SIMILARITY).
  RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK
  (POTENTIAL).
  (POTENTIAL).
   (POTENTIAL)
   (POTENTIAL)
  . .) (POTENTIAL)
   (POTENTIAL)
  (POTENTIAL)
  (POTENTIAL)
   (POTENTIAL)
   16;
  Length 467;
  EMBL, C. 1180.

HSSP, P34752, IIRP.

SGD, S0001258, PH012.

(InterPor) IPR000560; ...

R Péam, PF00328; acid_phosphat, 1.

R PROSITE: PS000718; HIS_ACID_PHOSPHAT_1; 1.

DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; 1.

BY SIMILARITY.

ACID PHOSPHATASE PH012.

""Arolase; Glycoprotein; Signal; Multigene family.

"Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family.
""Arolase; Glycoprotein; Signal; Multigene family."
"""Arolase; Multigene family."
"""Arolase; Multigene family."
""""Arolase; Multigene
  NUCLEOPHILIC ACCEPTOR (BY SI PROTON DONOR (BY SIMILARITY)
  65; Mismatches 203; Indels
   BEC606CDF39B845B CRC64;
  394 VRYVINDAVVPIETCSTGPGFSCEINDFYGYAEKRVAGTDFLK 436
   422 VRVLVNDRVVPLHGCGVDKLGRCKRDDF-----VEGLSFAR 457
  (GLCNAC. . .)
   (GLCNAC. . .)
   (GLCNAC. . .)
   (GLCNAC. . .)
  16.0%; Score 394; DB 1; 25.7%; Pred. No. 5.4e-24;
   (GLCNAC.
  (GLCNAC.
  (GLCNAC.
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  (GLCNAC
  296 YYQTGPGYDVVRSVGANLFNASVKLLKESEVQDQ---
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   EMBL; U00029; AAB69729.1; -. PIR; S48996; S48996.
   52699
  Query Match 16.0
Best Local Similarity 25.7
Matches 119; Conservative
   97
162
192
192
315
  356
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439
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  461 ,
467 AA;
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PPA3\_YEAST

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  13;
   Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.; "Analysis of a 70 kb region on the right arm of yeast chromosome II."; Yeast 10:1363-1381(1994).
  64; Gaps
   49 GTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATA 108
  42 GGAGPYFSFPGDYGISRDLPEGCEMKQLQMLARHGERYPTYSKGATIMKTWYKLSNYTRQ 101
  SEQUENCE FROM N.A.
MEDLINE-85037940; PubMed-6093051;
Bajwa W., Meyhack B., Rudolph H., Schweingruber A.-M., Hinnen A.;
"Structural analysis of the two tandemly repeated acid phosphatase
  NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
  -!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN
   -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
   Saccharomycetes;
   N-LINKED (GLCNAC. . .) (POTENTIAL).
  (POTENTIAL)
   (POTENTIAL)
   (POTENTIAL)
  (POTENTIAL)
   (POTENTIAL)
   (POTENTIAL)
   (POTENTIAL)
  (POTENTIAL)
  Length 467;
  CONSTITUTIVE ACID PHOSPHATASE
  Indels
   DED -> MKT (IN REF. 1).
05FBB80DEB41B0FF CRC64;
              01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CONSTITUTIVE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Sacc
Saccharomycetales; Saccharomycetaceae; Saccharomyces
   SGD; SUCCESTON SERVICES SERVIC
   (GLCNAC. . .)
   (GLCNAC. . .)
   (GLCNAC. . .)
  (GLCNAC. . .)
  (GLCNAC. . .
  61; Mismatches 192;
  15.8%; Score 391; DB 1; 27.0%; Pred. No. 9.4e-24;
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  Nucleic Acids Res. 12:7721-7739(1984)
   MEDLINE=95208357; PubMed=7900426;
   52776 MW;
  EMBL; X01080; CAA25557.1; -. EMBL; X78993; CAA55597.1; -. EMBL; Z35961; CAA85045.1; -.
   ORTHOPHOSPHATE
  PHO3 OR YBR092C OR YBR0813.
  Matches 117; Conservative
   PIR; S44674; PABYCC.
HSSP; P34752; 1IHP.
SGD; S0000296; PHO3.
   467 AA;
  Local Similarity
   SEQUENCE FROM N.A.
  NCBI_TaxID=4932;
  genes in yeast.
  STRAIN=S288C
  ACT_SITE
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  Query Match
  CARBOHYD
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198 ----TLSENSSSGANTLAAKSSCPNWNSNANNDILMSYSRDYLENISDRLNDENKGLNLS 253
   49 GTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATA 108
  109 FKGKYAFLKT-YNYTL-------GADDLTPF-GEQQMVNSGIKFYRRYKALAR 152
   --- DDVEANFTAVFAPPIRARLEAHLPGVNLT 253
   254 DEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGP 313
  314 AQGVGFVN---ELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFF 370
   Gaps
   Ol-FEB-1994 (Rel. 28, Last sequence update)
Ol-JUN-1994 (Rel. 29, Last annotation update)
3-PHYTASE B PRECURSOR (EC 3.1.3.8) (WAYO-INOSTIOL-HEXAPHOSPHATE
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
   153 KIVPF-IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD
  [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 20-101; 133-141 AND 376-399.
MEDLINE=93371452; PubMed=7916610;
Ehrlich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr.,
  (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL).
(POTENTIAL).
  : | | : | | :: | 309 SIGANLFNATVKLIRQSAH-------LDQKVWLSFTHDTDILNYLT
  371 ALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRV
   Ullah A.H.J.;
"Identification and cloning of a second phytase gene (phyB) from Aspergillus niger (ficuum).";
Biochem. Biophys. Res. Commun. 195:53-57(1993).
   (POTENTIAL).
   (POTENTIAL)
   (POTENTIAL)
   15.0%; Score 369; DB 1; Length 468; 25.3%; Pred. No. 5.4e-22; Live 60; Mismatches 175; Indels 110;
                              N-LINKED (GLCNAC. . . ) (POTINED (GLCNAC. . ) (POTINED (GL
  431 VPLHGCGVDKLGRCKRDDFVE-----GLSFARSGGNWEEC 465
   11: 1 : 1 : 1 404 VPIESCSSGPGFSCEEGTFYEYAKDRLRGVSF-----YEDC 439
  479 AA
  PRT;
163
193
193
202
202
238
1 251
5 316
397
457
N 462
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S3076 MW;
  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seq
01-JUN-1994 (Rel. 29, Last ann
3-PHYTASE B PRECURSOR (EC 3.1.:
  Best Local Similarity 25.3% Matches 117; Conservative
  STANDARD;
  212 HGLCTAFEESELG--
  PHOSPHOHYDROLASE B).
          163
193
202
238
251
316
357
391
457
462
  Aspergillus niger.
   PHYB_ASPNG
                           CARBOHYD
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  16;
  158 IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
  218 FEESELG------DDVEANFTAVFAPPIR---ARLEAHLPGVNLTDEDVVNLMD 262
  322
   380
   L----DRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDKGTVVRLVLNEAVLPFNDC 413
   NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONG (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
  109 EYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
  202 SESEVMGADSLTPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLIV 261
  108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GEQQMVNSGIKFYRRYKAL--ARKIVPF 157
  49 GTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAY-SALIEAIQKNAT 107
  Gaps
  ------FGYNYSTNAALNII
   263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAOGVGFVNE
   323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY--NGTKP
   317 SLTLLNQGP-----KEAGP-----LFFNFAHDTNITPILAALGVLIPNEDLP
   381 LSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC
  FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
                                       -; - CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE. -; - SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
  DB 1; Length 479;
   REQUIRED FOR BINDING SUBSTRATE (BY SIMILARITY).
  Indels
  395D4DA2B50FDFC4 CRC64;
  156;
  14.7%; Score 362.5; DB 1
28.3%; Pred. No. 1.8e-21;
  54; Mismatches
   Pfam: PF001328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
   3-PHYTASE B.
   :|| ||| :| ||| |||
169 F-SSGYGRVIETARKFGEGF------
   Hydrolase; Glycoprotein; Signal.
  MM.
   EMBL; L20567; AAA02934.1; -.
  52611
  Best Local Similarity 28.3
Matches 119; Conservative
   82
106
1106
1227
2250
442
458
   19
   81
  AA;
                            FROM PHYTATE.
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   InterPro;
  ACT_SITE
  CARBOHYD
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   15;
  53 GPYSERVSY----GIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINTT 108
  49 GTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASK-AYSALIEAIQKNAT 107
  91; Gaps
   MEDLINE-94040796; PubMed-8224894; Paloheimo M.T., Cantrell M.A., Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A., Mattrien-Olinonen A., Nevalainen H., Rambosek J.A.; Mistrien-Olinonen A., Nevalainen H., Rambosek J.A.; William and sequencing of the genes encoding phytase (phy) and Pt. S.-optimum acid phosphatase (aph) from Aspergillus niger var.
   Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
   MEDLINE-99264417; PubMed-10329192;
Kostrewa D., Wyss M., D'Arcy A., van Loon A.P.;
"Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
   J. MOI. Biol. 288:965-974(1999).
  SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
  -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + ORTHOPHOSPHATE.
                       Last sequence update)
Last annotation update)
(EC 3.1.3.8) (MYO-INOSTHOL-HEXAPHOSPHATE
(PH 2.5 OPTIMUM ACID PHOSPHATASE).
  Length 479;
  Indels
  -LINKED (GLCNAC. ..).
4F8E0F3778CC3B08 CRC64;
   N-LINKED (GLCNAC. ..)
   3-PHYTASE B. NUCLEOPHILIC ACCEPTOR. PROTON DONOR.
   14.4%; Score 354.5; DB 1; 27.9%; Pred. No. 8e-21;
  ; Pred. No. 8e-21;
53; Mismatches 159;
  pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HTS_ACID_PHOSPHAT_1; 1.
Hydrolase; Glycoprotein; Signal; 3D_structure.
   BY SIMILARITY.
  N-LINKED
N-LINKED
   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
  441
298
421
191 N-
315 N-
52678 MW;
     Created)
   EMBL; L02420; AAA16897.1; -.
  Best Local Similarity 27.9%
Matches 117; Conservative
   PIR; JN0890; JN0890.
PDB; IQFX; 19-APR-00.
InterPro; IPR000560; -.
   -!- SUBUNIT: HOMODIMER.
   82
337
387
472
01-FEB 1994 (Rel. 28, C
01-FEB-1994 (Rel. 28, L
30-MAY-2000 (Rel. 39, L
3-PHYTASE B PRECURSOR (
   3-PHOSPHOHYDROLASE B)
  Gene 133:55-62(1993).
   Aspergillus awamori
  2.4-A resolution.";
   479 AA;
  NCBI_TaxID=105351;
   SEQUENCE FROM N.A.
   FROM PHYTATE
  STRAIN-ALK0243;
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   109 EYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPF 168
  158 IRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTA 217
   218 FEESELG------DDVEANFTAVFAPPIR---ARLEAHLPGVNLTDEDVVNLMD 262
   263 MCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNE 322
  323 LIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY--NGTKP 380
108 AFKGKYAFLKTYNYTL-----GADDLT-PF-GEQQMVNSGIKFYRRYKAL-ARKIVPF 157
   202 SESEVMGADSLTPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMV 261
   317 SLTLLNQGPKE-------AGSLFFNFAHDTNITPILAALGVLIPNEDLP 358
   381 LSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEA----EKEPLVRVLVNDRVVPLHGC 436
  359 L----DRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDC 413
  ACID PHOSPHATASE PHO1.

NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).

PROTON DONOR (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
   169 F-SSGYGRVIETARKFGEGF-----FGYNYSTNAALNII
   Gene 163:19-26(1995).
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN ALCOHOL + ORTHOPHOSPHATE.
   -!- INDUCTION: BY PHOSPHATE STARVATION.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
   Payne W.E., Gannon P.M., Kaiser C.A., "An inducible acid phosphatase from the yeast Pichia pastoris: characterization of the gene and its product.";
  PROSITE; PS0028; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Signal; Multigene family.
   01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ACID PHOSPHATASE PHO1 PRECURSOR (EC 3.1.3.2).
  POTENTIAL.
   PRT;
   MEDLINE=96001238; PubMed=7557473;
  (Rel. 34, Created)
(Rel. 34, Last sequ
   EMBL; U28658; AAA85503.1; -.
  STANDARD;
  Pichia pastoris (Yeast).
   InterPro; IPR000560; -
   84
345
163
196
256
  SEQUENCE FROM N.A.
   NCBI_TaxID=4922;
   23
84
345
163
196
256
  PPA1_PICPA
P52291;
  01-0CT-1996
  ACT_SITE
CARBOHYD
  ACT_SITE
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   PPA1_PICPA
   CHAIN
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21;
  This SWISS-PROT entry is copyright. It is produced through a collaboration
  68 SEI-----ESCTIDQAHLLMRHGERYPSTNVGKQLEALYQKLLDADVEVPTGPLSFFQDY 122
  123 DYFVSDAAWYEQETTKGFYSGLNTAFDFGTTLRERYDHLINTSEEGKKL--SVWAGSQER 180
  181 VVDTAKYFAQGFMKSNYTD------MVEVVALEEEKSQGLNSLTARISCPNYNSHI 230
  61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIE-AIQKNATAFKGKYAFLKTY 119
   120 NYTLG----ADDLTPFGEQQMVNSGIKF----YRRYKAL-----ARKIVPFIRASGSDR 165
   166 VIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPE---GAGYNNTLDHGLCT----A 217
   218 FEESELGDDV---EANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSD 274
  275 ATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQD 334
  ----SFCDVLSREALLYTAYLRDLGWYNVGNGNPLGKTIGYVYAN------ 321
   335 HTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTK-PLSTTSVESIEETD 393
  Gaps
  6 VLLSIATL---FGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPF--FSLADE 60
  394 GYSASWTVPFAARAYVEMMQC---EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVE
 N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
AES55B8E27718C2C CRC64;
  Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyceties;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
   :06
   Length 468;
  79; Mismatches 200; Indels
   01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
REPRESSIBLE ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
  14.2%; Score 350; DB 1; 25.2%; Pred. No. 1.8e-20;
  52690 MW;
  Matches 124; Conservative
   STANDARD;
321
360
453
  452 GLSFARSGGNWEE 464
  434 RLEALNEDSDFAE 446
  Similarity
  SEQUENCE FROM N.A. STRAIN-CBS 2359/152;
   468 AA;
   NCBI_TaxID=28985;
  PPA5_KLULA
P52289;
  Query Match
 CARBOHYD
             CARBOHYD
                           CARBOHYD
   SEQUENCE
  Best Local
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  PPA5_KLULA
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STANDARD;

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   16;
   NUCLEDPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
  394 GYSASWIVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF---- 449
   370 IQQLSWVTPMGGRIFTEKLKC--GNASYVRYIINDVIIPVPGCTSGPGFSCPIEDFDDXI 427
   119 YNYTLGADDLTPFGEQOMVNSGIKFYRRY-------KALARKIVPFIR---- 159
   105 -----NDPLEVFNDYEFFVSNTKYFDQLTNSTDVDPSNPYAGAKTAQHLGKYIAYNYGD 158
   LFSDSNPVFTSSSGRVH--QTAKYVVSSLEEELDIQLDLQIIQENETSGANSLTPADSCM 216
   217 AFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLT - DEDVVNLMDMCPFDTVARTSD 274
  217 TY-NGDLGDEYFENATLPYLTDIKNRWMKKNSNLNLTLEHDDIELLVDWCAFETNVKGSS 275
  275 ATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQD 334
  AV-----CDLFERNDLVAYSYYANVNNFYRRGAGNPMSNPIGSVLVNASYNLLTQADELD 330
  HTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY-NGTKPLSTTSVESIEETD 393
   59 DESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKT 118
  1 MLSILLGLLSLSGTHAAPISK-----DNGTVCYALNNSTTDESIFSLLNGQGPHYDYP 53
  7 LLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCF-----PEISHLWGTYSPFFSLA 58
   160 -ASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEG--AGYNNTLDHGLCT
  (POTENTIAL)
   DB 1; Length 469;
   REPRESSIBLE ACID PHOSPHATASE
   Indels
  863B528D0740AA7E CRC64;
  13.7%; Score 337.5; DB 1; 24.6%; Pred. No. 1.8e-19; tive 70; Mismatches 208;
  GLCNAC
  N-LINKED
  ×
  EMBL; 233995; CAA83964.1; -.
  52532
   Best Local Similarity 24.6
Matches 121; Conservative
   16
469
77
73
33
31
32
32
129
229
  428 TNRLNGIDYVSS 439
  450 ---VEGLSFARS 458
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  51 YSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSA------LIE 100
   101 AIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQOMVNSGIKFYRRYKALARKIVPF 157
  50; Gaps
  43 HKPYF-----YGPSIDFPTTCKIKQVHTLQRHGSRNPT-GGNAAFDAVGIANFQQRLLNG 96
   "Isolation and characterization of the structural gene for secreted acid phosphatase from Schizosaccharomyces pombe.";
J. Biol. Chem. 261:2936-2941(1986).
  NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
   Elliott S., Chang C., Schweingruber M.E., Schaller J., Rickli E.E.,
   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
   Rieger M., McDougall R.C., Rajandream M.A., Barrall B.G.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
   ALCOHOL + ORTHOPHOSPHATE.

- SUBCELLULAR LOCATION: CELL WALL.

- INDUCTION: REPRESED BY PHOSPHATE AND WEAKLY BY THIAMINE.

- INDUCTION: REPRESED BY PHOSPHATE AND WEAKLY BY THIAMINE.

- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
   (POTENTIAL)
   Length 453;
   60; Mismatches 187; Indels
   7CF891256EB154D1 CRC64;
   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
  13.3%; Score 328; DB 1; 25.8%; Pred. No. 9.7e-19;
   ACID PHOSPHATASE
  08, Last sequence update)
40, Last annotation update)
  PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hydrolase; Glycoprotein; Cell wall; Signal.
  ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2).
  N-LINKED
  SEQUENCE FROM N.A.
MEDLINE=86140050; PubMed=3005272;
  InterPro; IPR000560; -
Pfam; PF00328; acid_phosphat; 1.
   (Rel. 08, Created)
  ..
Σ
   EMBL; M11857; AAA35321.1; -.
EMBL; AL137099; CAB68657.1; -
  50557
  Conservative
   18
453
69
330
330
151
183
1193
410
429
   (Rel. 08,
  PIR; A25326; A25326.
  Schizosaccharomyces.
   PHO1 OR SPBP4G3.02.
   Similarity
   HSSP; P34752; 11HP
   SEQUENCE FROM N.A.
  NCBI_TaxID=4896;
  01-AUG-1988
  01-OCT-2000
   Matches 103;
  01-AUG-1988
  STRAIN=972;
PPA1_SCHPO
P08091;
  ACT_SITE
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RESULT 13 PPA,1\_SCHPO

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16;
                          NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
   99 IDIFQNKLLNGSIPVNFSYPENPLYFVKHWTPVIKAENADQLSSSGRIELFDLGRQVFER 148
   98 -----LIEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRR 146
   147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPE--GA 204
  205 GYNNTLDHGLCTAFEESELGDD-VEANFTA---VFAPPIRARLEAHL-PGVNLTDEDVVN 259
   260 IMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGF 319
   320 VNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTK 379
  380 PLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVD 439
  359 PEHPLETDKNIFTYSLKTSSFVPFAGNLITELFLC-SDNKYYVRHLVNQQVYPLTDCGYG 417
   63; Mismatches 184; Indels 63; Gaps
   46 HLWGTYS----PFFSLADESALSPDVPKGCRVTFVQVLSRHGARYPT--SSASKAYSA-- 97
   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdit; 13: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                THIAMINE-REPRESSIBLE ACID PHOSPHATASE
  STRAIN=BRISTOL N2;
Matthews P., 1.loyd C.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN ALCOHOL + ORTHOPHOSPHATE.
   12.3%; Score 303.5; DB 1; Length 463; 26.7%; Pred. No. 9e-17;
  F48EAFF8BB6B234A CRC64;
  PPAX_CAEEL STANDARD, PRT; 755 AA. Q09549; Q17843; Q1.01-NOV-1995 (Rel. 32, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2).
   MW.:
18
463
340
340
104
1186
221
221
221
221
433
433
458
52118 %
  Matches 113; Conservative
  Caenorhabditis elegans.
  1
19
69
98
104
1221
221
221
433
433
439
453
453
   Best Local Similarity
   [1]
SEQUENCE FROM N.A.
   NCBI_TaxID=6239;
  440 KLG 442
  418 PSG 420
             CHAIN
ACT_SITE
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   22;
  261 MDMCPFDTVARTSDA--TQLSPFCD-LFTHDEWIQYDYLQSLGKYYG-----YGAGNP 310
   : | : | | : | | | : | | : | | : | | : | | : | | : | | | : | | | : | | | : | | | : | : | | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
  57 LADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFL 116
   332 LAIEKSFMSEV-DNMKLEFVQTIWRHGDR-----SALEGLFPISEKNWTFGGG---- 378
  117 KTYNYTLGADDLTPFGEQQMVNSGIKFYRRY------KALARKIVPFIRASGSDRVI 167
  168 ASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNTLD-------HGL- 214
  430 ISAMSLLYG-----MFPPGA-----WNI---OGVDYPNDVDWQQGFTFIPVHVDGID 473
   -----CTAFEE----SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNL 260
  578 KPSIVDGIDIPQEVSTLQGGPLLNEIFERGREKIRCVADAENCSIDYLKPLKF----Y 631
   Gaps
   NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY
   Ouery Match 5.8%; Score 142; DB 1; Length 755; Best Local Similarity 23.1%; Pred. No. 0.0014; Matches 94; Conservative 53; Mismatches 132; Indels 128;
   PY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
; E7F3050115A235EB CRC64;
   357 ADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPF 403
   EMBL; 247072; CAA87370.1; -... EMBL; 254342; CAA87370.1; JOINED. EMBL; 254342; CAA87370.1; JOINED. EMBL; 247072; CAA91156.1; JOINED. WORMPEP; P26C11.1; CE05732. InterPro; IPR005560; -... Pfam. PF00328; acid_phosphat; 1... PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1... PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1...
   Hypothetical protein; Hydrolase.
ACT_SITE 356 356 NUC1
  755 AA; 87783 MW;
  ACT_SITE
ACT_SITE
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Search completed: October 26, 2001, 15:18:05 Job time: 451 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2001, 15:17:26 ; Search time 75.85 Seconds (without alignments) 814.587 Million cell updates/sec Run on:

Title: Perfect score:

US-09-488-265-31
2468
1 MGVFVVLLSIATLFGSTSGT......DFVEGLSFARSGGNWEECFA 467 Sequence:

BLOSUM62:-Gapop 10.0 , Gapext 0.5 Scoring table:

425026 seqs, 132305027 residues Searched:

425026 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL\_16:\*

1: Sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_mammal:\*
5: sp\_mammal:\*
5: sp\_mhc:\*
5: sp\_plage:\*
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5: sp\_vorganelle:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| SUMMAKLES | 1 DB ID Description      |      | n   | 3 Q9UUZ7 | 3 093838 | 3 09HE00 | 3 000100 | 3 000085 | 300000 | 3 000107 | 3 00#846 | 2 U91846 09y846 | 3 074677 | 3 060172 | 5 09VV72 | ======================================= | 110000 | 0 0304.Z1 | 11 09Z2L6 | 4 095172 | 4 O9UNW1 | 4 090GA3 | 00000 |
|-----------|--------------------------|------|-----|----------|----------|----------|----------|----------|--------|----------|----------|-----------------|----------|----------|----------|-----------------------------------------|--------|-----------|-----------|----------|----------|----------|-------|
| *         | Query<br>Match Length DB | 10 Y | 400 |          |          | 467      | `.       |          | 466    |          |          |                 |          |          | 460      | 451                                     | 197    | , ,       | 4 8 I     | 487      | 487      | 487      | 153   |
| æ         | Query<br>Match           | 3 34 | 0.0 | 74.8     | 74.6     | 74.1     | 73.8     | 71.0     | 69.3   | 54.1     | 12       |                 | 13.0     | 12.6     | 8.3      | 7.9                                     | 7      |           | 9.7       | 9./      | 7.6      | 7.5      | 7 7   |
|           | Score                    | 1990 | 0 1 | 1847     | 1841     | 1828     | 1822     | 1752     | 1710   | 1334.5   | 338 5    |                 | 0.400    | 311.5    | 204.5    | 196                                     | 196    | 001       | 188       | TRR      | 187      | 185      | 181   |
|           | Result<br>No.            | -    | + 0 | 7        | m        | 4        | 2        | 9        | 7      | 80       | σ        | , ,             | 7        | П        | 12       | 13                                      | 14     | · u       | 7.        | QT.      | 17       | 18       | 19    |

| Q9w438 drosophila<br>Q92170 gallus gall<br>Q9utxl schizosacch<br>O04509 arabidopsis<br>Q9jjd5 mus musculu | Q19076 caenorhabdi<br>Q91mg5 mus musculu<br>Q94xg5 mus musculu<br>Q46334, comamonas t<br>Q2525 caenorhabdi | Q9qxh7 mus musculu C24719 comamonas t 000838 leishmania 000839 leishmania Q20826 caenorhabdi | 0                                              | Valugo nomo saplen<br>Q9nph0 homo saplen<br>Q19175 caenorhabdi<br>Q20330 caenorhabdi<br>Q26446 methanobact<br>Q19461 caenorhabdi |
|-----------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| Q9W438<br>Q92170<br>Q9UTX1<br>O04509<br>Q9JJD5                                                            | Q19076<br>Q9JMG5<br>Q9QXG5<br>Q46334<br>Q22555                                                             | Q9QXH7<br>O24719<br>O00838<br>O00839<br>Q20826                                               | 09P2C1<br>047871<br>019709<br>09R6Y7<br>09ILX9 | 20100<br>09NPH0<br>019175<br>020330<br>026446<br>019461                                                                          |
| 5<br>13<br>10<br>11                                                                                       |                                                                                                            |                                                                                              | 47577                                          |                                                                                                                                  |
| 453<br>449<br>198<br>468<br>274                                                                           | 449<br>374<br>381<br>513<br>380                                                                            | 381<br>513<br>683<br>707<br>730                                                              | 758<br>827<br>354<br>763<br>1013               | 428<br>452<br>1225<br>642<br>408                                                                                                 |
| 7.3<br>7.2<br>6.8<br>6.1<br>5.8                                                                           |                                                                                                            | 4444                                                                                         | 4 4 4 4 4 4<br>4 4 6 6 6 6 6                   | 4444                                                                                                                             |
| 180.5<br>177.5<br>168.5<br>149.5                                                                          | 130<br>128.5<br>127.5<br>124.5<br>118                                                                      | 113.5<br>112.5<br>110<br>110<br>109.5                                                        | 108.5<br>108.5<br>107<br>103.5                 | 103<br>103<br>102.5<br>101.5                                                                                                     |
| 20<br>22<br>23<br>24                                                                                      | 22<br>22<br>23<br>23<br>23                                                                                 | 30 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                       | , w w w w w w w w w w w w w w w w w w w        | 444422                                                                                                                           |

# ALIGNMENTS

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5;
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
   60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTA1QANATDFKGKFAFLKTV 119
   120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179
   181 KLADPGANPHQASPVINVIIPEGAGYŅNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  Gaps
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59
   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-067-2000 (TrEMBLrel. 15, Last annotation update)
MYO-INOSITOL HEXAPHOSPHATE PHOSPHOHYDROLYASE PRECURSOR (EC 3.1.3.8).
ASPERGILLUS niger.
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
NCBL_TaxID=5061;
                          SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
   Hongning W., Qi W., Jing X.; PCR, cloning and characterization of the phytase (phyA) gene of
   (POTENTIAL).
  (POTENTIAL).
   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
   3;
3-PHYTASE A. REQUIRED FOR BINDING SUBSTRATE (BY
   (POTENTIAL)
  (POTENTIAL)
  76.5%; Score 1888; DB 3; Length 465; 76.9%; Pred. No. 4.5e-144; Live 35; Mismatches 71; Indels 2
   PROTON DONOR (BY SIMILARITY).
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   N-LINKED (GLCNAC. . .) (P. 86FC1D9058C9B2C9 CRC64;
  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC...) (
  467 AA
  PRT;
   MW.
   50836
   Best Local Similarity 76.9
Matches 359; Conservative
  PRELIMINARY;
  82
359
359
339
4412
104
119
205
228
   337
350
374
465
   SEQUENCE FROM N.A.
  465 AA;
  DISULFID
   ACT_SITE
DISULFID
   Query Match
  CARBOHYD
  CARBOHYD
   SEQUENCE
               ACT_SITE
  CARBOHYD
  CARBOHYD
   CARBOHYD
   CARBOHYD
   DISULFID
  DISULFID
  CARBOHYD
   ACT_SITE
   090027
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420
  240
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  241 QRLENDLSGYSLTDTEVTYLMDMCSFDTISTSTYDTKLSPFCDLFTHDEWINYDYLQSLK 300
  61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAİQKNATAFKGKYAFLKTYN 120
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP
  ö
   74.8%; Score 1847; DB 3; Length 467; 74.1%; Pred. No. 9.2e-141;
tive 45; Mismatches 76; Indels
   STRAIN=SK-57;
Magashima T., Kondo H., Anazawa H., Terasaki Y.;
Magashima T., Kondo H., Anazawa H., Terasaki Y.;
Submitted (JAN-1999) to the EMBL/Genbank/DDBJ databases.
EMBL, AR022700; CAR19824.1;
HSSP; P34722, LHPP.
InterPro; IPPR000560;
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
         Submitted (DEC'1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF218813; AAF25481.1; -.
HSSP; P34752; 11HP.
   467 AA; 51029 MW; F4300A8F165EBF92 CRC64;
   Last sequence update)
Last annotation update)
  Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
  POTENTIAL
  Created)
  PRT;
Aspergillus niger (China Strain).";
   Pfam; PF00328; acid_phosphat; 1.
   01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-2000 (TrEMBLrel. 13,
  Signal; Lyase; Hydrolase.
   Best_Local Similarity 74.1
Matches 346; Conservative
   PRELIMINARY;
   01-MAY-1999 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.
   InterPro; IPR000560; -.
   SEQUENCE FROM N.A.
  Aspergillus niger.
  NCBI_TaxID=5061;
  SEQUENCE
   PHYTASE.
  Query Match
  093838;
  093838
   SIGNAL
   301
  RESULT
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  61 SAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEBIQQNATTFEGKYAFLKTYN 120
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
   61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  KYYGYGAGNPLGPAQGYGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  Gaps
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDIVDGGYQCFPEISHLWGTYSPFFSLADE 60
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
   0;
  0;
   74.6%; Score 1841; DB 3; Length 467; 73.2%; Pred. No. 2.8e-140; Live 49; Mismatches 76; Indels (
   Length 467;
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  77; Indels
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SEQUENCE 467 AA; 51028 MW; 7A38AD543EDC265C CRC64;
   Zhang L., An L., Wang Y., Yuan X.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AY013315; AAG40685.1; -- SEQUENCE 467 AA, 51012 MW; 3F69AD543COB565B CBC64.
  4 U885.1; -. 51012 MW; 3F69AD543C0B565B CRC64;
   Last sequence update)
Last annotation update)
   74.1%; Score 1828; DB 3; 73.0%; Pred. No. 3.2e-139;
   467 AA
   49; Mismatches
   Created)
  PRT;
  (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 16, I
   Query Match
Best Local Similarity 73.08
Matches 341; Conservative
  Conservative
   PRELIMINARY;
  Similarity
   Aspergillus ficuum.
   SEQUENCE FROM N.A.
   NCBI_TaxID=5058;
   342;
   01-MAR-2001
   01-MAR-2001
  01-MAR-2001
   Query Match
   Local
   PHYTASE
  00не0
   09HEO
   Matches
  61
   RESULT
   09HEQ0
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  Q
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  οy
   qq
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240
   360
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
           121 YSLGADDLTPFGEQELVNSGVKFYQFYESLTRNIVPFIRSSGSSRVIASGNKFIEGFQST 180
   181 KLKDPRAQPGQSSPKIDVVISEASTSNNTLDPGTCTVFEDSELADDIEANFTATFVPSIR 240
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
   HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
   -!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL, U60412; AAB58465.1; -
HSSP; P34752; 11HP.
  01-JUL-1997 (TrEMBLrel. 04, Last Sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
3-PHYTASE PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE) (3 PHYTASE) (MYO-INOSITOL HEXAKISPHOSPHATE
   REQUIRED FOR BINDING SUBSTRATE (BY
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
   466 AA.
  POTENTIAL.
   3-PHYTASE.
   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last segments)
   Hydrolase; Glycoprotein; Signal.
   PRELIMINARY;
  InterPro; IPR000560; -.
  466
  40
414
465
282
444
27
105
120
   Aspergillus terreus.
   SEQUENCE FROM N.A.
   NCBI_TaxID=33178;
  PHOSPHOHYDROLASE)
   16
82
  83
361
31
71
   215
264
436
27
105
120
  ACT_SITE
DISULFID
DISULFID
  DISULFID
  ACT_SITE
  ACT_SITE
  DISULFID
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0;
  FROM PHYTATE (BY SIMILARITY).

CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
   360
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
  61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   Gaps
  Mitchell D.B., Vogel K., Welmann B.J., Pasamontes L., Loon A.P., "The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fundi Aspergillus terreus and
  Microbiology 143:245-252(1997).
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
   KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel., 04, Last sequence update)
01-MAY-2000 (TrEMBLrel., 13, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE PHOSPHOHYDROLASE A).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                       (POTENTIAL)
   0
   73.8%; Score 1822; DB 3; Length 466; 72.3%; Pred. No. 9.6e-139;
   Indels
  LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECF 466
   F2AECECIAF7C22C4 CRC64;
  (GLCNAC. . .)
  83;
 (GLCNAC.
                          (GLCNAC.
   466 AA
   46; Mismatches
 N-LINKED (
N-LINKED (
N-LINKED (
N-LINKED (
N-LINKED (
   PRT;
   STRAIN=9A1;
MEDLINE=97177792; PubMed=9025298;
                          339 339 N-
352 352 N-
376 376 N-
466 AA; 51055 MW;
  genes for two novel phytase
Myceliophthora thermophila.
  Query Match 73.8°
Best Local Similarity 72.3°
Matches 337; Conservative
   PRELIMINARY;
  207 :
230
339
352
376
  Aspergillus terreus
   SEQUENCE FROM N.A.
  NCBI_TaxID=33178;
                  CARBOHYD
                               CARBOHYD
   CARBOHYD
  SEQUENCE
     CARBOHYD
  CARBOHYD
   000085;
   000085
   9
  421
  301
  301
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121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
  121 YSLDSEELTPFGRNQLRDLGAQFYERYNALTRHINPFVRATDASRVHESAEKFVEGFQTA 180
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  241 QRLEADLPGVQLSTDDVVNLMAMCPFETVSLTDDAHTLSPFCDLFTATEWTQYNVLLSLD 300
   KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
   HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  361 HDSNLVSIFWALGLYNGTAPLSQTSVESVSQTDGYAAAWTVPFAARAYVEMMQCRAEKEP 420
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  0; Gaps
        -i- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF 2.5 TO 7.5, WITH MAXIMAL ACTIVITY AT PH 5.5. ALSO ACCEPT 4- NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO MORE ACIDIC PH VALUES.

-i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY. BEMBL; US9805; AAB52507.1; -...
  REQUIRED FOR BINDING SUBSTRATE (BY SIMILARITY). NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROJON DONOR (BY SIMILARITY).
  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
   71.0%; Score 1752; DB 3; Length 466; 69.3%; Pred. No. 4.2e-133;
  Indels
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECF 466
  LINKED (GLCNAC. . .) (Position (Position )
   Pfan; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
  87;
  AA
   Best Local Similarity 69.3%; Pred. No. 4.2e
Matches 323; Conservative 56; Mismatches
   3-PHYTASE A
  POTENTIAL.
-!- SUBCELLULAR LOCATION: SECRETED.
   Hydrolase; Glycoprotein; Signal.
   51093 MW;
   PRELIMINARY;
  19
466
82
  414
465
282
282
444
1120
200
3330
335
335
335
335
   83
361
40
  InterPro; IPR000560;
   466 AA;
   83
361
31
71
  20
82
  Query Match
   ACT_SITE
  ACT_SITE
   DISULFID
   DISULFID
   DISULFID
  DISULFID
  CARBOHYD
  CARBOHYD
  CARBOHYD
   CARBOHYD
   CARBOHYD
   CARBOHYD
  SEQUENCE
   960000
  SIGNAL
   301
   361
  CHAIN
  421
  61
   RESULT
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"Cloning of the phytases from Emericella nidulans and the thermophilic fungus Talaromyces thermophilus.";
  -!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)0 = D-MYO-
   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. .) (POTENTIAL).
  INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE

-I- MISCELLANEOUS: HAS POTENTIAL AS FOOD AND FEED ADDITIVE. IT CAN FACILITATE THE DEGRADATION OF PHYTIN IN SOYBEAN AND OTHER SEEDS
   POTENTIAL.
3 PHTTASE A.
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
   Biochim. Biophys. Acta 1353:217-223(1997).
    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSTTOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSTTOL HEXARISPHOSPHATE BLANCAPHOHYDROLASE A).
   USED AS FOOD FOR MONOGASTRIC ANIMALS.

-1 - SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY:
EMBL; US9802; AAB96873.1; -.
HSSP; P34752; 11HP.
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Talaromyces.
  MEDLINE-98007872; Pubmed-9349716;
Pasamontes L., Haiker M., Henriquez-Huecas M., Mitchell D.B.,
van Loon A.P.G.M.;
  FC4575B521A5C929 CRC64;
   InterPro; IPR000560; --
Pfam; PF00328; acid_phosphat; 1.
PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
  Hydrolase; Glycoprotein; Signal
  51450 MW;
   Talaromyces thermophilus.
   461
278
440
  STRAIN=ATCC 20186;
  SEQUENCE FROM N.A.
   466 AA;
  NCBI_TaxID=28565;
   FROM PHYTATE.
  15
79
357
28
68
212
261
432
   335
348
372
  ACT_SITE
   DISULFID
  SITE
   DISULFID
   DISULFID
  CARBOHYD
   DISULFID
   DISULFID
   CARBOHYD
   CARBOHYD
   CARBOHYD
   CARBOHYD
   SEQUENCE
   SIGNAL
  CHAIN
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3
   DESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKT 118
  YNYTLGADDLIPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQ 178
   179 SAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPP 238
  1 MGVFVVLLS--1ATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLA 58
   8; Gaps
69.3%; Score 1710; DB 3; Length 466; 68.9%; Pred. No. 1e-129; 1ve 45; Mismatches 93; Indels 6
                       Matches 323; Conservative
              Similarity
Query Match
              Local
   59
  26
   119
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  q
   δ
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  δ
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-!- CATALYTIC ACTIVITY: MYO-INOSITOL HEXAKISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,2,4,5,6-PENTAKISPHOSPHATE + PHOSPHATE.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- MISCELLANEOUS: SHOWS ACTIVITY WITH PHYTIC ACID AT A PH RANGE OF 3.5 TO 8.5, WITH MAXIMAL ACTIVITY BETWEEN PH 5.5 AND 6.0. ALSO ACCEPT 4-NITROPHENYL PHOSPHATE AS SUBSTRATE WITH A PH OPTIMA SHIFTED TO MORE ACIDIC PH VALUES.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
-- SIMILARITY: ABB25508.1;
-- GENBL: 105908; ABB25508.1;
239 IRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQS 298
           299 LGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYAD 358
   359 FSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEK 418
  SIMILARITY).
NUCLEOPHILIC ACCEPTOR (BY SIMILARITY). PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'SIMILARITY.
N'LINKED (GLCNAC. ..) (POTENTIAL).
   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
3-PHYTASE A PRECURSOR (EC 3.1.3.8) (MYO-INOSITOL-HEXAPHOSPHATE 3-PHOSPHOHYDROLASE A) (3 PHYTASE A) (MYO-INOSITOL HEXAKISPHOSPHATE
   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Chaetomiaceae; Thielavia.
NCBI_TaxID=78579;
   REQUIRED FOR BINDING SUBSTRATE (BY
   EPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
  487 AA.
  POTENTIAL.
3-PHYTASE A.
  POLY-SER.
  POLY-GLY.
  01-JUL-1997 (TrEMBLrel. 04, Created)
  PRT;
  SEQUENCE FROM N.A.
MEDLINE=97177792; PubMed=9025298;
  Hydrolase; Glycoprotein; Signal
  Thielavia heterothallica.
   PRELIMINARY;
  487
270
433
75
  76
368
35
421
  PHOSPHOHYDROLASE A).
   InterPro; IPR000560;
   IHP
  FROM PHYTATE
   423
   267
   76
368
26
64
   HSSP; P34752;
  DISULFID
  ACT_SITE
DISULFID
   ACT_SITE
   DISULFID
  CARBOHYD
  ACT SITE
   DISULFID
  CARBOHYD
  000107
   ω
  SIGNAL
   DOMAIN
   DOMAIN
                      236
   295
   419
   CHAIN
   RESULT
000107
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9

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074677
   RESULT 10
 CHAIN
  218
  165
   074677
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  δ
  g
   δ
   δλ
  Óγ
 FT
   δ
   9
   411 AARIYVEKMRCSGGGGGGGGGGGGGGROERVENDRVWTLKGCGADERGMCTLERFI 470
  FAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTS------DATQLSPFCD 283
   231 FAGPITARVNANLPGANLTDADTVALMDLCPFETVASSSSDPATADAGGGNGRPLSPFCR 290
   LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLIHSPVQDHTSTNHTLD 343
   SNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPF 403
  AARAYVEMMQC------EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFV 450
  118 TYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGF 177
  178 QSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEE---SELGDDVEANFTAV 234
  58 ADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK 117
  Gaps
   1 MGVFVVL---LSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSL 57
  Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
   54.1%; Score 1334.5; DB 3; Length 487;
53.3%; Pred. No. 2.1e-99;
Live 60; Mismatches 129; Indels 43;
   San Vicente A., Ferminan E., Dominguez A.;
"Isolation and characterization of KlPH03 a gene encoding a constitutive acid phosphatse from Kluyveromyces lactis.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ007502; CAB46490.1;
                         97D10EDC83D051DB CRC64;
  01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
  469 AA
   HSSP; P34755; IQFX.
InterPro; IPR000560; -.
Pfam; PF00128; acid_phosphat; 1.
PROSITE; PS00616; HTS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
   01-NOV-1999 (TrEMBLrel. 12, Created)
  PRT;
   ACID PHOSPHATASE (EC 3.1.3.2).
                         487 AA; 52537 MW;
  EGLSFARSGGNWEECFA 467
  471 ESMAFARGNGKWDLCFA 487
  Conservative
  PRELIMINARY;
  Similarity
   SEQUENCE FROM N.A.
   NCBI_TaxID=28985;
  STRAIN=2360/7
   Best Local Sim
Matches 265;
   Hydrolase.
             CARBOHYD
SEQUENCE
   Query Match
   CARBOHYD
  09Y846
  6
   235
   284
  291
   404
   451
  RESULT
Q9Y846
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17;
  Phonogara A., Merckelbach A., Keup P., Gellissen G., Hollenberg C.P.; "Cloning and characterization of the gene encoding a repressible acid phosphatase (PHO1) from the methylotrophic yeast Hansenula
  276 TQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDH 335
  277 V----CDLFERNDLVAXSYIANVNNFYRRGAGNPMSNPIGSVLVNASYNLLTQADELDN 331
  332 ------KVWLSFSHDTDIQQFISALGLIDNG---VTEYSLDQVDFQNI 370
   395 YSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF---- 449
   54 QSFGIPVEVPDQCTVEHVQMLARHGERYPTASKGKLWIALWDKLKEFQGQYNGPMEVFND 113
  114 YEFFVSNTKYFDQLTNSTDVDPSNPYAGAKTAQHLGKYIAYNYGDLFSDSNP-VFTSSSG 172
  RVIASAEKFIEGFQSAKLADPGANPHQASPVINV----IIPEG--AGYNNTLDHGLCTA 217
   FEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLT--DEDVVNLMDMCPFDTVARTSDA 275
  218 Y-NGDLGDEYFENATLPYLTDIKNRWMKKNSNLNLTLEHDDIELLVDWCAFETNVKGSSA 276
   336 TSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLY-NGTKPLSTTSVESIEETDG 394
  59 DESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKT 118
  119 YNY----TLGADDLT-----PF-GEQQMVNSGIKFYRRYKALARKIVPFIRASGSD 164
  7 LLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCF-----PEISHLWGTYSPFFSLA 58
   Gaps
  1 MLSILLSLESLSGTHAAPISK-----DNGTVCYALNSSTTDESIFRLLNGQGPHYDYP
  Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
  91;
  DB 3; Length 469;
   Mismatches 210; Indels
ACID PHOSPHATASE, 5C7ABF622CEA891C CRC64;
   01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) REPRESSIBLE ACID PHOSPHATASE (EC 3.1.3.2).
  Appl. Microbiol. Biotechnol. 50:77-84(1998).
EMBL. APO51161; AAC62537.1; -.
HSSP; P34755; 10FX.
InterPro; IPR000560; -.
Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
Hydrolase.
   13.7%; Score 338.5; DB 3 24.6%; Pred. No. 4.3e-19; tive 69; Mismatches 210
   442 AA
  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last anno
   PRT;
   STRAIN=ATCC34438;
MEDLINE=98386672; PubMed=9720203;
   469 A
52560 MW;
  Conservative
  PRELIMINARY;
   173 RVHQTAKYVVSSLEEE--
  450 -- VEGLSFARS 458
  429 NRLNGIDYVSS 439
   17 4
469 AA;
  Similarity
  SEQUENCE FROM N.A.
  NCBI_TaxID-4905;
   polymorpha."
  Matches 121;
                              SEQUENCE
  Query Match
   Local
   074677;
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6C41AF422C6D624A CRC64;

52758 MW;

463 AA;

SEQUENCE

g

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16;
  V---EANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCD 283
  66 DVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQK-NATAFKGKYAFLKTYNYTLG 124
   125 ADDLTPFGEQQMVNSGI----KF----YRRYKAL--ARKIVPFIRASGSDRVIASAEKFI 174
  115 DSDNYELETTRGLYSGLENAFKFGTYLRERYDSLVDTSSVLPIFAAS-EDRVVDTARSFG 173
  175 EGFQSAKLADPGANPHQASPVINVI----IPEGAGYNNTLDHGLC----TAFEESELGDD 226
   284 LFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGYGFVNELIARLTHSPVQDHTSTNHTLD 343
  Gaps
  NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTEWILAL).
   174 RGFFGPDYA-----TSCSIQVVNETDTSKGANALTTKDN--CPTYNSSFYDYSFGDE
  344 SNPATFPL---NATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWT
  Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S., Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN ALCOHOL + ORTHOPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL, AL022286; CAA18863.1; --
   83;
   Length 442;
   401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVE 451
  Indels
442 AA; ' 49370 MW; 7087D91A85B05C31 CRC64;
   SPBC21H7.03C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
   268 ALSREAFIALQYNNDVTKFYQFGPGYNMSAVAGGVYAN-----
   01-106-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 15, Last sequence update)
  DB 3;
   13.6%; Score 334.5; DB 3 25.8%; Pred. No. 8.3e-19; tive 63; Mismatches 159
  463 AA
  InterPro; IPR000560; -
Pfam; PF00328; acid_phosphat; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
  01-OCT-2000 (TrEMBLrel. 15, Last annotat
PROBABLE ACID PHOSPHATASE (EC 3.1.3.2).
   PRT;
   Conservative
   PRELIMINARY;
  Glycoprotein
   340
98
104
221
324
439
458
   69
  Schizosaccharomyces.
  Query Match
Best Local Similarity
  SEQUENCE FROM N.A.
   HSSP; P34755; 1QFX
  NCBI_TaxID=4896;
   98
104
221
324
439
458
   106;
  STRAIN=972;
  Hydrolase;
 SEQUENCE
   ACT_SITE
CARBOHYD
   CARBOHYD
CARBOHYD
CARBOHYD
  ACT_SITE
  CARBOHYD
   CARBOHYD
  060172
   Matches
  227
  308
  RESULT 11
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15;
  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamatides P.G., Scherer S.E., Lib Pw., Hoskins R.A., Galle R.E.,
A Amanatides P.G., Scherer S.E., Lib Pw., Hoskins R.A., Galle R.E.,
AS George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Baxu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakvo S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
   89 LNNFQEKLLNGSIPVNFSYPENPLCFIKQWTPVIDAENADQLSSRGRLELFDLGRQLYQR 148
  149 YYKLFDSYVYDINTAEQERVVESAKWFTYGLFGDKMYE-----KTNFILISEGKAA 199
  205 GYNNTLDHGLCTAFEESEL----GDDVEANFTAVFAPPIRARLEAHL-PGVNLTDEDVVN 259
   147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEG--A 204
  260 LMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGF 319
   320 VNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTK 379
  315 INNLADSL------RNVTNPDFDRK------VFLAFTHDSNIIPVEAALGFFPDIT 358
   Eukaryota; Metazoa; Arthropoda; Tracheata: Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
   Gaps
   PQNPLPTDKNIYTYSQKTSSFVPFAGNLITELFFC-SDSKYYVRHLVNQQVYPLIDCGYG 417
   46 HLWGTYS----PFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTS--SASKAYSA-- 97
  98 -----LIEAIQKNATAFKGKYAFLKTYNYTL---GADDLTPFGEQQMVNSGIKFYRR
   200 GANSLSMYNACPVFKDNNFHKNATDAAHAVWRNIFIEPIVNRLAKYFDSSYKLTINDVRS
   260 LFYICEYEIAIKDH-----SDFCSIFTPSEFLNFEYDSDLDQAYGGGPVSEWASTLGGAY
  380 PLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVD
   67;
        DB 3; Length 463;
  12.6%; Score 311.5; DB 3; Length 425.3%; Pred. No. 6.4e-17; ive 69; Mismatches 197; Indels
  Last sequence update)
Last annotation update)
  460 AA
  Created)
   418 PSGTSDGLCELQAYLNSPIRANSTSN 443
   Drosophila melanogaster (Fruit fly)
   440 KLGR----CKRDDFVEGLSFARSGGN 461
  PRT;
   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
Query Match 12.65
Best Local Similarity 25.35
Matches 113; Conservative
   PRELIMINARY;
   SEQUENCE FROM N.A.
   MIPP1 OR CG4123.
  NCBI_TaxID=7227;
   STRAIN-BERKELEY
   MIPP1 PROTEIN
   09VV72
  09VV72
   359
   RESULT 12
   Q9VV72
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Roller C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Rh Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Rh Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Rh Gotin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Rh Galali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Rh Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Rh Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Rh Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Rh Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Rh Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Rh Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Rh Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Rh Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rh Ye J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zhao Q., Zhao G.,
Rh Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Rh Globs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Rr Trhe genome sequence of Drosophila melanogaster.";
  329 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTWVSIFFALGLYNGTKPLSTTSVES 388
   389 IEETDGYSASWTVPFAARAYVEMMQCEA--EKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
  L-TSRRWKSSLIDPFAANFVAVKYDCPADLDREKVV-FFLNQQAVQLDWCSV---GLCKW 411
   162 YYQRTTESFKAFAEGLFGSQNAAHPVEIPKQDLLLRPYDYCSSFKNVNYKDEGSEYYK-- 219
  211 DHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPG--VNLTDEDVVNLMDMCPFDT 268
  259 -- OAWNVDRNSVWCGAFLPEQITVFEYLEDLKYYYGSGYGFPENAHLNCRLVODLLTHLS 316
  317 -NPVSPH------VVAHFGHSTGLLTLLTALGIQKDDIKLRADNYDS 356
  105 ALCOTDLIAIKLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTVLTANYNDT 161
   165 ---RVIASAEKFIEG-FQSAKLADPGANPHQ-----ASPVINV-IIPEGAGYNNTL 210
   -----FHQSKLYNDTLAD-----ISTRL-----GFLYTLEEADIKLMYDMCRYE- 258
  269 VARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLT 328
  66 DVPK-----GCRVTFVOVLSRHGARYPTSS----ASKAYSALIEAIOKNATAFKGK---- 112
  113 -----YAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVP-FIRASGSD- 164
  Gaps
  46 DIDKQYLVPGCQPQKMWIFHRHGTRLPKKSMINKASRV-AELRDLIINNYQVARTKPETD 104
   103;
  Query Match

8.3%; Score 204.5; DB 5; Length 460;
Best Local Similarity (23.9%; Pred. No. 2.7e-08;
Matches 106; Conservative 64; Mismatches 171; Indels 103.
  F00B25718E40807D CRC64;
  01-JAN-1998 (TrEMBLrel. 05, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
   451 AA
  447 DDFVE-----GLSFARSGG 460
   412 SDVLEKYKTIADADCGEYYCRTGG 435
   Pfam; PF00328; acid_phosphat; 1.
SEQUENCE 460 AA; 52685 MW; F
   FlyBase; FBgn0026061; Mippl.
  EMBL; AE003527; AAF49450.1;
  PRELIMINARY;
   IPR000560; -.
   [nterPro;
  SEQUENCE
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17;
   "Purification of an inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase activity from rat liver and the evaluation of its substrate
  TETRAKISPHOSPHATE TO INOSITOL 1,4,5-TRIPHOSPHATE AND INOSITOL 1,3,4,5,6-PETRAKISPHOSPHATE TO INOSITOL 1,4,5,6-TETRAKISPHOSPHATE AND THEN TO INOSITOL 1,4,5-TRISPHOSPHATE. DEPHOSPHORYLATES INOSITOL 14,5-TRISPHOSPHATE. TOWARDS A PARTICULAR
   Nogimori K., Hughes P.J., Glennon M.C., Hodgson M.E., Putney J.W. Jr.,
  1 : | : | : | : | : | : | 17 0 CLOGLLQTRESVDGGSRVAAALDQWPLWYDD---WMDGQLVEKGRQDMRQLALRLAALFP 130
  97 ALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVP 156
   --FIR-----ASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAG 205
  Indels 78; Gaps
  14 SPYFGTKTRYEDVNPWLLGDPVAPRRDPELLAGTCTPVQLVALIRHGTRYPTTKQIRKLR 73
  -----LADESA--ISPDVPKG-CRVTFVQVLSRHGARYPTSSASKAYS 96
   Sciurognathi; Muridae; Murinae; Rattus.
  SEQUENCE OF 11-451 FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
  MEDLINE-98028656; PubMed-9359836; Craxton A., Caffrey J.J., Burkhart W., Safrany S.T., Shears S.B.; "Molecular cloning and expression of a rat hepatic multiple inositol
  PROSITE; PF001328; acid_phosphat; 2.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; FALSE_NEG.
Hydrolase; Glycoprotein; Phosphorylation; Multifunctional enzyme.
ACT_SITE 59 59 NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
   S -> P (IN AAC53453).
PREVENT SECRETION FROM ER (POTENTIAL).
EB1C05512A03020B, CRC64;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
  -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-i- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY AND LIVER.
-i- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
EMBL; AF012714; AAC53453.1; -.
   (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HEPATIC MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE (EC 3.1.3.-)
  7.9%; Score 196; DB 11; Length 451;
21.3%; Pred. No. 1.3e-07;
  ::
  PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
   specificitty.";
J. Biol. Chem. 266:16499-16506(1991).
-!- FUNCTION: CATALYZES THE HYDROLYSIS OF INOSITOL 1,3,4,5-
   PHOSPHORYLATION (POTENTIAL)
  PHOSPHORYLATION (POTENTIAL)
   21.3%; Pred. No. 1.3e-07;
tive 72; Mismatches 187;
  N-LINKED
N-LINKED
  ::
   CATALYTIC ACTIVITY.
MEDLINE=91358435; PubMed=1653239;
   51592 MW;
  polyphosphate phosphatase.";
Biochem. J. 328:75-81(1997).
  91; Conservative
   Rattus norvegicus (Rat).
   59
65
146
176
201
218
  InterPro; IPR000560;
InterPro; IPR000886;
   PHOSPHATE GROUP
   451 AA;
   Similarity
  NCBI_TaxID=10116;
   52 SPFFS-----
  TISSUE=LIVER;
  Shears S.B.;
  Query Match
Best Local 9
   ACT_SITE
  CARBOHYD
   CARBOHYD
   CONFLICT
   SEQUENCE
  MOD RES
  MOD_RES
   MOD_RES
  VARIANT
  MOD_RES
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  MOD_RES
   MOD RES
   (MIPP).
   Matches
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21;
  Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endoberryota; Diptera; Brachycerya, Berygota; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
DLFCRENYGRLRLITSSKHRCVDSSAAFLQGLW--QHYHPGLPP----PDVSDMECDPPR 184
   PLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIF 369
  203
  221
   AGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPG--VNLTDEDVVNLM 261
  SEYYK-----FHQSKLYNDTLAD-----ISTRL----GFLYTLEEADIKLMY 259
  105 ALCQTDLIAIKLWKWN---SSITPDMEEYLTAQGYEDLRGTAKLYQRYYPTVLTANYNDT 161
  46 DIDKOYLVPGCQPQKMWIFHRHGTRLPKKSMINKASRV-AELRDLIINNYQVARTKPETD 104
   DMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVN 321
   206 YNNTL----DHGLCTAFEESELGDDVEANFTAVF-----APPIRARLE-----AHLPG
  185 VNDKLMRFFDH -- CEKFL -- -- TEVERNATALYHVEAFKTGPEMQTVLKKVAATLQVPV
  250 VNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGN
   294 AINSRSSCNLFQDIFLHLDKAVEQKQRSQ------PVSSSVILQFGHAETLLPLL
  370 FALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP----LVRVL
  ----RASGSDRVIASAEKFIEG-FQSAKLADPGANPHQ-----ASPVINV-IIPEG
   162 YYQFRHTDTQRTTESFKAFAEGLFGSQNAAHPVEIPKQDLLLRPYDYCSSFKNVNYKDEG
  110;
   DVPK-----GCRVTFVQVLSRHGARYPTSS----ASKAYSALIEAIQKNATAFKGK--
   ----YAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFI----
   Query Match 7.9%; Score 196; DB 5; Length 467; Best Local Similarity 22.8%; Pred. No. 1.3e-07; Matches 103; Conservative 66; Mismatches 172; Indels 1:
   Pfam: PF00328; acid_phosphat; 1.
SEQUENCE 467 AA; 53602 MW; 1A0571B9958B2632 CRC64;
  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE 1.
   467 AA
   PRT;
   PRELIMINARY;
  : |::|:|
402 LNEKVLPL 409
  426 VNDRVVPL 433
  NCBI_TaxID=7227;
  096421
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  RESULT 14
096421
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382 STISVESIEETDGYSASWIVPFAAR--AYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVD 439
                                -----VVXHFGHSTGLLTLLTALGIXKDDIKL 356
  ELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPL 381
   64 SPDVPK-----GCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAF 115
   123 AALAEWPLWYGD---WMDGQLVEKGRQDMRQLALRLAALFPDLFSRENYDRLRLITSSKH 179
   RVIASAEKFIEGFQSAKLADPGANPHQAS-----PVINVIIPEGAGYNNTLDHGLCTAF 218
   180 RCVDSSAAFLQGLW--QHYHPGLPPPDVSDMECGPPRINDKL-----MRFFDH--CEKF 229
   230 L----TDVERNETALY-----HVEAFKTGPEMOKVLKKVAATLQVPMNSLNADLIQVA 278
   261 MDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFV 320
  321 NELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKP 380
   11 ATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLAD--ESA----I 63
   357 RADNYDSL-TSRRWKSSLIDPFAANFVAVKYDLPADLDREKVV-FFLNQQAVQLDWCSV-
  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   21 AALLSSFARCSLPGRGD-----PVASVL---SPYFGTKTRYEDANPWLLV
  116 LKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVP--FIR-----ASGSD
  219 EESELGDDVEANFTAVFAPPIRARLEAHLPG--------VNLTDEDVVNL-
   279 FFTCSFDLAIKGVH----SPWCDVFDVDDARVLEYLNDLKQYWKRSYGYTINSRSSCNLF
   Indels 112;
  Length 481;
  MGD; MGI:1330200660; --
Interpro; IPR000560; --
Interpro; IPR000886; --
Pfam; PF00218; acid_phosphat; 2.
Pfam; PF0021E; PS00014; ER_TARGET; UNKNOWN_1.
   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
MULTIPLE INOSITOL POLYPHOSPHATE PHOSPHATASE.
  7.6%; Score 188; DB 11;
Local Similarity 20.8%; Pred. No. 6.2e-07;
nes 99; Conservative 70; Mismatches 196;
  481 AA
   | | | | | : | : | | 414 --GLCKWSDVLEKYKTIADADCGEYYCRTGG 442
  440 KLGRCKRDDFVE-----GLSFARSGG 460
                     DLLTHLS-NPVSPH----
  PRELIMINARY;
  [1]
SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
  MINPP1 OR MIPP
  STRAIN=129;
  Query Match
  0922L6
  RESULT 15
   Matches
   165
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381 LSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP----LVRVLVNDRVVPL 433 | : : | : : | : : | : : | : : | : : | : : | : : | 384 LTAYNFEE-QVNRKFRSGHIVPYASNLIFVLYHCDNAQSPEEQFQIQLLLNEKVLPL 439 QQ QQ

Search completed: October 26, 2001, 15:17:26 Job time: 3977 sec

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October 26, 2001, 16:40:04; Search time 57.24 Seconds (without alignments) 494.609 Million cell updates/sec
   US-09-488-265-31
2468
1 MGVEVVLLSIATLFGSTSGT......DFVEGLSFARSGGNWEECFA 467
   (SIDSI/) (SIDSISSIPSI/) (SIDSI/) (SIDSI
  /SIDS1/gcgdata/geneseq/geneseqp/AA1980.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:*/SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
   412676
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
  412676 seqs, 60623988 residues
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
  A_Geneseq_0601:*
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   Perfect score:
   Scoring table:
  Database :
  Sequence:
  Searched:
   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description              | Consensus phytase- | Consensus phytase | Mutant phytase-10, | Consensus phytase | Consensus phytase | Consensus phytase | Phytase-10, a cons | Consensus phytase | Consensus phytase- | ı        |          |  |
|-----------|--------------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|-------------------|--------------------|----------|----------|--|
| SUMMAKIES | ID                       | AAY43170           | AAB20527          | AAY69569           | AAB20534          | AAB20533          | AAB20524          | AAY69566           | AAB20532          | AAY43169           | AAB20526 | AAB20531 |  |
|           | th DB                    | 67 20              | 67 21             | 67 21              | 67 21             | 67 21             | 467 21            | 67 21              | 67 21             | 67 20              | 67 21    | 67 21    |  |
|           | Query<br>Match Length DB | 100.0 4            |                   |                    |                   |                   |                   |                    |                   |                    |          |          |  |
|           | Score                    | 2468               |                   |                    |                   |                   |                   |                    |                   |                    |          |          |  |
|           | Result<br>No.            | н                  | 7                 | Э                  | 4                 | S                 | 9                 | 7                  | 8                 | თ                  | 10       | 11       |  |

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113<br>2362<br>114<br>23162<br>114<br>23162<br>117<br>23108<br>119<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108<br>23108 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| <br><b>ოოოოოო ფაფაფა</b> | 2002<br>2002<br>118<br>1184<br>1187<br>1187                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 2244<br>665<br>7244<br>725<br>725<br>725<br>725<br>725<br>725<br>725<br>725<br>725<br>725 |                              | AAY 69557<br>AAB 20536<br>AAB 20536<br>AAY 69565<br>AAY 43171<br>AAY 43171<br>AAY 9505<br>AAW 8439905<br>AAW 8439905<br>AAY 6950<br>AAB 20507<br>AAB 20507<br>AAY 69551<br>AAY 69551                                                        | ·                       | Initial consensus<br>Mutant Aspergillus<br>Consensus phytase<br>Initial consensus<br>A. fumigatus phyta<br>Aspergillus fumiga<br>Aspergillus fumiga                                                                                                                                                                                                                              |
| <br>r43                  | LT 13170 AAY43170 St. AAY43170; 06-JAN-2000 Consensus p                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | stan<br>00<br>phy<br>anim | rd; P<br>irst<br>se-10<br>feed                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Protein; 467 A entry)  0-thermo(3)-Q5                                                     | 1; 4{<br>)<br>no(3;<br>arat: | 7 AA<br>-Q50                                                                                                                                                                                                                                | T-K91A protein sequence | nce.<br>, transgenic plant,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| \$                       | Synthetic. WO9944380-71 30-SEP-1999. 23-MAR-1998; 19-JUN-1998; 22-JAN-1999; 22-JAN-1999; 22-JAN-1999; 22-JAN-1999; WPI; 1999-59 N-PSDB; AAZ3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | o,   ·                    | 11. 99WO-1. 98BK-(-) 98BK-(-) 98BK-(-) 98BK-(-) 99BK-(-) |                                                                                           | 54<br>76<br>93.              |                                                                                                                                                                                                                                             |                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

27-JUL-2000

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The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed additive (phytase) simultaneously.
  This sequence represents the consensus phytase-10-thermo(3)-Q50T-K91A.
   Gaps
  0;
  Length 467;
   0; Indels
Preparing animal feed using a thermostable phytase
  Ouery Match 100.0%; Score 2468; DB 20; Best Local Similarity 100.0%; Pred. No. 2.6e-237;
  0; Mismatches
                                     Example 3; Fig 10; 71pp; English.
  Matches 467; Conservative
   467 AA;
   Sequence
  Query Match
  61
   61
δ
  임
  ŏ
   g
  ò
  g
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ó 240 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 121 YTLGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420 241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 181 kladpganphqaspvinviipegagynntldhglctafeeselgddveanftavfappir KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467 181 361 301 241

> ò Dp δy g Qγ qq ŏ g δ g

Consensus phytase 10 thermo 3 q50t, k91a protein SEQ ID NO:31. AAB20527 standard; Protein; 467 AA. (first entry) 05-DEC-2000 AAB20527 RESULT 

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

WO200043503-A1.

Synthetic.

LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467 241 181 301 361 361 421 δλ QQ δλ g g g QΥ Óχ Qγ Qy δy

increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate especificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and 61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 61 saispdvpkgcrvtfvqvlsrhgaryptssaskaysalieaiqknatafkgkyaflktyn 120 121 YTLGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFOSA 180 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420 hdntmvsiffalglyngtkplsttsvesieetdgysaswtvpfaarayvemmqceaekep 420 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360 Gaps 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60 The present invention describes improved phytases, preferably with ; Score 2468; DB 21; Length 467; Pred. No. 2.6e-237; 0; Indels Mismatches Claim 4; Fig 8a-c; 240pp; English. 0 100.0%; 21-JAN-2000; 2000WO-DK00025 99DK-0000092 99DK-0001340 compound foods and feeds 467; Conservative (NOVO ) NOVO NORDISK AS WPI; 2000-491161/43. Query Match Best Local Similarity Matches 467; Conserv 467 AA; N-PSDB; AAA73234 22-JAN-1999; 21-SEP-1999; Lehmann M; nvention. Sednence 

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The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphorydrolase) and one or more stabilising agents including xylitol or ribitol: polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a feed composition for monogastric animals (e.g., pigs, poultry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphorus is present in animal feed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phosphate, resulting in the addition of extra
  Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; mutein.
  1..26
/note= "Phytase signal peptide from Aspergillus terreus
cbs16.46"
  New stabilized enzyme formulation, useful for feed compositions for
   27..467
/note= "Mature phytase-10-thermo[3]-050T-K91A"
   Mutant phytase-10, phytase-10-thermo[3]-050T-K91A.
  (HOFF ) HOFFMANN LA ROCHE & CO AG F.
   Location/Qualifiers
                              AAY69569 standard; Protein; 467 AA
   Talaromyces thermophilus ATCC20186.
Myceliophthora thermophila.
Paxillus involutus NN005693.
  Example 5; Fig 19; 101pp; English.
  Aspergillus fumigatus ATCC32722.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC26906.
  Aspergillus niger var. awamori.
Aspergillus niger str. NRRL3135.
Aspergillus fumigatus ATCC13073.
   Aspergillus fumigatus ATCC32239
  Brugger R, Lehmann M, Wyss M;
  Aspergillus terreus cbs16.46.
  99EP-0111949,
  98EP-0111960
  pediades NND09289.
   (first entry)
  Trametes pubescens NN9343.
  Peniophora lycii NN006113.
   Aspergillus terreus 9A1
  Thermomyces lanuginosa
  Emericella nidulans
  monogastric animals
  WPI; 2000-099429/09
  29-JUN-1998;
  05-JAN-2000.
  23-JUN-1999
   EP969089-A1
   AAY69569;
   Synthetic
  Agrocybe
  Peptide
   Protein
               AAY69569
RESULT
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;
phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents a mutant phytase-10 consensus sequence, phytase-10-thermo[3]-050T-K91A, which has a temperature optimum and melting point 4 degrees Celsius higher than that of phytase-10 (AAX69566). Its specific activity with phytate as a substrate is also strongly increased.
   SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
   KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP
  YTLGADDLTPFGEQOMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA
  .;
0
   100.0%; Score 2468; DB 21; Length 467; 100.0%; Pred. No. 2.6e-237; ive 0; Mismatches 0; Indels 0;
   LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  Conservative
   Query Match
Best Local Similarity
Matches 467; Conserv
  467 AA;
  Sequence
  121
   301
  361
   61
   421
  61
   301
     δŽ
   g
   δ
  qq
  δ
   g
   ŏ
   qq
  δ
  g
   δλ
   Op
  QY
  q
   ŏλ
   QQ
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Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure. Consensus phytase 10 thermo 5 Q50T K91A protein SEQ ID NO:97. (first entry) Synthetic. 

WO200043503-A1

AAB20534 standard; Protein; 467 AA

AAB20534

05-DEC-2000

AAB20534;

us-09-488-265-31.rag

S

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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate observage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
  Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -
   61 saispdvpkgcrvtfvqvlsrhgaryptssaskaysalieaiqknatafkgkyaflktyn 120
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   121 ytlgaddltpfgeqqmvnsgikfyrrykalarkivpfirasgsdrviasaekfiegfgsa 180
   Gaps
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   present invention describes improved phytases, preferably with
  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
  ·;
  99.5%; Score 2456; DB 21; Length 467; 99.6%; Pred. No. 4.1e-236; 1ve 0; Mismatches 2; Indels 0;
   LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   Disclosure; Fig 25a-c; 240pp; English.
   99DK-0001340
                                   2000WO-DK00025
  . 99DK-0000092
  Matches 465; Conservative
   (NOVO ) NOVO NORDISK AS.
  WPI; 2000-491161/43.
   Best Local Similarity
  467 AA;
   N-PSDB; AAA73293.
                               21-JAN-2000;
   22-JAN-1999;
21-SEP-1999;
27-JUL-2000
  Lehmann M;
  invention
  Sequence
  Query Match
  61
   121
  361
   361
   421
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present invention.
   Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
  Phytase; mutant; thermostability; mutation; mutagenesis; pH stability, temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   0; Gaps
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   1 mgvfvvllsiatlfgstsgtalgprgnshscdtvdggyqcfpeishlwgtyspffslade 60
  Score 2451; DB 21; Length 467; Pred. No. 1.3e-235;
   Indels
   Consensus phytase 10 thermo 5 Q50T protein SEQ ID NO:95.
  Pred. No. 1.3e
0; Mismatches
   Disclosure; Fig 24a-c; 240pp; English.
                                    AAB20533 standard: Protein: 467 AA.
   Query Match 99.3%;
Best Local Similarity 99.4%;
Matches 464; Conservative 0
   99DK-0000092.
  food; feed; phytate; manure.
  21-JAN-2000; 2000WO-DK00025.
  (first entry)
  compound foods and feeds
   (NOVO ) NOVO NORDISK AS
   WPI; 2000-491161/43.
  467 AA;
  N-PSDB; AAA73292
  WO200043503-A1.
  22-JAN-1999;
  21-SEP-1999;
  05-DEC-2000
   27-JUL-2000.
  Lehmann M;
   Synthetic.
   AAB20533;
  Sednence
  61
RESULT
AAB20533
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   q
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360
121 ytlgaddltpfgeggmvnsgikfyrrykalarkivpfirasgsdrviasaekfiegfgsa 180
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
   KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   301
  361
  361
  qq
                    δ
                                      q
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   ò
  οy
   q
  ŏ
  g
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AAB20524 standard; Protein; 467 AA AAB20524; AAB20524 RESULT 

(first entry) 05-DEC-2000

Consensus phytase 10 SEQ ID NO:26.

Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile, temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate; food; feed; phytate; manure.

Synthetic

WO200043503-A1 .27-JUL-2000 21-JAN-2000; 2000WO-DK00025.

99DK-0001340. 99DK-0000092 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS

Lehmann M;

WPI; 2000-491161/43. N-PSDB; AAA73232. Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds -

Claim 1; Fig 5a-c; 240pp; English.

The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods of an beu used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, substrate binding, position specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it

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into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   300
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
   Gaps
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
  ;
0
   Length 467;
  Indels
   LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  99.2%; Score 2448; DB 21;
98.9%; Pred. No. 2.6e-235;
11ve 2; Mismatches 3;
  Best Local Similarity 98.9
Matches 462; Conservative
  467 AA;
                          invention.
   Sequence
  Query Match
  61
   61
  361
   421
  AAY69566
  SSSSXS
   δ
   g
  δ
  g
  ò
   q
   δ
  Оp
  QΫ
   qq
  ò
   Db
   δy
   qq
  δ
```

Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; phytase-10. Talaromyces thermophilus ATCC20186. Myceliophthora thermophila. Paxillus involutus NN005693. Aspergillus terreus 9A1.
Aspergillus terreus cbs16.46.
Aspergillus niger var. awamori.
Aspergillus miger str. NRR13135.
Aspergillus funigatus ATCC13073.
Aspergillus funigatus ATCC32722.
Aspergillus funigatus ATCC36128.
Aspergillus funigatus ATCC36128.
Aspergillus funigatus ATCC36128.
Emericella nidulans. Phytase-10, a consensus phytase. AAY69566 standard; protein; 467 Trametes pubescens NN9343.
Agrocybe pediades NN009289. 19-APR-2000 (first entry) AAY69566; A 

 241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

g

g

KYYGYGAGNPLGPAQGYGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

301

OY OY Db

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and pelleting. The present sequence represents a consensus sequence, designated phytase-10, which was derived from the mature phytase aguences from a variety of fungi (AANF0544, AANF0548, AANF05563 and AANF05564) and the Basidiomycetes phytase consensus AAXF05563 and additionally contains the Aspergillus terreus cbs116.46 signal peptide at
  feed composition for monogastric animals (e.g., pigs, poutry) and provides a monogastric animals (e.g., pigs, poutry) and provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphorus is present in animal feed in the form of phystate phosphorus, monogastric animals are unable to utilise this form of phosphorus, monogastric animals are unable phosphate to the feed of such animals. Phytase enhances the nutritional value of plant material without the need for adding additional phosphate to the feed. The level of phosphate pollution in the environment is reduced by adding phytase to animal feed, as the animal can make use of the incorpus of phosphate pollution in the animal can make use of the incorpus of phosphate formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage
   The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hexakisphosphate phosphohydrolase) and one or more stabilising agents including xylitol; polyethylene glycols with a molecular weight of 600 to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a
   1..20
/note= "Phytase signal peptide from Aspergillus terreus
cbs16.46"
   can withstand feed processing methods such as extrusion, expansion
  New stabilized enzyme formulation, useful for feed compositions for
  27..467
/note= "Mature phytase-10 consensus"
  (HOFF ) HOFFMANN LA ROCHE & CO AG 'F.
  Location/Qualifiers
   Example 4; Fig 17; 101pp; English.
   Brugger R, Lehmann M, Wyss M;
  99EP-0111949.
  98EP-0111960.
Peniophora lycii NN006113.
   Thermomyces lanuginosa.
   WPI; 2000-099429/09
   monogastric animals
  467 AA;
   N-PSDB; AAZ59642
  the N-terminus.
   23-JUN-1999-
   29-JUN-1998;
  05-JAN-2000.
  EP969089-A1
  Synthetic
   Sequence
  Peptide
   Protein
   and
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The present invention describes improved phytases, preferably with increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce
   phytases with improved properties such as temperature stability, ability and substrate specificity, for use in pharmaceuticals and
   Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
  Consensus phytase 3 thermo 11 Q50T K91A protein SEQ ID NO:93.
   Disclosure; Fig 23a-c; 240pp; English.
                               AAB20532 standard; Protein; 467 AA
  food; feed; phytate; manure.
   21-JAN-2000; 2000WO-DK00025
  99DK-0000092.
   pH stability and substrate compound foods and feeds -
   05-DEC-2000 (first entry)
   (NOVO ) NOVO NORDISK AS.
   WPI; 2000-491161/43.
N-PSDB; AAA73291.
  WO200043503-A1.
  22-JAN-1999;
  21-SEP-1999;
  27 - JUL- 2000.
  Lehmann M;
   Synthetic.
  AAB20532;
  Novel
ω
 RESULT
```

; 0

0; Gaps

Score 2448; DB 21; Length 467; pred. No. 2.6e-235; 2; Mismatches 3; Indels 0;

99.2%;

Best Local Similarity 98.9 Matches 462; Conservative

oy Oy

Query Match

61

g

1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60

```
;
0
   Phytase; animal feed preparation; thermostable phytase; transgenic plant;
pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present
   SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   180
   180
   240
  240
   300
   300
  360
  Gaps
  1 MGVFVVLLSIĄTLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  9
  YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA
  KLADPGANPHQASPYINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
  ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
  KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
   ;
  Length 467;
  Indels
   Consensus phytase-1-thermo(8)-Q50T-K91A protein sequence.
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   95.9%; Score 2367; DB 21;
llarity 95.7%; Pred. No. 3.1e-227;
Conservative 8; Mismatches 12;
   AAY43169 standard; Protein; 467 AA.
  98DK-0000806.
98DK-0001176.
99DK-0000091.
99DK-0000093.
  99WO-DK00154
   98DK-0000407
   06-JAN-2000 (fjrst entry)
  AA;
   Similarity
   consensus sequence.
   467
   WO9948380-A1
  19-JUN-1998;
18-SEP-1998;
22-JAN-1999;
22-JAN-1999;
   447;
   22-MAR-1999;
  23-MAR-1998;
  invention
   Synthetic
  Sequence
  AAY43169;
   Query Match
Best Local S
   Matches
   σ
  61
   61
  181
  121
   121
  241
   361
  241
  301
   AAY43169
   RESULT
 d
  δy
  g
   οy
   g
  δ
   QQ
   δ
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  ò
   g
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   Db
  Ω
   g
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This sequence represents the consensus phytase-1-thermo(8)-050T-K91A. The invention relates to a process for preparing animal feed by agglomerating feed ingredients with a thermostable phytase, which is added before or during agglomeration. The thermostable phytase is useful for expression in transgenic plants. These plants are useful in the preparation of animal feed itself. The thermostable phytase allows animal feed to be produced more efficiently, in addition to improved phytase-expressing transgenic plants. These plants provide a feed ingredient and a feed additive (phytase) simultaneously.
   Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate;
  240
  240
   300
  Gaps
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   9
  YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA
   KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
   ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
   KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
  HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP
  ;
0
   Length 467;
   Consensus phytase 1 thermo 8 q50t, k91a protein SEQ ID NO:29.
  Indels
   LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   Preparing animal feed using a thermostable phytase
  95.7%; Score 2362; DB 20; 95.5%; Pred. No. 9.7e-227;
  13;
  8; Mismatches
  AA
   Example 3; Fig 9; 71pp; English.
  AAB20526 standard; Protein; 467
   05-DEC-2000 (first entry)
   Best Local Similarity 95.5
Matches 446; Conservative
(NOVO ) NOVO-NORDISK
  WPI; 1999-591030/50.
  467 AA;
   N-PSDB; AAZ31520
                          ŝ
                          Petersen
  AAB20526;
  Sequence
  Query Match
   181
   181
   301
  61
   61
   121
   241
  301
  241
  361
   421
  AAB20526
  RESULT
δ
   g
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  δŏ
  Op
  δ
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   Qγ
  셤
  δλ
   a
  δy
  QQ
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specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
  food; feed; phytate; manure.
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Synthetic.

WO200043503-A1

27-JUL-2000.

21-JAN-2000; 2000WO-DK00025.

99DK-0000092 99DK-0001340. 22-JAN-1999; 21-SEP-1999;

(NOVO ) NOVO NORDISK AS.

Lehmann M;

WPI; 2000-491161/43.

N-PSDB; AAA73233

Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and compound foods and feeds

Claim 5; Fig 7a-c; 240pp; English.

increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate observage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate. The present sequence represents a phytase sequence from the present present invention describes improved phytases, preferably with 

467 AA; Sequence

; 0 121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120 Gaps 1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60 1 mgvfvvllsiatlfgstsgtalgprgnshscdtvdggyqcfpeishlwgtyspyfslade 60 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 0 Length 467; Indels Score 2362; DB 21; Pred. No. 9.7e-227; 8; Mismatches 13; 95.78; Matches 446; Conservative Query Match Best Local Similarity 61 61 241 181 301 g g q g ò q g ò ò ò

; 0

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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, pH stability, pH profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, pharmaceutical compositions or compound food or feeds run feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates and/or inositol and inorganic phosphate.
   Phytase; mutant; thermostability; mutation; mutagenesis; pH stability, temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
  vel phytases with improved properties such as temperature stability, stability and substrate specificity, for use in pharmaceuticals and
361 HDNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVVFFAARAYVEMMQCEAEKEP 420
                  0; Gaps
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  The present sequence represents a phytase sequence from the present
   The present invention describes improved phytases, preferably with
  Length 467;
   Indels
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  Consensus phytase 3 thermo 11 Q50T protein SEQ ID NO:91.
  Query Match 95.7%; Score 2362; DB 21; Best Local Similarity 95.5%; Pred. No. 9.7e-227; Matches 446; Conservative 8; Mismatches 13;
  Disclosure; Fig 22a-c; 240pp; English.
  A.
  AAB20531 standard; Protein; 467
   99DK-0000092.
99DK-0001340.
   food; feed; phytate; manure.
  21-JAN-2000; 2000WO-DK00025.
   05-DEC-2000 (first entry)
   compound foods and feeds
   (NOVO ) NOVO NORDISK AS.
  WPI; 2000-491161/43.
  467 AA;
  N-PSDB; AAA73290.
  WO200043503-A1.
   22-JAN-1999;
  21-SEP-1999;
   27-JUL-2000
  Synthetic.
  Lehmann M;
  invention.
   AAB20531;
  Sequence
   11
  Novel
   AAB20531
   RESULT
   δ
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  Q
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Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation; thermostable; animal feed; monogastric animal; phytate phosphorus; phosphate availibility; consensus; mutant; mutein.
  /note= "Phytase signal peptide from Aspergillus terreus
cbs16.46"
           181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
  KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG
  /note= "Mature phytase-1-thermo[8]-050T-K91A"
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  Mutant phytase-1, phytase-1-thermo[8]-Q50T-K91A.
  Location/Qualifiers
   AA.
  Talaromyces thermophilus ATCC20186. Mycellophthora thermophila.
   Aspergillus terreus cbs16,46.
Aspergillus niger var. awamori.
Aspergillus niger var. akspergillus niger str. NRRL3135.
Aspergillus fumigatus ATCC13073.
Aspergillus fumigatus ATCC3722.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC58128.
Aspergillus fumigatus ATCC58128.
   AAY69568 standard; protein; 467
   99EP-0111949
   98EP-0111960.
  19-APR-2000 (first entry)
  Aspergillus terreus 9A1
   Emericella nidulans.
  23-JUN-1999;
  29-JUN-1998;
  05-JAN-2000
   EP969089-A1
   Synthetic.
   Peptide
   Protein
                       61
  301
  AAY69568
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   δy
   g
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   δ
   qq
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The invention relates to a novel stabilised dry or liquid enzyme formulation, comprising phytase (myo-inositol hoxakisphosphate) to physphohydrolase) and one or more stabilising agents including to physphohydrolase) and one or more stabilising agents including to the phosphohydrolase) and one or more stabilising agents including to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic, of glutaric and succinic acid; carboxymethylcellulose; and sodium alginate. The stabilised phytase formulation is used in a method for preparing a provides a monogastric animal with its dietary requirements of phosphorus. Although a large amount of phosphate is present in animal teed in the form of phytate phosphorus, monogastric animals are unable to utilise this form of phytate phosphorus, monogastric animals are unable to the feed of such animals. Phytase enhances the nutritional phosphate to the feed of such animals. Phytase enhances the nutritional phosphate to the feed of such animals. Phytase enhances the nutritional content of phosphate liberated from phytate phosphorus using the reduced by adding phytase to animal feed, as the animal can make use of the inorganic phosphate liberated from phytate phosphorus using the enzyme. The phytase formulation of the invention has an improved thermostability and can therefore remain stable during long-term storage and can withstand feed processing methods such as extrusion, expansion and pelleting. The present sequence represents a mutant phytase-I consensus sequence, phytase-I-thermof81-050T-K91A, which has a that that that that the consensus sequence of phytase-I-thermof81-050T-K91A, which has a
  61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
   HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  Gaps
  9
  New stabilized enzyme formulation, useful for feed compositions for
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE
  ;
0
   95.7%; Score 2362; DB 21; Length 467; 95.5%; Pred. No. 9.7e-227; 1ve 8; Mismatches 13; Indels 0;
                   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
  Example 5; Fig 19; 101pp; English.
   Brugger R, Lehmann M, Wyss M;
  Best Local Similarity 95.5
Matches 446; Conservative
   2000-099429/09
   monogastric animals
  467 AA;
  N-PSDB; AAZ59715
  Sequence
   Query Match
  301
  301
   361
   361
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  Ωp
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   QQ
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increased thermostability, and methods for producing them. The methods can be used for producing phytases with improved properties e.g. temperature stability, ph stability, ph profile, temperature profile, specific activity, substrate specificity, substrate cleavage pattern, substrate binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate, and end level of released phosphate. The phytases can be used to produce pharmaceutical compositions or compound food or feeds. The feed can be used to reduce levels of phytate in animal manure, by converting it into lower inositol phosphates. The present sequence represents a phytase sequence from the present
   Novel phytases with improved properties such as temperature stability, pH stability and substrate specificity, for use in pharmaceuticals and
   Phytase; mutant; thermostability; mutation; mutagenesis; pH stability; temperature stability; pH profile; temperature profile; reaction rate; specific activity; substrate specificity; substrate cleavage pattern; substrate binding; position specificity; phytate degradation rate;
  present invention describes improved phytases, preferably with
              421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA
  Consensus phytase 10 (Fcp10) SEQ ID NO:24.
   Example 2; Fig 4a-d; 240pp; English.
   AAB20523 standard; Protein; 441 AA.
   food; feed; phytate; manure.
  21-JAN-2000; 2000WO-DK00025
   99DK-0000092
   99DK-0001340.
   (first entry)
   compound foods and feeds
   NOVO ) NOVO NORDISK AS.
  WPI; 2000-491161/43.
  441 AA;
   WO200043503-A1.
  22-JAN-1999;
   21-SEP-1999;
   05-DEC-2000
  27-JUL-2000.
  Lehmann M;
   Synthetic.
   invention
  Sequence
   AAB20523;
  RESULT 13
   δ
                                    D
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consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is useful for improving protein properties by altering their sequence. The consensus protein and mutein are useful in food, feed or pharmaceutical compositions. This sequence is a mutant phytase protein of the invention which does not appear in the specification but has been created from the protein represented in AAW93380.
  NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
   DIVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
   LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
  ESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
   Phytase; consensus; myo-inositol hexakisphosphate; hydrolysis; food; feed additive; variant; mutein; feed; pharmaceutical.
  This invention describes a novel process for the preparation of a
   Preparation of a consensus protein, especially a phytase - using programs to compare evolutionary similarity of sequences
   Fungal consensus phytase protein mutant Q50T.
  AA.
  AAW93382 standard; Protein; 467
  Claim 9; Page -; 30pp; English.
  (HOFF ) HOFFMANN LA ROCHE AG F.
   421 ddfveglsfarsggnweecfa 441
   447 DDFVEGLSFARSGGNWEECFA 467
  98EP-0113176.
   97EP-0112688
   (first entry)
  WPI; 1999-134647/12.
   24-JUL-1997;
  15-JUL-1998;
  24-FEB-1999-
   11-JUN-1999
  EP897985-A2
   Lehmann M;
  Fungi.
Synthetic.
  AAW93382;
  14
   387
  207
  181
   267
   327
   AAW93382
   g
  Qγ
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467 AA;

Sequence

PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146 

qq

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27 NSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86 

94.1%; Score 2322; DB 21; 98.9%; Pred. No. 8.6e-223; iive 2; Mismatches 3;

Best\_Local Similarity 98.9 Matches 436; Conservative

Query Match

; 0

0; Gaps

Length 441; Indels

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ö
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
   HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  0; Gaps
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
     Length 467;
                          Indels
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  93.8%; Score 2314; DB 20;
93.6%; Pred. No. 5.9e-222;
live 11; Mismatches 19;
                      437; Conservative
Query Match
Best Local Similarity
            Best Loca
Matches
   301
  361
   QQ
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  qq
  В
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   Qγ
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  δ
  g
   δ
   g
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consensus; myo-inositol hexakisphosphate; hydrolysis; food;
  Preparation of a consensus protein, especially a phytase - using programs to compare evolutionary similarity of sequences
   feed additive; variant; mutein; feed; pharmaceutical
  Fungal phytase protein consensus DNA.
                 AAW93380 standard; Protein; 467
  (HOFF ) HOFFMANN LA ROCHE AG
   97EP-0112688
  98EP-0113176
  11-JUN-1999 (first entry)
   WPI; 1999-134647/12.
  N-PSDB; AAX23022.
   24-JUL-1997;
  EP897985-A2.
   24-FEB-1999.
  15-JUL-1998;
   Lehmann M;
  Synthetic.
                                  AAW93380;
  Phytase;
  Fungi
       AAW93380
RESULT
```

Claim 8; Fig 2; 30pp; English.

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                           consensus protein. The specific example given in the specification is that of a fungal phytase (myo-inositol hexakisphosphate) which hydrolyses phytase to valuable feed additives, with a fully defined amino acid sequence given in the specification, or variant or mutein. The method is consensus protein and mutein properties by altering their sequence. The compositions. This sequence represents the consensus phytase protein in the method of the invention.
   61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
  360
  Gaps
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR
  301 KYYGYGAGNPLGPAQGYGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS
               invention describes a novel process for the preparation of a
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP
   ö
   Length 467;
   Indels
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   93.5%; Score 2308; DB 20;
93.4%; Pred. No. 2.3e-221;
live 11; Mismatches 20;
  Query Match 93.5%
Best Local Similarity 93.4%
Matches 436; Conservative
   467 AA;
   Sequence
  421
X 0 0 0 0 0 0 0 0 0 0 X 8
   δŏ
  g
   Op
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  a
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   ò
  qq
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Search completed: October 26, 2001, 16:40:05 Job time: 4956 sec

OM protein - protein search, using sw model

Run on:

(without alignments)
295.232 Million cell updates/sec October 26, 2001, 16:40:47; Search time 32.57 Seconds

US-09-488-265-31

Perfect score:

1 MGVEVVLLSIATLEGSTSGT.......DEVEGLSFARSGGNWEECFA 467 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 197339; seqs, 20590346 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/FCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMADIES

| IES       | Description   | -425-1 Sequence 1. April | -425-2 Sequence 2 | -724-8 Segment 2 | -8 Seguence 8 | -2 Segmence | 32 Seguence 32 | Sequence 20 | C endemos | -448-32 | -825-3 Secuence 3 | .642-3 Sections 3 | .855-3 Segmence 3 | .855-1 Sedilence 1 | -855-2 Sections 2 | .825-2 Sequence 2 | .642-2 Seguence 2 | .359-30 Sequence 30 | -359-22 Sedilence 22 | 4 Seguence 24 | -654-2 Sequence 2 | -358A-2 Seguence 2 | -359-28 Section 29 | .359-26 Sequence 26, | .539G-2 | 72 acree 2 acree 2 acree 2 acree 2 acree 2 | , sequence /, | 26.0    |
|-----------|---------------|--------------------------|-------------------|------------------|---------------|-------------|----------------|-------------|-----------|---------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|---------------------|----------------------|---------------|-------------------|--------------------|--------------------|----------------------|---------|--------------------------------------------|---------------|---------|
| SUMMARIES | ID            | US-09-121                | US-09-121         | US-07-923        | -08-60        |             | US-08-151      | -08         | US-08-693 | 4       | -08-8             | US-09-163         | -09-1             | -09-1              | -09-1             | à                 | -09-16            | -08-99              | -08-9                | US-08-993     | US-09-221         | US-08-989          | -08                | -08-993              | 77-627  | -07-627                                    | -07-923       | 609-80- |
|           | 90. ч         | 1 4                      |                   |                  |               |             |                |             |           | 2       |                   | 7                 | 4                 | *                  | 3 4               |                   |                   |                     |                      |               |                   |                    |                    |                      |         |                                            | ٠<br>-        |         |
|           | Length DB     | 441                      | 46                | 46               | 46            | 46.         | 46             | 46          | 46        | 46      | . 467             | 46                | 467               | 44                 | 44                | 47                | 47                | 44                  | 453                  | 439           | 439               | 439                | 442                | 442                  | 468     | 446                                        | 479           | 479     |
| dФ        | Query         | . 8                      | 87.9              | 75.0             | 75.0          | 5           |                | •           | •         | 74.9    | 74.9              | 74.9              | 74.6              | 72.9               | 72.7              | 56.0              | 26.0              | 34.3                | 33.8                 | 33.7          | 33.7              | 33.7               | 33.4               | 33.0                 | 14.5    | 14.4                                       | 14.4          | 14.4    |
|           | Score         | 2182                     | 2170              | 1852             | 1852          | 1852        | 1848           | 1848        | 1848      | 1848    | 1848              | 1848              | 1841              | 1799               | 1794              | 1381              | 1381              | 845.5               | 833.5                | 830.5         | 830.5             | 830.5              | 825                | 814                  | 359     | 354.5                                      | 354.5         | 354.5   |
|           | Result<br>No. | н.                       | 7                 | m                | 4             | 2           | φ              | 7           | 90        | o (     | 10                | 11                | 12                | 13                 | 14                | 15                | 16                | 17                  | 18                   | 19            | 20                | 21                 | 22                 | 23                   | 24      | 25                                         | 26            | 27      |



|   | Segmence 4 Appli | , 0              | 7               | Sequence // Appli | òα              | ò'n             | , 6               | Segmence 32; Appl | 0 0              | ץ<br>ע           | ۰, د            | . 0              | 0 0              | ,                | Sequence 2, Appli | , i              | 7                                        | Sequence 5, Appli | Sequence 1, Appli |  |
|---|------------------|------------------|-----------------|-------------------|-----------------|-----------------|-------------------|-------------------|------------------|------------------|-----------------|------------------|------------------|------------------|-------------------|------------------|------------------------------------------|-------------------|-------------------|--|
|   | US-08-374-652C-4 | US-08-993-359-32 | US-08-680-506-7 | US-08-241-853-8   | US-08-850-917-8 | US-08-680-506-3 | US-08-374-652C-32 | US-08-241-853-10  | US-08-850-917-10 | PCT-US93-09636-6 | US-08-758-213-1 | US-08-692-787-48 | US-09-002-100-48 | 118-09-146-283-2 | US-08-579-823A-2  | IIS-00-344-105-2 | 2 - CC - 3 - 4 - C - CC - CC - CC - CC - | 0-604-222-604-2   | US-09-171-878-1   |  |
|   | 2                | 3                | e<br>e          | 1                 | 2               | т<br>ж          | 7                 | 3                 | 3                | 2                | 1               | 2                | 4                | 7                | m                 | 7                | , ,                                      | n                 | 4                 |  |
|   | 479              | 6                | 44              | 11                | 11              | 318             | 77                | 113               | 113              | 23(              | 386             | 386              | 386              | 515              | 515               | 7                | 7257                                     | 7                 | 675               |  |
| , | 14.4             | 7.5              | 7.2             | 4.9               | 4.9             | 4.9             | 4.7               | 4.5               | 4.5              | 4.0              | 4.0             | 4.0              | 4.0              | 4.0              | 4.0               | 4.0              | 0.0                                      | ) (               | æ.<br>            |  |
|   | 354.5            | 185.5            | 177.5           | 122               | 122             | 120             | 115               | 111               | 111              | 66               | 66              | 66               | 66               | 66               | 66                | 66               | 7.5                                      |                   | 33.5              |  |
|   | 28               | 29               | 30              | 31                | 32              | 33              | 34                | 35                | 36               | 37               | 38              | 39               | 40               | 41               | 42                | 43               | 44                                       | • [               | 4 5               |  |

RESULT

|       |                 |                                     |                    |                      |                            |                                        |                                          |                                           |                                 |                                            | •                               |                          |                             |             |             |           |                               |          | Segmence                                                  |                             |                 |  |
|-------|-----------------|-------------------------------------|--------------------|----------------------|----------------------------|----------------------------------------|------------------------------------------|-------------------------------------------|---------------------------------|--------------------------------------------|---------------------------------|--------------------------|-----------------------------|-------------|-------------|-----------|-------------------------------|----------|-----------------------------------------------------------|-----------------------------|-----------------|--|
| 17007 | US-09-121-425-1 | Sequence 1, Application US/09121425 | Patent No. 6153418 | GENERAL INFORMATION: | APPLICANT: Lehmann, Martin | TITLE OF INVENTION: Consensus Phytases | FILE REFERENCE: consensus phytases 13239 | CURRENT APPLICATION NUMBER: US/09/121,425 | CURRENT FILING DATE: 1998-07-23 | EARLIER APPLICATION NUMBER: EPO 97112688.3 | EARLIER FILING DATE: 1997-07-24 | NUMBER OF SEQ ID NOS: 20 | SOFTWARE: PatentIn Ver. 2.0 | SEQ ID NO 1 | LENGTH: 441 | TYPE: PRT | ORGANISM: Artificial Sequence | FEATURE: | OTHER INFORMATION: Description of Artificial Sequencescon | OTHER INFORMATION: sequence | US-09-121-425-1 |  |
| •     | D               | ••                                  | ••                 | •-                   | •-                         | •-                                     | ••                                       | •-                                        | ••                              | •-                                         | ••                              | ٠.                       | •-                          | ••          | •-          | •-        | •-                            | ••       | ••                                                        | ••                          | Ď               |  |

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0; Gaps NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266 DIVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386 27 NSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86 Length 441; 20; Indels Query Match 88.4%; Score 2182; DB 4; Best Local Similarity 93.0%; Pred. No. 5.7e-217; Matches 410; Conservative 11; Mismatches 20; Query Match 207 181 267 241 327 δλ q δ qq δ g δλ οq δλ Q οy

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461 NWAECFA 467
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   2,
  281 FCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
  181 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGYGFANELIARLTRSPVQDHTSTNH 340
  341 TLDSNPATFPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYSASWT 400
   401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGG 460
  401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460
   YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
  101 YTLGADDLTPFGENQWVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160
  ...-----VIIPEGAGYNNTLDHGLCTAFEE 220
   221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 280
   ----TYN 100
  SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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85.4%; Pred. No. 1.1e-215;
Live 11; Mismatches 20; Indels 40; Gaps
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  1 MGVFVVLLSIATLEGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   OTHER INFORMATION: Description of Artificial Sequence:consensus OTHER INFORMATION: sequence
  APPLICAMT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
13239
FILE REPERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER PILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
   Sequence 2, Application US/09121425
Patent No. 6153418
   447 DDFVEGLSFARSGGNWEECFA 467
  ORGANISM: Artificial Sequence
  181 KLADPGANPHQASPVIN-----
  Best Local Similarity 85.4%
Matches 416; Conservative
  GENERAL INFORMATION:
  461 NWEECFA 467
   SEQ ID NO 2
LENGTH: 467
  US-09-121-425-2
  US-09-121-425-2
   Query Match
  TYPE: PRT
  FEATURE
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61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
  1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  75.0%; Score 1852; DB 1; Length 467; 74.3%; Pred. No. 7.9e-183;
  APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Turunen, Marja K.
APPLICANT: Pagerst m, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
  Indels
  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
   ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600 CITY: Washington
  42; Mismatches
  NAME: Cimbala, Michele A.
REGISTATION NUMBER: 33.851
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
   Nevalainen, Helena K.M.
Paloheimo, Marja T.
Miettinen-Oinonen, Arja S.K.
Torkkeli, Tuula K.
Cantrell, Michael
   FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION APPLICATION
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
  APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
  APPLICATION NUMBER: UK 8610600 FILING DATE: 30-APR-1986 ATTORNEY/AGENT INFORMATION:
            Sequence 8, Application US/07923724
Patent No. 5780292
   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
  TELEPHONE: (202) 371-2600 TELEFAX: (202) 371-2540 INFORMATION FOR SEO ID NO: 8: SEQUENCE CHARACTERISTICS:
   : 467 amino acids amino acid
   Query Match
Best Local Similarity 74.39
Matches 347; Conservative
  CURRENT APPLICATION DATA:
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  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
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   CLASSIFICATION:
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  TOPOLOGY:
  LENGTH:
   COUNTRY:
  APPLICANT:
  APPLICANT:
APPLICANT:
US-07-923-724-8
   APPLICANT:
  APPLICANT:
  STATE:
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121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
                      181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
   241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
   361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m. Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
   Sterne, Kessler, Goldstein & Fox
  STREET: 1100 New York Avenue, Suite 600
  Miettinen-Oinonen, Arja S.K.
   APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
   APPLICATION NUMBER: US/08/609,426A FILING DATE: 01-MAR-1996 CLASSIFICATION: 435
  APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
  US 07/496,155
  UMBER: US 07/044,077
29-APR-1987
   APPLICANT: Nevalainen, Helena K.M. APPLICANT: Paloheimo, Maria T.
  OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 8, Application US/08609426A Patent No. 5830733
   APPLICATION NUMBER: UK 8610600 FILING DATE: 30-APR-1986
   Paloheimo, Marja T.
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
   FILING DATE: 19-MAR-1990
  ATTORNEY/AGENT INFORMATION:
   PRIOR APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  PRIOR APPLICATION DATA:
   Reed, Grant E.
  APPLICATION NUMBER:
   Washington
  GENERAL INFORMATION:
  U.S.A.
   FILING DATE:
   20005
   ADDRESSEE:
  US-08-609-426A-8
  APPLICANT:
  COUNTRY:
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  APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: HOUSTON, CHRISTINE S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINATY CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
   61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEALQKNATAFKGKYAFLKTYN 120
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  .;
0
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  Query Match 75.0%; Score 1852; DB 2; Length 41 Best Local Similarity 74.3%; Pred. No. 7.9e-183; Matches 347; Conservative 42; Mismatches 78; Indels
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  S: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
  APPLICANT: NEVALAINEN, HELENA K.M.
APPLICANT: PALOHEIMO, MARJA T.
APPLICANT: FAGERSTROM, RICHARD B.
APPLICANT: MIETTINEN-OINONEN, ARJA S.
   Sequence 2, Application US/08374652C Patent No. 5834286
   TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acids
  APPLICANT: RAMBOSEK, JOHN A. APPLICANT: PIDDINGTON, CHRIS
   TURUNEN, MARJA K.
  TOPOLOGY: linear
MOLECULE TYPE: protein
  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
   STREET: 1100 NEW CITY: WASHINGTON
   GENERAL INFORMATION:
  ADDRESSEE:
  US-08-609-426A-8
   RESULT 5
US-08-374-652C-2
   APPLICANT:
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  241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300
  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
   HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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  61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKXAFLKTYN 120
   YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
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  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   SOFTWARE: PatentIn Release #1.0, Version #1.30
   1050.071001
  AREAL PRING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
TITING DATE: 31-JUL-1992
   CLASSIFICATION DATA:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
  APPLICATION NUMBER: US/08/374,652C FILING DATE: 24-MAY-1995 CLASSIFICATION: 435
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
  Floppy disk
   LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not releyant
   CURRENT APPLICATION DATA:
   ; TOPOLOGY: not releva:
; MOLECULE TYPE: protein
US-08-374-652C-2
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                  20002
                   COUNTRY:
   Query Match
STATE:
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  DB 1; Length 467;
   Query Match
74.9%; Score 1848; DB 1; Length 41
Best Local Similarity 74.3%; Pred. No. 2e-182;
Matches 347; Conservative 42; Mismatches 78; Indels
   APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Rillem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
NUMBER OF SEQUENCES: 52
  PatentIn Release #1.0, Version #1.25
   NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
  E: Morrison & Foerster
545 Middlefield Road, Suite 200
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,574
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  07/688,578
                                 Sequence 32, Application US/08151574 Patent No. 5436156
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
INFORMATION FOR SEQ ID NO: 32:
  FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
   : 467 amino acids amino acid
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  PRIOR APPLICATION DATA:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison
   COMPUTER READABLE FORM:
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  APPLICATION NUMBER:
   CITY: Menlo Park
STATE: California
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  ZIP: 94025-3471
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   FILING DATE:
  SOFTWARE:
  TOPOLOGY:
                    JS-08-151-574-32
  COUNTRY:
  LENGTH:
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Murashige, Kate H
   TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
  467 amino acids
   TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Diskette
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  MOLECULE TYPE: protein
FRAGMENT TYPE: internal
  single
  CORRESPONDENCE ADDRESS:
  REGISTRATION NUMBER:
   TYPE: amino acid
   STRANDEDNESS: Sil
   COUNTRY: USA
ZIP: 94304-1018
   CA
   TELEFAX:
   US-08-693-709-2
  LENGTH:
  g
   δλ
   δ
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  0
301 KYYGYGAGNPLGPAQGVĞFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
                        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
   61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
  Gaps
   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
   Sequence 20, Application US/08146424

Patent No. 5553963

GENERAL INFORMATION:
APPLICANT: VAN OOLJEN, ALBERT J. J.
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: FOR NOW, PETER C.
APPLICANT: SIJMONS, PETER C.
APPLICANT: YERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
UNMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
   Ouery Match 74.9%; Score 1848; DB 1; Length 467; Best Local Similarity 74.3%; Pred. No. 2e-182; Matches 347; Conservative 42; Mismatches 78; Indels (
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146 474
   44615-20011.24
   O2-NOV-1993
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
   ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
   REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: 44!
TELECOMMUNICATION: INFORMATION:
   TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
   TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
   467 amino acids
  KENNEDY, BILL
   MOLECULE TYPE: protein
  California
  ZIP: 94304-1018
   amino acid
  linear
  USA
   FILING DATE:
   US-08-146-424-20
   TOPOLOGY:
   US-08-146-424-20
  COUNTRY:
   LENGTH:
  CITY:
STATE:
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241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
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   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   Sequence 2, Application US/08693709
Patent No. 5770413
CENERAL INFORMATION:
APPLICANT: VAN OOIJEN, ALBERT J.J.
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: FEW, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: SIJMONS, PETER C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
NUMBER OF SEQUENCES: 28
   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,709
FLING DATE: 07-AUG-1996
CLASSIFICATION: 800
   24615-20011.10
  ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146,424
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
  29,959
   REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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   241 QRLENDLSGVTLFDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300
   301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
   61 SVISPEVPAGCRVTFAQVĻSRHGARYPTDSKGKKYSALIEEIQQNATTEDGKYAFLKTVN 120
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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  Query Match 74.9%; Score 1848; DB 1; Length 467; Best Local Similarity 74.3%; Pred. No. 2e-182; Marches 347; Conservative 42; Mismatches 78; Indels (
  421 LVRVLVNDRVVPLHGCPVDALGRCIRDSFVRGLSFARSGGDWAECFA 467
   Cloning and Expression of Microbial Phytase
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   3: Morrison & Foerster
2000 pennsylvania Ave. N.W., Suite 5500
  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
   APPLICATION NUMBER: US/08/419,448
  APPLICANT: Robert F.M. Van Gorcom APPLICANT: Willem Van Hartingsveldt
  APPLICANT: Perrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and E
  Sequence 32, Application US/08419448 Patent No. 5863533 GENERAL INFORMATION:
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
NAME/KET: Signal Sequence
LOCATION: 1...23 '
OTHER INFORMATION: 1
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  Matches 347; Conservative
   CURRENT APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES:
   Washington
   RY: USA
20006-1888
   ADDRESSEE:
  SOFTWARE:
SOFTWARE:
   US-08-419-448-32
   COUNTRY:
   STREET:
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  E: No. 58661180 No. 5866118disk of No. 5866118th America, Inc. 405 Lexington Avenue, Suite 6400
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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  361 HDNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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   1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
  0; Gaps
   APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
   74.9%; Score 1848; DB 2; Length 4 74.3%; Pred. No. 2e-182; Live 42; Mismatches 78; Indels
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
   24615-20026.10
   Sequence 3, Application US/08819825 Patent No. 5866118
                CLASSIFICATION: 435
ATJORNEY/AGENT INFORMATION:
NAME: MATSHIGE, Rate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
10-APR-1995
   LENGIH: 467 amino acids
  Best Local Similarity 74.39
Matches 347; Conservative
  ZIP: 10174-6401
COMPUTER READABLE FORM:
  MOLECULE TYPE: protein
   CORRESPONDENCE ADDRESS:
   amino acid
   linear
   GENERAL INFORMATION:
  New York
  New York
 FILING DATE:
   ADDRESSEE:
   COUNTRY:
  US-08-419-448-32
   TOPOLOGY:
  US-08-819-825-3
  STREET:
  STATE:
   Query Match
   RESULT 10
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
  TELBFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
   COMPUTER: IBM Compatible
  FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
   467 amino acids
   SEQUENCE CHARACTERISTICS:
  MEDIUM TYPE: Diskette
  STRANDEDNESS: single
TOPOLOGY: linear
  COMPUTER READABLE FORM:
   OPERATING SYSTEM:
   amino acid
   New York
   COUNTRY: U.S.A. ZIP: 10174-6401
  New York
   CLASSIFICATION:
  FILING DATE:
           ADDRESSEE:
  US-09-163-642-3
  LENGTH:
  US-09-155-855-3
  RESULT
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   SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
   121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
   181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
  241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
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   361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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   Query Match 74.9%; Score 1848; DB 2; Length 467; Best Local Similarity 74.3%; Pred. No. 2e-182; Matches 347; Conservative 42; Mismatches 78; Indels (
   APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Rlotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
   REFERENCE/DOCKET NUMBER: 4758.200-US TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
  ; Sequence 3, Application US/09163642; Patent No. 6221644
  33,728
  TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
   ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,7
   LENGTH: 467 amino acids
   SEQUENCE CHARACTERISTICS:
   Diskette
  STRANDEDNESS: single
   amino acid
  ; TOPOLOGY: linear
US-08-819-825-3
   GENERAL INFORMATION:
MEDIUM TYPE:
   US-09-163-642-3
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No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
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  181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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  301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
  361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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  Length 467;
  Query Match 74.9%; Score 1848; DB 4; Length 4 Best Local Similarity 74.3%; Pred. No. 2e-182; Matches 347; Conservative 42; Mismatches 78; Indels
  421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
                       405 Lexington Avenue, Suite 6400
  NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
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Matches
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   YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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  .;
0
   TITLE OF, INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
   APPLICANT: ANAZAWA, Hidharu
APPLICANT: ANAZAWA, Fidharu
APPLICANT: NAGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 81356/124
CURRENT APPLICATION NUMBER: U5/09/155,855
   Length 467;
   421 LVRVLVNDRVVPLHGCPVDALGRCIRDSFVKGLSFARSGGDWGECFA 467
  Indels
   421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
  74.6%; Score 1841; DB 4;
73.2%; Pred. No. 1.1e-181;
tive 49; Mismatches 76;
  CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION UNMARER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER PULICATION NUMBER: JP 084314
EARLIER FILING DATE: 1996-04-05
SOFTWARE: PELLO DAIS: 7
SOFTWARE: PATENTIN VET: 2.0
  49; Mismatches
  Sequence 1, Application US/09155855 Patent No. 6139902
Sequence 3, Application US/09155855 Patent No. 6139902
   APPLICANT: ANAZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
PPLLICANT: NAGASHIMA, Tadashi
APPLICANT: TANGE, Tatsuya
   ; ORGANISM: Aspergillus niger US-09-155-855-3
  Conservative
  APPLICANT: KONDO, Hidemasa
  APPLICANT: KONDO, Hidemasa
   Query Match
Best Local Similarity
Matches 342; Conserva
                                  GENERAL INFORMATION:
  GENERAL INFORMATION:
   RESULT 13
US-09-155-855-1
   467
  TYPE: PRT
  SEO ID NO 3
  121
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387 ESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
   DIVARISDAIQLSPFCDLFIHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
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  147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
  Gaps
  27 NSHSCDIVDGGYQCFPEISHLWGIYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86
   APPLICANT: ANAZAWA, Hideharu
APPLICANT: KANEKO, Syunichi
APPLICANT: NAGASHIWA, Tadashi
APPLICANT: TANGE, Tatsuya
TITLE OF INVERTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REPERENCE: 81356/124
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   Length 443;
  Indels
   72.9%; Score 1799; DB 4;
74.8%; Pred. No. 2.2e-177;
tive 47; Mismatches 64;
   CURRENT PELLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1966-04-05
SARLIER FILING DATE: 1966-04-05
SOFTWBER OF SEQ ID NOS: 7
SOFTWBER OF SEQ ID NOS: 7
         CURRENT APPLICATION NUMBER: US/09/155,855
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: WO PCT/JP97/01175
EARLIER FILING DATE: 1997-04-04
EARLIER FILING DATE: 1996-04-05
EARLIER FILING DATE: 1996-04-05
NUMBER OF SEO ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
  Sequence 2, Application US/09155855 Patent No. 6139902
  447 DDFVEGLSFARSGGNWEECFA 467
   ; ORGANISM: Aspergillus niger
US-09-155-855-1
  Conservative
  GENERAL INFORMATION:
APPLICANT: KONDO, Hidemasa
FILE REFERENCE: 81356/124
  Local Similarity
nes 330; Conserv
  RESULT 14
US-09-155-855-2
  443
   TYPE: PRT
   Query Match
  SEQ ID NO 1
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   267
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Search completed: October 26, 2001, 16:40:47
Job time: 4958 sec
  ö
  ; OTHER INFORMATION: Xaa at positions 2 & 3 may be any amino acid or unknown US-09-155-855-2
  NUMBER OF SEQUENCES: '5.
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
  90 SASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRYKA 149
  150 LARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYNNT 209
  210 LDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTV 269
  246 STSTVDTKLSPFCDLFTHEEWINYDYLQSLNKYYGHGAGNPLGPTQGVGYANELIARLTH 305
  Gaps
   SPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESI 389
   30 SCDIVDGGYQCFPEISHLMGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYPTS 89
   270 ARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTH
  390 EETDGYSASWTVPFAARAYVEMMOCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDF
  .<u>`</u>
   72.7%; Score 1794; DB 4; Length 443; 75.1%; Pred. No. 7.2e-177; tive 47; Mismatches 62; Indels
   APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION POLYPEPTIGES Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
  SYSTEM: DOS
FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
  Sequence 2, Application US/08819825
Patent No. 5866118
  426 VKGLSFARSGGDWGECFA-443
   450 VEGLSFARSGGNWEECFA, 467
  IBM Compatible
                                TYPE: PRT
ORGANISM: Aspergillus niger
   Matches 329; Conservative
   ZIP: 10174-6401.
COMPUTER REDABLE FORM:
MEDIUM TYPE: Dieber
  Diskette
   Query Match
Best Local Similarity
  OPERATING SYSTEM:
  GENERAL INFORMATION:
   CITY: New York
STATE: New York
  SOFTWARE:
   US-08-819-825-2
SEQ ID NO 2
  FEATURE:
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178 QSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVE-ANFTAVFA 236
   58 ADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK 117
   TYNYTLGADDLIPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGF 177
   237 PPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDAT----QLSPFCDLFTHDEWIQ 292
   EMMQC------EAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSG 459
   352 NATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE--SIEETDGYSASWTVPFAARAYV 409
   293 YDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLT-HSPVQDHTSTNHTLDSNPATFPL 351
   1 MGVF-VVLLSIATLFGSTSGTALGP--RGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSL 57
   38;
   Length 475;
  Indels
  61; Mismatches 107;
   56.0%; Score 1381; DB 2; 57.7%; Pred. No. 3.8e-134;
            NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPFAX: 212 867 0298
ATTORNEY/AGENT INFORMATION:
  LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS: single
  SEQUENCE CHARACTERISTICS:
   INFORMATION FOR SEQ ID NO:
   Best Local Similarity 57.7
Matches 281; Conservative
   ; TOPOLOGY: linear
MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-819-825-2
   460 GNWEECF 466
  469 GHWDRCF 475
   Query Match
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